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PATENT APPLICATION

NOVEL METHODS OF DIAGNOSIS OF METASTATIC COLORECTAL CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC COLORECTAL CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

The present application is related to USSN 60/272,206, filed February 27, 2001, USSN 60/281,149, filed April 2, 2001, and USSN 60/284,555, filed April 17, 2001, all of which are herein incorporated by referenced in their entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in metastatic colorectal cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of metastatic colorectal cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit metastatic colorectal cancer.

BACKGROUND OF THE INVENTION

Cancer of the colon and/or rectum (referred to as "colorectal cancer") are significant in Western populations and particularly in the United States. Cancers of the colon and rectum occur in both men and women most commonly after the age of 50. These develop as the result of a pathologic transformation of normal colon epithelium to an invasive cancer. There have been a number of recently characterized genetic alterations that have been implicated in colorectal cancer, including mutations in two classes of genes, tumor-suppressor genes and proto-oncogenes, with recent work suggesting that mutations in DNA repair genes may also be involved in tumorigenesis. For example, inactivating mutations of both alleles of the adenomatous polyposis coli (APC) gene, a tumor suppressor gene, appears to be one of the earliest events in colorectal cancer, and may even be the initiating event. Other genes implicated in colorectal cancer include the MCC gene, the p53 gene, the DCC (deleted in colorectal carcinoma) gene and other chromosome 18q genes, and genes in the TGF-β signaling pathway. For a review, see *Molecular Biology of Colorectal Cancer*, pp. 238-299, in *Curr. Probl. Cancer*, Sept/Oct 1997; see also Willams, *Colorectal Cancer*

(1996); Kinsella & Schofield, *Colorectal Cancer: A Scientific Perspective* (1993); *Colorectal Cancer: Molecular Mechanisms, Premalignant State and its Prevention* (Schmiegel & Scholmerich eds., 2000); *Colorectal Cancer: New Aspects of Molecular Biology and Their Clinical Applications* (Hanski *et al.*, eds 2000); McArdle *et al., Colorectal Cancer* (2000); Wanebo, *Colorectal Cancer* (1993); Levin, *The American Cancer Society: Colorectal Cancer* (1999); *Treatment of Hepatic Metastases of Colorectal Cancer* (Nordlinger & Jaeck eds., 1993); *Management of Colorectal Cancer* (Dunitz *et al.*, eds. 1998); *Cancer: Principles and Practice of Oncology* (Devita *et al.*, eds. 2001); *Surgical Oncology: Contemporary Principles and Practice* (Kirby *et al.*, eds. 2001); Offit, *Clinical Cancer Genetics: Risk Counseling and Management* (1997); *Radioimmunotherapy of Cancer* (Abrams & Fritzberg eds. 2000); Fleming, *AJCC Cancer Staging Handbook* (1998); *Textbook of Radiation Oncology* (Leibel & Phillips eds. 2000); and *Clinical Oncology* (Abeloff *et al.*, eds. 2000).

Imaging of colorectal cancer for diagnosis has been problematic and limited. In addition, metastasis of the tumor to the lumen, and metastasis of tumor cells to regional lymph nodes are important prognostic factors (*see, e.g., PET in Oncology: Basics and Clinical Application* (Ruhlmann *et al.* eds. 1999). For example, five year survival rates drop from 80 percent in patients with no lymph node metastases to 45 to 50 percent in those patients who do have lymph node metastases. A recent report showed that micrometastases can be detected from lymph nodes using reverse transcriptase-PCR methods based on the presence of mRNA for carcinoembryonic antigen, which has previously been shown to be present in the vast majority of colorectal cancers but not in normal tissues. Liefers *et al.*, *New England J. of Med.* 339(4):223 (1998). In addition, colorectal cancers often metastasize to the liver. However, the lack of information about the gene expression exhibited by these cancers limits the ability to effectively diagnose and treat the disease.

Thus, methods for diagnosis and prognosis of metastatic colorectal cancer and effective treatment of colorectal cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of metastatic colorectal cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, colorectal cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in metastatic colorectal disease and other metastatic cancers.

SUMMARY OF THE INVENTION

The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in metastatic colorectal cancer cells. Such genes and the proteins they

encode are useful for diagnostic and prognostic purposes, and also as targets for screening for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include, early detection of colon cancers, monitoring and early detection of relapse following treatment of colon cancers, monitoring response to therapy of colon cancers, determining prognosis of colon cancers, directing therapy of colon cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous colon adenomas. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1-26. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1-26.

In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

In one embodiment, the polynucleotide is immobilized on a solid surface.

In one embodiment, the patient is undergoing a therapeutic regimen to treat metastatic colorectal cancer. In another embodiment, the patient is suspected of having metastatic colorectal cancer.

In one embodiment, the patient is a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides methods of detecting polypeptide encoded by a metastatic colorectal cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with an antibody that specifically binds a polypeptide encoded by a sequence at least 80% identical to a sequence as shown in Tables 1-26.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26., thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated transcript to a level of the metastatic colorectal cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, wherein the polypeptide specifically binds to the metastatic colorectal cancer-associated antibody, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated antibody to a level of the metastatic colorectal cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of metastatic colorectal cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a metastatic colorectal cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the metastatic colorectal cancer-associated polypeptide to a level of the metastatic

colorectal cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-26.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-26.

In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a metastatic colorectal cancer cell in a biological sample from a patient, the method comprising contacting the biological sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to metastatic colorectal cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1-26.

In another aspect, the present invention provides a method for identifying a compound that modulates a metastatic colorectal cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a metastatic colorectal cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a metastatic colorectal cancer-associated cell to treat colorectal cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having colorectal cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-26. in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of colorectal cancer.

In one embodiment, the control is a mammal with colorectal cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

In another aspect, the present invention provides a method for treating a mammal having colorectal cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having colorectal cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of colon and/or rectal cancer (*e.g.*, colorectal cancer), including metastatic colorectal cancers, as well as methods for screening for compositions which modulate colorectal cancer. By "metastatic colorectal cancer" herein is meant a colon and/or rectal tumor or cancer that is classified as Dukes stage C or D (*see, e.g.*, Cohen *et al., Cancer of the Colon*, in *Cancer: Principles and Practice of Oncology*, pp. 1144-1197 (Devita *et al.*, eds., 5th ed. 1997); see also *Harrison's Principles of Internal Medicine*, pp. 1289-129 (Wilson *et al.*, eds., 12th ed., 1991). "Treatment, monitoring, detection or modulation of metastatic colorectal cancer" includes treatment, monitoring, detection, or modulation of metastatic colorectal disease in those patients who have metastatic colorectal

disease (Dukes stage C or D). In Dukes stage A, the tumor has penetrated into, but not through, the bowel wall. In Dukes stage B, the tumor has penetrated through the bowel wall but there is not yet any lymph involvement. In Dukes stage C, the cancer involves regional lymph nodes. In Dukes stage D, there is distant metastasis, e.g., liver, lung, etc.

Tables 1-26 provide UniGene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in metastasizing colorectal cancer samples. Tables 1-26 also provide an exemplar accession number that provides a nucleotide sequence that is part of the UniGene cluster. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic colorectal cancer vs. known primary tumor samples from Dukes B stage survivors. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio provided represents primary tumor samples from known Dukes B stage survivors vs. liver metastasis samples from patients with metastatic colorectal cancer. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less. Survivors are subjects who have been disease free for five years or longer.

In Tables 1-26, the ratio provided represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are overexpressed in the metastatic samples, as the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. In Tables 1-26, the ratio represents liver metastasis samples from patients with known metastatic disease vs. tissue samples from normal colon tissue. In these samples, the identified genes are underexpressed in the metastatic samples, as the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

One of skill will recognize that although the sequences identified in Tables 1-26 exhibited increased or decreased expression in metastasizing colorectal cancer samples, the sequences of the invention, and their encoded proteins, can be used to diagnose, treat or prevent cancers in patients with Dukes stage A or B colorectal cancers. Alteration of gene

expression for a gene in Tables 1-26 may be more likely or less likely to indicate that the subject will progress to metastatic disease. The sequences can also be used to diagnose, treat or prevent precancerous or benign conditions such as precancerous colon adenomas. Alteration of gene expression for a gene in Tables 1-26 may or may not indicate that the subject is more likely to progress to cancer or to metastatic disease. Thus, although the specification focuses primarily on metastasizing colorectal cancer, the methods described below can also be applied to non- metastasizing colorectal cancers (*e.g.*, Dukes stages A and B) and precancerous or benign conditions (*e.g.*, precancerous adenomas) as well.

Definitions

The term "metastatic colorectal cancer protein" or "metastatic colorectal cancer polynucleotide" or "metastatic colorectal cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-26 and conservatively modified variants thereof or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a UniGene cluster of Tables 1-26. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "metastatic colorectal cancer polypeptide" and a "metastatic colorectal cancer polynucleotide," include both naturally occurring or recombinant.

A "full length" metastatic colorectal cancer protein or nucleic acid refers to a metastatic colorectal cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type metastatic colorectal cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a metastatic colorectal cancer protein, polynucleotide or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (*see, e.g.,* NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions

and/or additions, as well as those that have substitutions, as well as naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short

words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (*see, e.g.,* Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules

or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (*see, e.g.,* the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogenous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine,

norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are typically conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g.,* Creighton, *Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g.,* Alberts *et al.*, *Molecular Biology of the Cell* (3rd ed., 1994) and Cantor & Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β-sheet and α-helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, *Carbohydrate Modifications in Antisense Research*, Sanghui &

Cook, eds.. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g. to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g. the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins

or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g.,

recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence,

wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification,

although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, *et al.*

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a metastatic colorectal cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the metastatic colorectal cancer protein or nucleic acid, e.g., an enzymatic, functional, physical, or chemical effect, such as the ability to decrease metastatic colorectal cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a metastatic colorectal cancer protein sequence, e.g., functional, enzymatic, physical and

chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the metastatic colorectal cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on metastatic colorectal cancer can also be performed using metastatic colorectal cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of metastatic colorectal cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for metastatic colorectal cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of metastatic colorectal cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using *in vitro* and *in vivo* assays of metastatic colorectal cancer polynucleotide and polypeptide sequences of the invention. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of metastatic colorectal cancer proteins of the invention, e.g., antagonists. Antisense nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate metastatic colorectal cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of metastatic colorectal cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the metastatic colorectal cancer protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then

determining the functional effects on activity, as described above. Activators and inhibitors of metastatic colorectal cancer can also be identified by incubating metastatic colorectal cancer cells with the test compound and determining increases or decreases in the expression of 1 or more metastatic colorectal cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more metastatic colorectal cancer proteins, such as colorectal cancer proteins encoded by the sequences set out in Tables 1-26.

Samples or assays comprising metastatic colorectal cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a metastatic colorectal cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. *See, e.g.,* Freshney, *Culture of Animal Cells a Manual of Basic Technique* pp. 231-241 (3rd ed. 1994).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (*see*, Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed. 1994)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen.

The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, *Fundamental Immunology*.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab')_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab')_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab')'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (*see Fundamental Immunology* (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (*see, e.g.,* McCafferty *et al.*, *Nature* 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (*see, e.g.,* Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4:72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy* (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce

antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g.,* McCafferty *et al.*, *Nature* 348:552-554 (1990); Marks *et al.*, *Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

Identification of metastatic colorectal cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different metastatic colorectal cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in metastatic colorectal cancer versus non-metastatic colorectal cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate metastatic colorectal cancer, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of metastatic colorectal cancer in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a

particular expression profile; e.g., screening can be done for drugs that suppress the metastatic colorectal cancer expression profile. This may be done by making biochips comprising sets of the important metastatic colorectal cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the metastatic colorectal cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the metastatic colorectal cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the metastatic colorectal cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in metastatic colorectal cancer, herein termed "metastatic colorectal cancer sequences." As outlined below, metastatic colorectal cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in metastatic colorectal cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the metastatic colorectal cancer sequences are from humans; however, as will be appreciated by those in the art, metastatic colorectal cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other metastatic colorectal cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Metastatic colorectal cancer sequences from other organisms may be obtained using the techniques outlined below.

Metastatic colorectal cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, metastatic colorectal cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the metastatic colorectal cancer sequences can be generated.

A metastatic colorectal cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid

or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying metastatic colorectal cancer-associated sequences, the metastatic colorectal cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue, or tumor tissue samples from patients who have been diagnosed with Dukes stage A or B cancer but have survived vs. metastatic tissue. Other suitable tissue comparisons include comparing metastatic colorectal cancer samples with metastatic cancer samples from other cancers, such as lung, breast, other gastrointestinal cancers, prostate, ovarian, etc. Samples of, e.g., Dukes stage B survivor tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal colon, but also including, and not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the metastatic colorectal cancer screen that are expressed in significant amounts in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, metastatic colorectal cancer sequences are those that are up-regulated in metastatic colorectal cancer; that is, the expression of these genes is higher in the metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (*see, e.g.,* Tables 1-26). "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. All UniGene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, *see, e.g.,* Benson, DA, *et al.*, Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, metastatic colorectal cancer sequences are those that are down-regulated in the metastatic colorectal cancer; that is, the expression of these genes is lower in metastatic tissue as compared to non-metastatic cancerous tissue or normal colon tissue (*see, e.g.,* Tables 1-26). "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

Informatics

The ability to identify genes that are over or under expressed in metastatic colorectal cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with metastatic colorectal cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see* Anderson, *Pharmaceutical Proteomics: Targets, Mechanism, and Function*, paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see* U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing metastatic colorectal cancer, i.e., the identification of metastatic colorectal cancer-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount *et al., Bioinformatics* (2001); *Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids* (Durbin *et al.*, eds., 1999); *Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins* (Baxevanis & Oeullette eds., 1998)); Rashidi & Buehler, *Bioinformatics: Basic Applications in Biological*

Science and Medicine (1999); *Introduction to Computational Molecular Biology* (Setubal *et al.*, eds 1997); *Bioinformatics: Methods and Protocols* (Misener & Krawetz, eds, 2000); *Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach* (Higgins & Taylor, eds., 2000); Brown, *Bioinformatics: A Biologist's Guide to Biocomputing and the Internet* (2001); Han & Kamber, *Data Mining: Concepts and Techniques* (2000); and Waterman, *Introduction to Computational Biology: Maps, Sequences, and Genomes* (1995).

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for metastatic colorectal cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The

comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example,

a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of metastatic colorectal cancer-associated proteins

Metastatic colorectal cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the metastatic colorectal cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus and/or in the organelles. Proteins containing one or more transmembrane domains that exclusively reside in organelles are also considered intracellular proteins. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (*see, e.g., Molecular Biology of the Cell* (Alberts, ed., 3rd ed., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein

interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (*see, e.g.*, Bateman *et al., Nuc. Acids Res.* 28:263-266 (2000); Sonnhammer *et al., Proteins* 28:405-420 (1997); Bateman *et al., Nuc. Acids Res.* 27:260-262 (1999); and Sonnhammer *et al., Nuc. Acids Res.* 26:320-322-(1998)).

In another embodiment, the metastatic colorectal cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive

hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (*see, e.g.* PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Metastatic colorectal cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ* or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the metastatic colorectal cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they often serve to transmit signals to various other cell types. The secreted protein may

function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Metastatic colorectal cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests.

Use of metastatic colorectal cancer nucleic acids

As described above, metastatic colorectal cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the metastatic colorectal cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The metastatic colorectal cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-26, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the metastatic colorectal cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/unigene/).

Once the metastatic colorectal cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire metastatic colorectal cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant metastatic colorectal cancer nucleic acid can be further-used as a probe to identify and isolate other metastatic colorectal cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant metastatic colorectal cancer nucleic acids and proteins.

The metastatic colorectal cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the metastatic colorectal

cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense applications. Alternatively, the metastatic colorectal cancer nucleic acids that include coding regions of metastatic colorectal cancer proteins can be put into expression vectors for the expression of metastatic colorectal cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to metastatic colorectal cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the metastatic colorectal cancer nucleic acids, i.e. the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical

equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize

sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (*see* 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of metastatic colorectal cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a metastatic colorectal cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of metastatic colorectal

cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis *et al.*, *PCR Protocols, A Guide to Methods and Applications* (1990).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (*see, e.g.*, literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see* Wu & Wallace, *Genomics* 4:560 (1989), Landegren *et al., Science* 241:1077 (1988), and Barringer *et al.*, *Gene* 89:117 (1990)), transcription amplification (Kwoh *et al., Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), self-sustained sequence replication (Guatelli *et al., Proc. Nat. Acad. Sci. USA* 87:1874 (1990)), dot PCR, and linker adapter PCR, etc.

Expression of metastatic colorectal cancer proteins from nucleic acids

In a preferred embodiment, metastatic colorectal cancer nucleic acids, e.g., encoding metastatic colorectal cancer proteins, are used to make a variety of expression vectors to express metastatic colorectal cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see, e.g.,* Ausubel, *supra*, and *Gene Expression Systems* (Fernandez & Hoeffler, eds, 1999)) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the metastatic colorectal cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the metastatic colorectal cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The metastatic colorectal cancer proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a metastatic colorectal cancer protein, under the appropriate conditions to induce or cause expression of the metastatic colorectal cancer protein. Conditions appropriate for metastatic colorectal cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli, Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the metastatic colorectal cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (*see, e.g.,* Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation,

polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, metastatic colorectal cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the metastatic colorectal cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis, E. coli, Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, metastatic colorectal cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, metastatic colorectal cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae, Candida albicans* and *C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis* and *K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The metastatic colorectal cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies,

if the desired epitope is small, the metastatic colorectal cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the metastatic colorectal cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the metastatic colorectal cancer protein is a metastatic colorectal cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the metastatic colorectal cancer protein is purified or isolated after expression. Metastatic colorectal cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the metastatic colorectal cancer protein may be purified using a standard anti-metastatic colorectal cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes, *Protein Purification* (1982). The degree of purification necessary will vary depending on the use of the metastatic colorectal cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the metastatic colorectal cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of metastatic colorectal cancer proteins

In one embodiment, the metastatic colorectal cancer proteins are derivative or variant metastatic colorectal cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative metastatic colorectal cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the metastatic colorectal cancer peptide.

Also included within one embodiment of metastatic colorectal cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the metastatic colorectal cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell

culture as outlined above. However, variant metastatic colorectal cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the metastatic colorectal cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed metastatic colorectal cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of metastatic colorectal cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a metastatic colorectal cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the metastatic colorectal cancer proteins as needed. Alternatively, the variant may be designed or reorganized such that the biological activity of the metastatic colorectal cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of metastatic colorectal cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a metastatic colorectal cancer polypeptide with an

organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a metastatic colorectal cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking metastatic colorectal cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-metastatic colorectal cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the γ-amino groups of lysine, arginine, and histidine side chains (Creighton, *Proteins: Structure and Molecular Properties*, pp. 79-86 (1983)), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the metastatic colorectal cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence metastatic colorectal cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express metastatic colorectal cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to metastatic colorectal cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence metastatic colorectal cancer polypeptide (for O-linked glycosylation sites). The metastatic colorectal cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the metastatic colorectal cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the metastatic colorectal cancer polypeptide is by chemical or enzymatic coupling of glycosides

to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin & Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

Removal of carbohydrate moieties present on the metastatic colorectal cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, *et al.*, *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge *et al.*, *Anal. Biochem.*, 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura *et al.*, *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of metastatic colorectal cancer comprises linking the metastatic colorectal cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Metastatic colorectal cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a metastatic colorectal cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a metastatic colorectal cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the metastatic colorectal cancer polypeptide. The presence of such epitope-tagged forms of a metastatic colorectal cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the metastatic colorectal cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a metastatic colorectal cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field *et al.*, *Mol. Cell. Biol.* 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto (Evan *et al.*, *Molecular and Cellular Biology* 5:3610-3616 (1985));

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (*Paborsky et al., Protein Engineering* 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (*Hopp et al., BioTechnology* 6:1204-1210 (1988)); the KT3 epitope peptide (Martin *et al., Science* 255:192-194 (1992)); tubulin epitope peptide (Skinner *et al., J. Biol. Chem.* 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth *et al., Proc. Natl. Acad. Sci. USA* 87:6393-6397 (1990)).

Also included are other metastatic colorectal cancer proteins of the metastatic colorectal cancer family, and metastatic colorectal cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related metastatic colorectal cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the metastatic colorectal cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to metastatic colorectal cancer proteins

In a preferred embodiment, when a metastatic colorectal cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the metastatic colorectal cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller metastatic colorectal cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-26 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler & Milstein, *Nature* 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-26, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, pp. 59-103 (1986)). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of Tables 1-26 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to metastatic colorectal cancer protein are capable of reducing or eliminating a biological function of a metastatic colorectal cancer protein, as is described below. That is, the addition of anti-metastatic colorectal cancer protein antibodies (either polyclonal or preferably monoclonal) to metastatic colorectal cancer tissue (or cells containing metastatic colorectal cancer) may reduce or eliminate the metastatic colorectal cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the metastatic colorectal cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)). Humanization can be essentially performed following the method of Winter and co-workers (Jones *et al.*, *Nature* 321:522-525 (1986); Riechmann *et al.*, *Nature* 332:323-327 (1988); Verhoeyen *et al.*, *Science* 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom & Winter, *J. Mol. Biol.* 227:381 (1991); Marks *et al.*, *J. Mol. Biol.* 222:581 (1991)). The techniques of Cole *et al.* and Boerner *et al.* are also available for the preparation of human monoclonal antibodies (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy,* p. 77 (1985) and Boerner *et al.*, *J. Immunol.* 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in virtually all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10:779-783 (1992); Lonberg *et al.*, *Nature* 368:856-859 (1994); Morrison, *Nature* 368:812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14:845-51 (1996); Neuberger, *Nature Biotechnology* 14:826 (1996); Lonberg & Huszar, *Intern. Rev. Immunol.* 13:65-93 (1995).

By immunotherapy is meant treatment of metastatic colorectal cancer with an antibody raised against a metastatic colorectal cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the metastatic colorectal cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted metastatic colorectal cancer protein.

In another preferred embodiment, the metastatic colorectal cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory,

antibodies used for this treatment typically bind the extracellular domain of the metastatic colorectal cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane metastatic colorectal cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the metastatic colorectal cancer protein. The antibody may be an antagonist of the metastatic colorectal cancer protein or may prevent activation of the transmembrane metastatic colorectal cancer protein. In some embodiments, when the antibody prevents the binding of other molecules to the metastatic colorectal cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, metastatic colorectal cancer is treated by administering to a patient antibodies directed against the transmembrane metastatic colorectal cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be any number of molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of the metastatic colorectal cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the metastatic colorectal cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with metastatic colorectal cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to metastatic colorectal cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with metastatic colorectal cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like.

Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against metastatic colorectal cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane metastatic colorectal cancer proteins not only serves to increase the local concentration of therapeutic moiety in the metastatic colorectal cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the metastatic colorectal cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the metastatic colorectal cancer protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The metastatic colorectal cancer antibodies of the invention specifically bind to metastatic colorectal cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM, preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding is also important.

Detection of metastatic colorectal cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the metastatic colorectal cancer phenotype. Expression levels of genes in normal tissue (i.e., not undergoing metastatic colorectal cancer) and in metastatic colorectal cancer tissue (and in some cases, for varying severities of metastatic colorectal cancer that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may

be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus metastatic colorectal cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, *Nature Biotechnology* 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the metastatic colorectal cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to metastatic colorectal cancer genes, i.e., those identified as being important in a metastatic colorectal cancer phenotype, can be evaluated in a metastatic colorectal cancer diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

The metastatic colorectal cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the metastatic colorectal cancer protein are detected. Although DNA or RNA encoding the metastatic colorectal cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a metastatic colorectal cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a metastatic colorectal cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, metastatic colorectal cancer proteins, including intracellular, transmembrane or secreted proteins, find use as markers of metastatic colorectal cancer. Detection of these proteins in putative metastatic colorectal cancer tissue

allows for detection or diagnosis of metastatic colorectal cancer. In one embodiment, antibodies are used to detect metastatic colorectal cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the metastatic colorectal cancer protein is detected, e.g., by immunoblotting with antibodies raised against the metastatic colorectal cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the metastatic colorectal cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the metastatic colorectal cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the metastatic colorectal cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of metastatic colorectal cancer proteins. Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing metastatic colorectal cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of metastatic colorectal cancer proteins. Antibodies can be used to detect a metastatic colorectal cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous metastatic colorectal cancer protein or vaccine.

In a preferred embodiment, *in situ* hybridization of labeled metastatic colorectal cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue

samples, including metastatic colorectal cancer tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g.,* Ausubel, *supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to metastatic colorectal cancer, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, metastatic colorectal cancer probes may be attached to biochips for the detection and quantification of metastatic colorectal cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing metastatic colorectal cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, *et al.*, *Science* 279:84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the metastatic colorectal cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified metastatic colorectal cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the metastatic colorectal cancer phenotype or an identified physiological function of a metastatic colorectal cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput

screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified the differentially expressed genes herein, a variety of assays may be applied. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in metastatic colorectal cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the metastatic colorectal cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing metastatic colorectal cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in metastatic colorectal cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in metastatic colorectal cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the metastatic colorectal cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the metastatic colorectal cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of metastatic colorectal cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more metastatic colorectal cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-26. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate metastatic colorectal cancer, modulate metastatic colorectal

cancer proteins, bind to a metastatic colorectal cancer protein, or interfere with the binding of a metastatic colorectal cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the metastatic colorectal cancer phenotype or the expression of a metastatic colorectal cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a metastatic colorectal cancer phenotype, e.g., to a normal tissue fingerprint. In another embodiment, a modulator induces a metastatic colorectal cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a metastatic colorectal cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a metastatic colorectal cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of

chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al., J. Med. Chem.* 37(9):1233-1251 (1994)).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent No. 5,010,175, Furka, *Pept. Prot. Res.* 37:487-493 (1991), Houghton *et al.*, *Nature*, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al., Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al., J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al., J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al., J. Amer. Chem.* Soc. 116:2661 (1994)), oligocarbamates (Cho, *et al., Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al., J. Org. Chem.* 59:658 (1994)). *See, generally,* Gordon *et al., J. Med. Chem.* 37:1385 (1994), nucleic acid libraries (*see, e.g.,* Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.,* U.S. Patent 5,539,083), antibody libraries (*see, e.g.,* Vaughn *et al., Nature Biotechnology* 14(3):309-314 (1996), and PCT/US96/10287), carbohydrate libraries (*see, e.g.,* Liang *et al., Science* 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.,* benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.,* 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual

synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.,* ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of metastatic colorectal cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (*see, e.g.,* Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of metastatic colorectal cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the

assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the metastatic colorectal cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a metastatic colorectal cancer expression pattern leading to a normal expression pattern, or to modulate a single metastatic colorectal cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated metastatic colorectal cancer tissue reveals genes that are not expressed in normal tissue or metastatic colorectal cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for metastatic colorectal cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated metastatic colorectal cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of metastatic colorectal cancer cells, that have an associated metastatic colorectal cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral

construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., metastatic colorectal cancer tissue may be screened for agents that modulate, e.g., induce or suppress the metastatic colorectal cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on metastatic colorectal cancer activity. By defining such a signature for the metastatic colorectal cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of metastatic colorectal cancer polypeptide activity, or of metastatic colorectal cancer or the metastatic colorectal cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of metastatic colorectal cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian metastatic colorectal cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a colorectal cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the metastatic colorectal cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively

binds to the metastatic colorectal cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the metastatic colorectal cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "metastatic colorectal cancer proteins." The metastatic colorectal cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the metastatic colorectal cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a metastatic colorectal cancer protein and a candidate compound, and determining the binding of the compound to the metastatic colorectal cancer protein. Preferred embodiments utilize

the human metastatic colorectal cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative metastatic colorectal cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the metastatic colorectal cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the metastatic colorectal cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the metastatic colorectal cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the metastatic colorectal cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all

or a portion of the metastatic colorectal cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e., a metastatic colorectal cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the metastatic colorectal cancer protein and thus is capable of binding to, and potentially modulating, the activity of the metastatic colorectal cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the metastatic colorectal cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the metastatic colorectal cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the metastatic colorectal cancer proteins. In this embodiment, the methods comprise combining a metastatic colorectal cancer protein and a competitor in a first sample. A second sample comprises a test compound, a metastatic colorectal cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the metastatic colorectal cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the metastatic colorectal cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native metastatic colorectal cancer protein, but cannot bind to modified metastatic colorectal cancer proteins. The structure of the metastatic colorectal cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a metastatic colorectal cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a metastatic colorectal cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising metastatic colorectal cancer proteins. Preferred cell types include almost any cell. The cells contain a

recombinant nucleic acid that encodes a metastatic colorectal cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate metastatic colorectal cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the metastatic colorectal cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting metastatic colorectal cancer cell division is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In another embodiment, a method of inhibiting metastatic colorectal cancer is provided. The method comprises administration of a metastatic colorectal cancer inhibitor. In a further embodiment, methods of treating cells or individuals with metastatic colorectal cancer are provided. The method comprises administration of a metastatic colorectal cancer inhibitor.

A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of metastatic colorectal cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, *Culture of Animal Cells a Manual of Basic Technique* (3rd ed., 1994),

herein incorporated by reference. *See also*, the methods section of Garkavtsev *et al.* (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (^{3}H)-thymidine at saturation density can be used to measure density limitation of growth. *See* Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a metastatic colorectal cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined autoradiographically. *See*, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (*see, e.g.*, Temin, *J. Natl. Cancer Insti.* 37:167-175 (1966); Eagle *et al.*, *J. Exp. Med.* 131:836-879 (1970)); Freshney, *supra*. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (*see, e.g.*, Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor

angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. *See, e.g.,* Folkman, *Angiogenesis and Cancer, Sem Cancer Biol.* (1992)).

Various techniques which measure the release of these factors are described in Freshney (1994), *supra*. Also, *see*, Unkless *et al.* , *J. Biol. Chem.* 249:4295-4305 (1974); Strickland & Beers, *J. Biol. Chem.* 251:5694-5702 (1976); Whur *et al.*, *Br. J. Cancer* 42:305-312 (1980); Gullino, *Angiogenesis, tumor vascularization, and potential interference with tumor growth.* in *Biological Responses in Cancer*, pp. 178-184 (Mihich (ed.) 1985); Freshney *Anticancer Res.* 5:111-130 (1985).

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate metastatic colorectal cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. *See, e.g.,* Freshney (1984), *supra*.

Tumor growth in vivo

Effects of metastatic colorectal cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the metastatic colorectal cancer gene is disrupted or in which a metastatic colorectal cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous metastatic colorectal cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous metastatic colorectal cancer gene with a mutated version of the metastatic colorectal cancer gene, or by mutating the endogenous metastatic colorectal cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (*see, e.g.,* Capecchi *et al., Science* 244:1288 (1989)). Chimeric targeted mice can be derived according to Hogan *et al., Manipulating the Mouse Embryo: A Laboratory Manual,* Cold Spring Harbor Laboratory (1988) and *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (*see, e.g.,* Giovanella *et al., J. Natl. Cancer Inst.* 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (*see, e.g.,* Bradley *et al., Br. J. Cancer* 38:263 (1978); Selby *et al., Br. J. Cancer* 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a metastatic colorectal cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth. Additionally, human tumor cells expressing the genes of the invention may be injected into immune compromised animals. Growth of these tumors, or xenografts, is compared to growth of similar human tumor cell that do not express the genes of the invention. These animals may also be used to binding assays and efficacy studies for therapeutic compounds that modulate metastatic colorectal cancer, such as antibodies or small molecules.

Polynucleotide modulators of metastatic colorectal cancer

Antisense Polynucleotides

In certain embodiments, the activity of a metastatic colorectal cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a metastatic colorectal cancer

protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the metastatic colorectal cancer protein mRNA. *See, e.g.,* Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for metastatic colorectal cancer molecules. A preferred antisense molecule is for a metastatic colorectal cancer sequence in Tables 1-26, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein & Cohen (*Cancer Res.* 48:2659 (1988 and van der Krol *et al.* (*BioTechniques* 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of metastatic colorectal cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g.,* Castanotto *et al.*,

Adv. in Pharmacology 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel *et al.*, *Nucl. Acids Res.* 18:299-304 (1990); European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g.*, WO 94/26877; Ojwang *et al.*, *Proc. Natl. Acad. Sci.* USA 90:6340-6344 (1993); Yamada *et al.*, *Human Gene Therapy* 1:39-45 (1994); Leavitt *et al.*, *Proc. Natl. Acad. Sci. USA* 92:699-703 (1995); Leavitt *et al.*, *Human Gene Therapy* 5:1151-120 (1994); and Yamada *et al.*, *Virology* 205: 121-126 (1994)).

Polynucleotide modulators of metastatic colorectal cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of metastatic colorectal cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating metastatic colorectal cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-metastatic colorectal cancer antibody that reduces or eliminates the biological activity of an endogenous metastatic colorectal cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a metastatic colorectal cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the metastatic colorectal cancer sequence is down-regulated in metastatic colorectal cancer, such state may be reversed by increasing the amount of metastatic colorectal cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous metastatic colorectal cancer gene or administering a gene encoding the metastatic colorectal cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the

incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the metastatic colorectal cancer sequence is up-regulated in metastatic colorectal cancer, the activity of the endogenous metastatic colorectal cancer gene is decreased, e.g., by the administration of a metastatic colorectal cancer antisense nucleic acid.

In one embodiment, the metastatic colorectal cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to metastatic colorectal cancer proteins. Similarly, the metastatic colorectal cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify metastatic colorectal cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a metastatic colorectal cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The metastatic colorectal cancer antibodies may be coupled to standard affinity chromatography columns and used to purify metastatic colorectal cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the metastatic colorectal cancer protein.

Methods of identifying variant metastatic colorectal cancer-associated sequences

Without being bound by theory, expression of various metastatic colorectal cancer sequences is correlated with metastatic colorectal cancer. Accordingly, disorders based on mutant or variant metastatic colorectal cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant metastatic colorectal cancer genes, e.g., determining all or part of the sequence of at least one endogenous metastatic colorectal cancer genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the metastatic colorectal cancer genotype of an individual, e.g., determining all or part of the sequence of at least one metastatic colorectal cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced metastatic colorectal cancer gene to a known metastatic colorectal cancer gene, i.e., a wild-type gene.

The sequence of all or part of the metastatic colorectal cancer gene can then be compared to the sequence of a known metastatic colorectal cancer gene to determine if any

differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the metastatic colorectal cancer gene of the patient and the known metastatic colorectal cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the number of copies of the metastatic colorectal cancer gene in the genome.

In another preferred embodiment, the metastatic colorectal cancer genes are used as probes to determine the chromosomal localization of the metastatic colorectal cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the metastatic colorectal cancer gene locus.

Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a metastatic colorectal cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*; Lieberman, *Pharmaceutical Dosage Forms* (vols. 1-3, 1992), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd, *The Art, Science and Technology of Pharmaceutical Compounding* (1999); and Pickar, *Dosage Calculations* (1999)). As is known in the art, adjustments for metastatic colorectal cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the metastatic colorectal cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above,

including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the metastatic colorectal cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a metastatic colorectal cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that metastatic colorectal cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. It is also recognized that, after delivery to other

sites in the body (*e.g.*, circulatory system, lymphatic system, or the tumor site) the metastatic colorectal cancer modulators of the invention may need to be protected from excretion, hydrolisis, proteolytic digestion or modification, or detoxification by the liver. In all these cases, protection is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier or by modifying the molecular size, weight, and/or charge of the modulator. Means of protecting agents from digestion degradation, and excretion are well known in the art.

The compositions for administration will commonly comprise a metastatic colorectal cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., *Remington's Pharmaceutical Science* (15th ed., 1980) and Goodman & Gillman, *The Pharmacologial Basis of Therapeutics* (Hardman *et al.*, eds., 1996)).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacologial Basis of Therapeutics*, *supra*.

The compositions containing modulators of metastatic colorectal cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its

complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present metastatic colorectal cancer protein-modulating compounds can be administered alone or in combination with additional metastatic colorectal cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-26, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of metastatic colorectal cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Berger & Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 (Berger), Ausubel *et al.*, eds., *Current Protocols* (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd ed., Vol. 1-3, 1989.

In a preferred embodiment, metastatic colorectal cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above.

Similarly, metastatic colorectal cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the metastatic colorectal cancer coding regions) can be administered in a gene therapy application. These metastatic colorectal cancer genes can include antisense applications, either as gene therapy (i.e., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Metastatic colorectal cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (*see, e.g.*,Vitiello, *et al.*, *J. Clin. Invest.* 95:341 (1995)), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.,* Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, (1991); Alonso *et al.*, *Vaccine* 12:299-306 (1994); Jones *et al.*, *Vaccine* 13:675-681 (1995)), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.,* Takahashi *et al.*, *Nature* 344:873-875 (1990); Hu *et al.*, *Clin Exp Immunol.* 113:235-243 (1998)), multiple antigen peptide systems (MAPs) (*see, e.g.*, Tam, *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413 (1988); Tam, *J. Immunol. Methods* 196:17-32 (1996)), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, *et al.*, In: *Concepts in vaccine development (*Kaufmann, ed., p. 379, 1996); Chakrabarti, *et al.*, *Nature* 320:535 (1986); Hu *et al.*, *Nature* 320:537 (1986); Kieny, *et al.*, *AIDS Bio/Technology* 4:790 (1986); Top *et al.*, *J. Infect. Dis.* 124:148 (1971); Chanda *et al.*, *Virology* 175:535 (1990)), particles of viral or synthetic origin (*see, e.g.*, Kofler *et al.*, *J. Immunol. Methods.* 192:25 (1996); Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993); Falo *et al.*, *Nature Med.* 7:649 (1995)), adjuvants (Warren *et al.*, *Annu. Rev. Immunol.* 4:369 (1986); Gupta *et al.*, *Vaccine* 11:293 (1993)), liposomes (Reddy *et al.*, *J. Immunol.* 148:1585 (1992); Rock, *Immunol. Today* 17:131 (1996)), or, naked or particle absorbed cDNA (Ulmer, *et al.*, *Science* 259:1745 (1993); Robinson *et al.*, *Vaccine* 11:957 (1993); Shiver *et al.*, In: *Concepts in vaccine development* (Kaufmann, ed., p. 423, 1996); Cease & Berzofsky, *Annu. Rev. Immunol.* 12:923 (1994) and Eldridge *et al.*, *Sem. Hematol.* 30:16 (1993)). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit,

MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.,* U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode metastatic colorectal cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.,* Shata *et al.*, *Mol Med Today* 6:66-71 (2000); Shedlock *et al.*, *J Leukoc Biol* 68:793-806 (2000); Hipp *et al.*, *In Vivo* 14:571-85 (2000)).

Methods for the use of genes as DNA vaccines are well known, and include placing a metastatic colorectal cancer gene or portion of a metastatic colorectal cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a metastatic colorectal cancer patient. The metastatic colorectal cancer gene used for DNA vaccines can encode full-length metastatic colorectal cancer proteins, but more preferably

encodes portions of the metastatic colorectal cancer proteins including peptides derived from the metastatic colorectal cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a metastatic colorectal cancer gene. For example, metastatic colorectal cancer-associated genes or sequence encoding subfragments of a metastatic colorectal cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the metastatic colorectal cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment metastatic colorectal cancer genes find use in generating animal models of metastatic colorectal cancer. When the metastatic colorectal cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense RNA directed to the metastatic colorectal cancer gene will also diminish or repress expression of the gene. Animal models of metastatic colorectal cancer find use in screening for modulators of a metastatic colorectal cancer-associated sequence or modulators of metastatic colorectal cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the metastatic colorectal cancer protein. When desired, tissue-specific expression or knockout of the metastatic colorectal cancer protein may be necessary.

It is also possible that the metastatic colorectal cancer protein is overexpressed in metastatic colorectal cancer. As such, transgenic animals can be generated that overexpress the metastatic colorectal cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of metastatic colorectal cancer and are additionally useful in screening for modulators to treat metastatic colorectal cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, metastatic colorectal cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative metastatic colorectal cancer polypeptides or polynucleotides, small molecules inhibitors of metastatic colorectal cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of metastatic colorectal cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a metastatic colorectal cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing metastatic colorectal cancer-associated activity. Optionally, the kit contains biologically active metastatic colorectal cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

Table 1

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	ExAccn	UnigeneID	Unigene Title	Ratio BS_Mets	Top 3 expressing cell lines
103989	AA314779	Hs.105484	ESTs; Weakly similar to LITHOSTATHINE 1	15.77	EB_cells, HT29_cells, HMEC
101169	L15533	Hs.423	pancreatitis-associated protein	11.98	HMEC (total RNA), Fibroblasts 2, Fibroblasts 2
101880	M97925	Hs.72887	defensin; alpha 5; Paneth cell-specific	9.24	Fibroblasts 2, MB231_cells, MB-MDA-453
129462	D84239	Hs.111732	IgG Fc binding protein	8.57	EB_cells, OVCAR_cells, HS578T_cells
131676	C20785	Hs.30514	ESTs	7.43	HMEC (total RNA), HMEC, Fibroblasts 2
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	7.15	HMEC, HMEC (total RNA), Fibroblasts 2
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	6.72	HMEC, HMEC (total RNA), Lu_AD_H23
101107	L08010	Hs.4158	regenerating islet-derived 1 beta (pancr	6.33	BT474_cells, Fibroblasts 2, MB231_cells
103466	Y00339	Hs.155097	carbonic anhydrase II	6.18	OVCAR_cells, MCF7, 293T_cells
102306	U33317	Hs.711	defensin; alpha 6; Paneth cell-specific	5.67	Fibroblasts 2, HMEC, HT29_cells
126419	AA451775	Hs.129064	H sapiens chromosome 19; cosmid F22162	5.14	HS578T_cells, HMEC (total RNA), HMEC
101198	L21998	Hs.315	mucin 2; intestinal/tracheal	5.1	EB_cells, HT29_cells, MB231_cells
107652	AA010195	Hs.52642	ESTs; Weakly similar to !!!! ALU CLASS F	4.94	HMEC (total RNA), HMEC, EB_cells
128145	AI498467	Hs.166669	ESTs; Weakly similar to sodium bicarbona	4.77	HS578T_cells, HMEC, Lu_SQ_H520
110660	H82117	Hs.28043	ESTs	4.54	HMEC, HS578T_cells, BT474_cells
111669	R19305	Hs.110347	H sapiens mRNA for alpha integrin bindin	4.52	HMEC, HS578T_cells, Caco2
124867	R68971	Hs.168500	ESTs	4.5	HMEC, HMEC (total RNA), HS578T_cells
127352	AA416577	Hs.189105	ESTs	4.41	HMEC, HMEC (total RNA), MB-MDA-435s
130736	T99385	Hs.18646	EST	4.29	HMEC, EB_cells, HMEC (total RNA)
128592	AA470056	Hs.113994	ESTs; Weakly similar to alternatively sp	4.18	HMEC (total RNA), HMEC, Fibroblasts 2
108092	AA045961	Hs.169355	ESTs; Weakly similar to TRANSCRIPTION RE	4.04	HMEC (total RNA), HMEC, Fibroblasts 2
133373	S72487	Hs.73946	endothelial cell growth factor 1 (platel	4.03	EB_cells, HMEC, HMEC (total RNA)
100572	HG2271		Profilaggrin	4.03	HMEC (total RNA), HMEC, Fibroblasts 2
115775	AA424030	Hs.46627	ESTs	4.02	HMEC, HMEC (total RNA), EB_cells
120811	AA346854	Hs.52788	fragile X mental retardation; autosomal	4.01	HMEC (total RNA), HMEC, Fibroblasts 2
111919	R39926	Hs.21031	ESTs	3.98	EB_cells, HMEC (total RNA), HMEC
117009	H85422	Hs.108556	ESTs	3.97	HMEC (total RNA), HMEC, Fibroblasts 2
101124	L10343	Hs.112341	protease inhibitor 3; skin-derived (SKAL	3.89	PC3_cells, RPWE_2, Caco2
106151	AA424958	Hs.33735	ESTs	3.88	EB_cells, HMEC, HMEC (total RNA)
134733	U03644	Hs.89421	CBF1 interacting corepressor	3.88	EB_cells, HMEC, HMEC (total RNA)
131739	AA449749	Hs.31386	ESTs; Highly similar to secreted apoptos	3.87	HS578T_cells, MB-MDA-435s, HT29_cells
116311	AA490469	Hs.48752	ESTs	3.84	HS578T_cells, HMEC, LNCaP_cells
134174	U05259	Hs.79630	CD79A antigen (immunoglobulin-associated	3.83	DU145_cells, Lu_AD_H23, MB231_cells
106753	AA476944	Hs.7331	ESTs	3.82	LNCaP_cells, Lu_SC_H345, DU145_cells
104842	AA039854	Hs.8065	H sapiens mRNA full length insert cDNA c	3.78	HS578T_cells, A549_cells, CALU6_cells
129161	N27334	Hs.181780	ESTs	3.75	HMEC (total RNA), HMEC, BT474_cells
105675	AA284767	Hs.252808	ESTs; Highly similar to pulmonary surfac	3.75	293T_cells, PRSC_con, HT29_cells
100547	HG2149		Mucin (Gb:M57417)	3.75	HMEC (total RNA), HMEC, Fibroblasts 2
116857	H65841	Hs.186550	ESTs	3.73	HS578T_cells, 293T_cells, HMEC
113222	T59670	Hs.10615	ESTs	3.7	HMEC, HS578T_cells, Caco2
118768	N74467	Hs.94304	EST	3.68	HMEC, HS578T_cells, OVCAR_cells
114542	AA055768	Hs.122576	ESTs	3.66	EB_cells, MCF7, LNCaP_cells
101640	M58459	Hs.180911	ribosomal protein S4; Y-linked	3.62	DU145_cells, RPWE_2, A549_cells
107754	AA017462	Hs.187571	ESTs	3.6	HMEC (total RNA), Fibroblasts 2, Fibroblasts 2
104668	AA007312	Hs.183852	ESTs; Weakly similar to polymerase [H.sa	3.58	HMEC (total RNA), HMEC, Fibroblasts 2
135377	C21382	Hs.99766	H sapiens mRNA; cDNA DKFZp564J0323 (from	3.56	HMEC, HMEC (total RNA), EB_cells
127083	Z44079	Hs.91608	otoferlin	3.53	HMEC (total RNA), HMEC, Fibroblasts 2
102329	U35407	Hs.158084	peroxisome receptor 1	3.51	HMEC, HMEC (total RNA), EB_cells
117882	N50101	Hs.124724	ESTs; Weakly similar to coded for by C.	3.47	HMEC (total RNA), HMEC, EB_cells
126405	U46278	Hs.122489	ESTs	3.46	LNCaP_cells, MCF7, DU145_cells
131378	AA463886	Hs.203910	small glutamine-rich tetratricopeptide r	3.45	EB_cells, HMEC, HMEC (total RNA)
111418	R01084	Hs.19081	ESTs	3.43	HS578T_cells, EB_cells, Lu_AD_H23
135398	AA194075	Hs.99908	nuclear receptor coactivator 4	3.4	HS578T_cells, EB_cells, HMEC
108710	AA121960		zm24g9.s1 Stratagene pancreas (#93728) H mRNA seq	3.4	EB_cells, HMEC, HMEC (total RNA)
105437	AA252191	Hs.25199	ESTs; Highly similar to match to ESTs AA	3.38	EB_cells, LNCaP_cells, RPWE_2
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	3.38	PC3_cells, EB_cells, HT29_cells
130436	M84526	Hs.155597	D component of complement (adipsin)	3.37	PRSC_con, EB_cells, Lu_AD_H23
112309	R55021		yj76d5.s1 Soares breast 2NbHBst H sapien	3.36	EB_cells, HMEC, HMEC (total RNA)
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	3.35	MB231_cells, HT29_cells, Lu_SC_H69
109012	AA156576	Hs.191466	ESTs	3.21	EB_cells, HMEC, HMEC (total RNA)
129989	AF005887	Hs.247433	activating transcription factor 6	3.19	HMEC (total RNA), HMEC, Lu_AD_H23
113466	T86945	Hs.16304	ESTs	3.18	HMEC, MB231_cells, Caco2
103029	X54489	Hs.789	GRO1 oncogene (melanoma growth stimulati	3.16	Lu_LC_H460, PC3_cells, Fibroblasts 2

109374	AA218727	Hs.210785	ESTs; Highly similar to Ibd1 [H.sapiens]	3.13	Caco2, A549_cells, MB231_cells
131403	R55750	Hs.26455	ESTs	3.13	HS578T_cells, HMEC, MB231_cells
113420	T83964	Hs.15400	ESTs	3.11	HMEC (total RNA), HMEC, EB_cells
112532	R69824	Hs.28313	ESTs	3.11	HMEC, HMEC (total RNA), EB_cells
117905	N50782	Hs.231713	EST	3.11	HMEC, HS578T_cells, Caco2
125349	T87826	Hs.164480	ESTs	3.1	HS578T_cells, EB_cells, MB-MDA-435s
107072	AA609113	Hs.177533	H sapiens mRNA; cDNA DKFZp586N0318 (from	3.1	Lu_SC_H69, MB-MDA-453, MB231_cells
118389	N64583	Hs.182385	ESTs	3.05	HMEC, HMEC, LNCaP_cells
117653	N38970	Hs.194214	ESTs	3.04	HMEC, HMEC (total RNA), Fibroblasts 2
101082	L05072	Hs.80645	interferon regulatory factor 1	3.04	EB_cells, PRSC_con, DU145_cells
126105	H75323	Hs.167614	ESTs	3.03	HS578T_cells, HMEC (total RNA), HMEC
120006	W90108	Hs.10848	KIAA0187 gene product	3.03	HMEC, HMEC (total RNA), EB_cells
127191	AA297581		EST113160 Gall bladder I H sapiens cDNA	3.02	HMEC, Lu_AD_H23, Lu_SQ_H520
106899	AA490107	Hs.21753	JM5 protein	3.02	EB_cells, HMEC (total RNA), HMEC
112784	R96306	Hs.191290	ESTs	3.02	EB_cells, HMEC, Lu_AD_358
113613	T93337	Hs.17167	ESTs; Highly similar to LRR FLI-I intera	3.02	HMEC (total RNA), EB_cells, HMEC
107631	AA007230	Hs.95026	ESTs	3.02	Lu_SC_H345, HS578T_cells, Lu_LC_H460
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	3.01	PC3_cells, EB_cells, HT29_cells
100695	HG315T		Beta-1-Glycoprotein 11, Pregnancy-Specif	3.01	Fibroblasts 2, Lu_AD_H23, MB-MDA-435s
102523	U53445	Hs.15432	downregulated in ovarian cancer 1	2.98	PRSC_con, Fibroblasts 2, HMEC
121588	AA416615	Hs.98242	ESTs	2.94	HMEC, HS578T_cells, BT474_cells
103714	AA047055	Hs.192943	ESTs	2.94	HS578T_cells, EB_cells, HMEC
104916	AA056588	Hs.16542	ESTs	2.93	HMEC (total RNA), Fibroblasts 2, HMEC
109928	H05961	Hs.26331	ESTs	2.92	HMEC, MB231_cells, HS578T_cells
104586	R78309	Hs.20787	ESTs	2.92	Caco2, Lu_AD_358, Lu_AD_358
101236	L29433	Hs.47913	coagulation factor X	2.91	HMEC, HS578T_cells, Caco2
134749	L10955	Hs.89485	carbonic anhydrase IV	2.9	BT474_cells, MCF7, HMEC (total RNA)
124703	R07294	Hs.109108	solute carrier family 22 (organic cation	2.9	HMEC, HMEC (total RNA), MB-MDA-435s
114108	Z38431	Hs.27038	ESTs; Moderately similar to X-linked ret	2.89	HMEC, HMEC (total RNA), EB_cells
107857	AA024687	Hs.61208	ESTs	2.88	HS578T_cells, MB231_cells, HMEC
111586	R10759	Hs.15177	ESTs	2.88	HS578T_cells, Lu_LC_H460, PRSC_con
127553	AA282433		H sapiens p60 katanin mRNA; complete cds	2.87	EB_cells, MB-MDA-435s, RPWE_2
129881	AA458952	Hs.197728	ESTs; Weakly similar to ZINC FINGER PROT	2.86	EB_cells, PC3_cells, HMEC
116852	H65459	Hs.38323	ESTs	2.85	HMEC, Caco2, HS578T_cells
133468	X03068	Hs.73931	major histocompatibility complex; class	2.82	MB-MDA-435s, BT474_cells, HT29_cells
130998	C00810	Hs.21970	guanine nucleotide binding protein (G pr	2.82	LNCaP_cells, Lu_SC_H345, EB_cells
124075	H05741	Hs.101643	ESTs	2.82	HMEC, HS578T_cells, HT29_cells
128108	AI247422	Hs.129966	ESTs	2.82	HS578T_cells, Lu_LC_H460, Lu_SC_H69
128096	R15413	Hs.164919	ESTs; Highly similar to PROTEIN KINASE C	2.8	MB231_cells, Lu_AD_H23, RPWE_2
126619	Z28861		HSBA7E032 STRATAGENE Human skeletal musc cDNA clone A7E03, mRNA seq.	2.77	HMEC, Lu_AD_H23, HMEC (total RNA)
114418	AA011383	Hs.177313	ESTs	2.77	HS578T_cells, EB_cells, MCF7
120383	AA228030	Hs.120234	ESTs	2.77	EB_cells, Fibroblasts 2, HMEC (total RNA)
126535	H73017	Hs.250723	ESTs; Weakly similar to atrophin-1 relat	2.76	Fibroblasts 2, PRSC_con, DU145_cells
119347	T64349		yc10d08.s1 Stratagene lung (#937210) H s	2.76	EB_cells, Lu_AD_H23, Lu_SC_H69
126219	N36368	Hs.141438	ESTs; Moderately similar to similar to C	2.76	Lu_AD_H23, HMEC (total RNA), MB-MDA-435s
125426	R43963	Hs.169355	ESTs; Weakly similar to TRANSCRIPTION RE	2.75	HMEC, HMEC (total RNA), Lu_SC_H69
103005	X52008	Hs.2700	glycine receptor; alpha 2	2.74	HS578T_cells, HMEC, MB-MDA-453
109170	AA180352	Hs.191472	ESTs	2.74	Fibroblasts 2, HMEC (total RNA), MB-MDA-435s
101125	L10373	Hs.82749	transmembrane 4 superfamily member 2	2.73	Lu_LC_H460, 293T_cells, EB_cells
130656	Z20481	Hs.17411	KIAA0699 protein	2.73	HMEC (total RNA), HMEC, Fibroblasts 2
122933	AA476728	Hs.107537	ESTs	2.72	HMEC, EB_cells, HMEC (total RNA)
126033	AA055978	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	2.71	Lu_SC_H345, Lu_SC_H69, 293T_cells
111644	R16539	Hs.223649	EST; Moderately similar to Cd-7 Metallo	2.71	EB_cells, HMEC, HMEC (total RNA)
133719	AA033790	Hs.75736	apolipoprotein D	2.71	Caco2, Fibroblasts 2, MB-MDA-435s
127555	AA582324	Hs.192857	ESTs	2.7	HMEC, HS578T_cells, HMEC (total RNA)
113321	T70580	Hs.13759	ESTs	2.69	HMEC (total RNA), Fibroblasts 2, PRSC_con
109326	AA210719	Hs.86414	ESTs	2.68	MB-MDA-435s, HS578T_cells, Lu_SC_H69
135003	H42527	Hs.92832	ESTs	2.68	HS578T_cells, EB_cells, PRSC_con
103650	Z70220		H.sapiens mRNA for 5'UTR for unknown pro	2.68	HMEC, HS578T_cells, PRSC_con
111507	R07728	Hs.191218	ESTs	2.67	HMEC (total RNA), HMEC, EB_cells
117084	H93081	Hs.41829	ESTs	2.67	HS578T_cells, HMEC, MB231_cells
103975	AA306264	Hs.176403	ESTs; Moderately similar to !!!! ALU SUB	2.67	DU145_cells, HS578T_cells, MB-MDA-435s
132850	R89741	Hs.58215	ESTs; Moderately similar to rhotekin [M.	2.66	HS578T_cells, EB_cells, 293T_cells
121599	AA416770	Hs.98255	EST	2.61	HMEC (total RNA), HMEC, EB_cells
124230	H63111	Hs.6655	ESTs	2.6	HMEC (total RNA), HMEC, Fibroblasts 2
114174	Z39055	Hs.27264	ESTs; Moderately similar to !!!! ALU SUB	2.58	Caco2, MB-MDA-453, A549_cells
128469	T23724	Hs.258677	EST	2.57	Lu_LC_H460, Lu_SC_H69, MB-MDA-435s
117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3	2.57	HMEC, HMEC (total RNA), EB_cells
129279	AA460551	Hs.184860	ESTs; Weakly similar to EG:87B1.6 [D.mel	2.57	HS578T_cells, EB_cells, HT29_cells
119817	W74257	Hs.159690	ESTs	2.57	HMEC, HMEC (total RNA), Lu_SC_H69
114445	AA019594	Hs.250493	ESTs; Weakly similar to KIAA0390 [H.sapi	2.56	HMEC, HT29_cells, Lu_LC_H460
120651	AA287286	Hs.99657	ESTs	2.55	HMEC, HMEC (total RNA), Fibroblasts 2
105707	AA291012	Hs.37617	ESTs; Weakly similar to KIAA0727 protein	2.55	HMEC (total RNA), EB_cells, BT474_cells
128483	T58588	Hs.5148	FLN29 gene product	2.54	HMEC, HS578T_cells, MB231_cells
125890	AA448739	Hs.116708	ESTs; Weakly similar to HYPOTHETICAL PRO	2.54	HMEC (total RNA), HMEC, OVCAR_cells

	134764	M74715	Hs.89560	iduronidase; alpha-L-	2.54	BT474_cells, PRSC_con, HT29_cells
	113404	T82323	Hs.70337	immunoglobulin superfamily; member 4	2.54	Caco2, HS578T_cells, HMEC
	129128	AA423854	Hs.108812	ESTs	2.54	BT474_cells, MB-MDA-435s, HMEC
	101428	M19684	Hs.184929	protease inhibitor 1 (alpha-1-antitrypsi	2.54	HMEC, HT29_cells, HMEC (total RNA)
5	103206	X72755	Hs.77367	monokine induced by gamma interferon	2.53	Fibroblasts 2, MB231_cells, HMEC (total RNA)
	132273	AA489716	Hs.43658	DKFZP586L151 protein	2.53	EB_cells, HMEC, HMEC (total RNA)
	108392	AA075124		zm86a1.s1 Stratagene ovarian cancer (#93 IMAGE:544776 3', mRNA seq	2.52	HMEC (total RNA), HMEC, HS578T_cells
	119508	W37895	Hs.45519	ESTs	2.52	Lu_SC_H69, CALU6_cells, 293T_cells
10	109828	F13763	Hs.19827	ESTs	2.52	PRSC_log, PRSC_con, HS578T_cells
	135096	N89775	Hs.132390	zinc finger protein 36 (KOX 18)	2.51	HMEC, HS578T_cells, HT29_cells
	130860	U66061	Hs.241395	protease; serine; 1 (trypsin 1)	2.51	OVCAR_cells, MB231_cells, PC3_cells
	105725	AA292228	Hs.199791	STAT induced STAT inhibitor 3	2.51	HS578T_cells, HT29_cells, HMEC
	110427	H48579	Hs.36275	EST	2.51	HS578T_cells, Caco2, Lu_LC_H460
15	123762	AA610013	Hs.244553	EST	2.51	HMEC (total RNA), HMEC, Fibroblasts 2
	126406	AA034096		zi06f05.r1 Soares_fetal_liver_spleen_1NF IMAGE:430017 5', mRNA seq.	2.5	Lu_AD_H23, HS578T_cells, Lu_AD_358
	129751	AA346065	Hs.111286	KIAA0714 protein	2.5	HMEC, HS578T_cells, Fibroblasts 2
	121704	AA418743	Hs.98306	ESTs	2.5	EB_cells, HMEC (total RNA), HMEC
20	112595	R77783	Hs.22404	protease; serine; 12 (neurotrypsin; moto	2.5	Fibroblasts 2, EB_cells, PRSC_con
	108499	AA083103		zn1b12.s1 Stratagene hNT neuron (#937233 IMAGE:5477 3', mRNA seq	2.5	LNCaP_cells, MB-MDA-453, HMEC
	131968	AA151333	Hs.36029	ESTs; Highly similar to basic helix-loop	2.5	Fibroblasts 2, A549_cells, 293T_cells
	112665	R85661	Hs.221447	ESTs	2.48	Lu_AD_H23, HMEC, Lu_LC_H460
25	115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	2.48	EB_cells, Caco2, MCF7
	105959	AA405540	Hs.7001	ESTs	2.48	OVCAR_cells, BT474_cells, Caco2
	125804	R79519	Hs.16899	ESTs	2.48	HMEC (total RNA), EB_cells, HMEC
	110102	H16681	Hs.180950	guanine nucleotide binding protein (G pr	2.46	HS578T_cells, HMEC, OVCAR_cells
	104680	AA009809	Hs.37599	ESTs	2.46	HMEC, HS578T_cells, Caco2
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	2.45	OVCAR_cells, 293T_cells, HMEC (total RNA)
	121712	AA419116	Hs.193663	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.45	Lu_SQ_H520, Lu_AD_H23, Lu_SC_H69
	129226	M96843	Hs.180919	inhibitor of DNA binding 2; dominant neg	2.44	MB-MDA-453, 293T_cells, Caco2
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor	2.43	HMEC, HMEC (total RNA), EB_cells
	106670	AA461174	Hs.5943	ESTs	2.43	EB_cells, HS578T_cells, Lu_SC_H69
35	119306	T26914	Hs.132785	EAP30 subunit of ELL complex	2.43	EB_cells, HMEC (total RNA), HMEC
	133507	X74295	Hs.74369	integrin; alpha 7	2.42	Fibroblasts 2, Caco2, EB_cells
	125713	AA367905	Hs.77356	transferrin receptor (p90; CD71)	2.41	HS578T_cells, Fibroblasts 2, Lu_AD_H23
	107438	W27841	Hs.17118	ESTs; Weakly similar to B0025.2 [C.elega	2.41	HMEC, HS578T_cells, MB231_cells
	101784	M83186	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.41	Fibroblasts 2, PRSC_con, PRSC_log
40	134578	AA194724	Hs.182418	endonuclease G	2.4	EB_cells, HMEC, Lu_AD_H23
	125105	T95642	Hs.189759	ESTs	2.4	EB_cells, A549_cells, HS578T_cells
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor	2.4	HMEC, HMEC (total RNA), EB_cells
	113118	T47906	Hs.220512	ESTs	2.39	MB-MDA-435s, HS578T_cells, HMEC
	104791	AA029046	Hs.30377	ESTs; Moderately similar to cAMP inducib	2.39	LNCaP_cells, OVCAR_cells, PC3_cells
45	115833	AA428269	Hs.125035	ESTs	2.38	Caco2, LNCaP_cells, CALU6_cells
	132223	R77451	Hs.4245	ESTs; Weakly similar to similar to S. ce	2.38	HMEC, HMEC (total RNA), EB_cells
	115836	AA428863	Hs.89388	ESTs	2.38	HS578T_cells, HMEC, PRSC_con
	101891	S45630	Hs.1940	crystallin; alpha B	2.38	HS578T_cells, OVCAR_cells, Lu_LC_H460
	132894	D82422	Hs.5944	ESTs	2.37	Caco2, MB-MDA-453, HT29_cells
50	106939	AA496048	Hs.26570	ESTs	2.35	LNCaP_cells, 293T_cells, EB_cells
	131104	W27770	Hs.258721	ESTs	2.35	HMEC (total RNA), HMEC, HT29_cells
	122355	AA443789	Hs.189324	ESTs	2.34	HMEC (total RNA), HMEC, EB_cells
	119343	T62873		yc3d2.s1 Stratagene lung (#93721) H sapi to contains Alu repetitive element;, mR	2.34	HS578T_cells, Lu_SC_H69, HT29_cells
55	115442	AA284722	Hs.89121	H sapiens mRNA; chromosome 1 specific tr	2.33	Lu_AD_H23, HMEC (total RNA), BT474_cells
	134286	T69384	Hs.68398	period (Drosophila) homolog 1	2.33	HMEC, HMEC (total RNA), MB231_cells
	125465	AI375276	Hs.158732	ESTs	2.33	HMEC (total RNA), EB_cells, HMEC
	127449	AI421866	Hs.75722	ribophorin II	2.33	Lu_AD_H23, HMEC (total RNA), HMEC
	110225	H23927	Hs.222381	ESTs	2.33	HS578T_cells, HMEC, Lu_LC_H460
60	119930	W86471	Hs.151624	hypocretin (orexin) receptor 2	2.32	HMEC, HMEC (total RNA), EB_cells
	125958	AI073357	Hs.12311	H sapiens clone 23570 mRNA seq	2.32	MB231_cells, HMEC (total RNA), HMEC
	119746	W70279	Hs.221189	ESTs; Weakly similar to 15-HYDROXYPROSTA	2.32	HMEC, HS578T_cells, MB231_cells
	108874	AA134112	Hs.107187	H sapiens DNA seq from cosmid ICK0721Q o L12 LIKE protein in an intron of the HS	2.32	Caco2, PRSC_con, LNCaP_cells
65	127368	AA434362	Hs.193326	ESTs	2.32	HMEC (total RNA), HS578T_cells, HMEC
	120437	AA243427	Hs.104311	ESTs	2.32	HMEC (total RNA), HMEC, MB-MDA-435s
	119867	W80852	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.32	Fibroblasts 2, HS578T_cells, MB-MDA-435s
	131205	J02947	Hs.2420	superoxide dismutase 3; extracellular	2.32	PRSC_con, EB_cells, Lu_AD_358
	133710	X76057	Hs.75694	mannose phosphate isomerase	2.31	293T_cells, LNCaP_cells, RPWE_2
70	104834	AA039331	Hs.16323	ESTs; Weakly similar to GAGE-7 [H.sapien	2.31	Caco2, HS578T_cells, HMEC
	113186	T56048	Hs.189674	ESTs	2.31	HMEC, Fibroblasts 2, HMEC (total RNA)
	113462	T86826	Hs.142528	ESTs	2.31	PC3_cells, HS578T_cells, HMEC
	104743	AA021157	Hs.33619	ESTs	2.3	HMEC (total RNA), HMEC, OVCAR_cells
	129667	Y00097	Hs.118796	annexin A6	2.3	PRSC_log, PRSC_con, HS578T_cells
75	111573	R10305	Hs.185683	ESTs	2.3	HMEC, HMEC (total RNA), EB_cells
	117523	N32626	Hs.145532	ESTs; Weakly similar to Gag polyprotein	2.29	EB_cells, Fibroblasts 2, HS578T_cells

115540	AA349954	Hs.56281	ESTs; Weakly similar to ASB-1 protein [H	2.29	Fibroblasts 2, BT474_cells, MB231_cells
101622	M55621	Hs.151513	mannosyl (alpha-1;3-)-glycoprotein beta-	2.29	PRSC_con, RPWE_2, PRSC_log
103535	Y13620	Hs.122607	B-cell CLL/lymphoma 9	2.28	Lu_SC_H69, Lu_AD_358, Lu_AD_H23
127482	AI337294	Hs.155014	ESTs	2.28	HS578T_cells, 293T_cells, CALU6_cells
104297	D31111	Hs.106005	ESTs; Highly similar to NY-REN-50 antige	2.27	EB_cells, DU145_cells, HT29_cells
112318	R55470	Hs.11067	ESTs	2.27	MB-MDA-453, LNCaP_cells, OVCAR_cells
101877	M97496	Hs.778	guanylate cyclase activator 1B (retina)	2.27	HT29_cells, BT474_cells, Caco2
100760	HG3576		Major Histocompatibility Complex, Class	2.26	MB-MDA-435s, MB231_cells, BT474_cells
102362	U39412	Hs.75932	N-ethylmaleimide-sensitive factor attach	2.26	LNCaP_cells, MB-MDA-453, Caco2
106142	AA424590	Hs.239631	Golgi transport complex protein (90 kDa)	2.26	HMEC, HS578T_cells, Caco2
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	2.26	LNCaP_cells, BT474_cells, Caco2
119336	T55340	Hs.208238	ESTs	2.26	HS578T_cells, EB_cells, HMEC
127619	AA627122	Hs.163787	ESTs	2.25	Lu_SQ_H520, Lu_LC_H460, Lu_SC_H69
104113	AA427510	Hs.181202	ESTs; Weakly similar to Wiscott-Aldrich	2.25	MB-MDA-435s, Fibroblasts 2, HMEC (total RNA)
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	2.25	Lu_SQ_H520, BT474_cells, Fibroblasts 2
118915	N91481	Hs.54713	ESTs	2.25	HMEC (total RNA), HMEC, MCF7
127556	AA679831	Hs.190228	ESTs	2.24	HS578T_cells, EB_cells, HMEC
128700	U59286	Hs.103982	small inducible cytokine subfamily B (Cy	2.24	HMEC, HS578T_cells, Fibroblasts 2
113674	T96374	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.24	A549_cells, DU145_cells, Lu_AD_358
133085	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.24	HS578T_cells, Fibroblasts 2, HT29_cells
106017	AA411882	Hs.26268	ESTs	2.24	MB-MDA-453, OVCAR_cells, 293T_cells
100582	HG2348		Peptide Yy	2.24	HMEC, HS578T_cells, HMEC (total RNA)
134811	N66357	Hs.89761	ATP synthase; H+ transporting; mitochond	2.23	Lu_SQ_H520, LNCaP_cells, Lu_AD_H23
102543	U57627	Hs.234776	oculocerebrorenal syndrome of Lowe	2.23	293T_cells, EB_cells, LNCaP_cells
127357	AA452788		zx39g11.r1 Soares_total_fetus_Nb2HF8_9w IMAGE:788900 5', mRNA seq.	2.23	HS578T_cells, RPWE_2, HMEC (total RNA)
135288	AA402930	Hs.97876	ESTs	2.23	HS578T_cells, 293T_cells, OVCAR_cells
105581	AA278850	Hs.28891	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.23	BT474_cells, BT474_cells, MB231_cells
103812	AA137107	Hs.124094	ESTs; Weakly similar to NFAT1-A [M.muscu	2.23	Lu_SC_H345, Lu_AD_H23, PRSC_con
117016	H87171	Hs.52170	ESTs	2.22	Fibroblasts 2, Lu_LC_H460, HMEC (total RNA)
114607	AA079342	Hs.129057	breast carcinoma amplified seq 1	2.22	BT474_cells, HT29_cells, HT29_cells
134000	U29091	Hs.7833	selenium binding protein 1	2.22	LNCaP_cells, MB-MDA-453, BT474_cells
111069	N58461	Hs.22036	ESTs	2.22	HMEC, Lu_SC_H345, HS578T_cells
129048	L27670	Hs.108287	intercellular adhesion molecule 4; Lands	2.21	Lu_AD_H23, HS578T_cells, Lu_SQ_H520
124995	T52700	Hs.110044	ESTs	2.2	Caco2, MB-MDA-453, HT29_cells
116678	F05063	Hs.251736	ESTs	2.2	HS578T_cells, BT474_cells, 293T_cells
118222	N62263	Hs.48501	EST	2.2	HS578T_cells, BT474_cells, MB231_cells
127888	AI149662	Hs.143590	ESTs	2.19	BT474_cells, CALU6_cells, MB231_cells
113790	W33178	Hs.26912	ESTs	2.19	HMEC, HMEC (total RNA), Fibroblasts 2
100097	AF002224		H sapiens Angelman Syndrome Gene, E6-AP from promoter P1, 5'UTR	2.19	HS578T_cells, CALU6_cells, 293T_cells
109151	AA176800	Hs.73452	ESTs	2.19	CALU6_cells, Lu_AD_H23, Lu_SC_H69
135368	AA086057	Hs.9964	ribosomal protein; mitochondrial; S12	2.19	OVCAR_cells, A549_cells, Lu_AD_H23
109016	AA156936	Hs.58069	ESTs; Highly similar to type II cAMP-dep	2.19	HS578T_cells, BT474_cells, A549_cells
124300	H92575	Hs.105959	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.18	Lu_AD_358, Lu_SC_H69, Lu_SC_H345
123450	AA598913	Hs.111207	ESTs	2.18	HMEC (total RNA), HMEC, MB-MDA-435s
117435	N27628		yw50b08.s1 Weizmann Olfactory Epithelium	2.18	LNCaP_cells, DU145_cells, Lu_SQ_H520
119860	W80709	Hs.58485	ESTs	2.18	HS578T_cells, MB231_cells, Caco2
123833	AA620717	Hs.112889	ESTs	2.18	Lu_AD_H23, Lu_SQ_H520, Lu_AD_358
107938	AA029446	Hs.53115	ESTs	2.17	Caco2, 293T_cells, 293T_cells
119380	T83659	Hs.184407	ESTs	2.16	Lu_AD_H23, Lu_AD_358, PRSC_con
114066	Z38152	Hs.26920	ESTs	2.15	HMEC (total RNA), HMEC, EB_cells
128748	T59001	Hs.10475	ESTs	2.15	HMEC, HT29_cells, MB231_cells
130414	M21121	Hs.241392	small inducible cytokine A5 (RANTES)	2.15	HS578T_cells, PC3_cells, A549_cells
123490	AA599723		TAP binding protein (tapasin)	2.15	HS578T_cells, EB_cells, Lu_SC_H69
112588	R77302	Hs.20226	ESTs	2.14	HMEC (total RNA), HMEC, Fibroblasts 2
110548	H58715	Hs.14706	ESTs	2.14	HMEC, HMEC (total RNA), HT29_cells
101581	M34996	Hs.198253	major histocompatibility complex; class	2.14	MB-MDA-435s, HMEC, HMEC
115248	AA278887	Hs.194530	ESTs; Weakly similar to unknown [H.sapie	2.14	HT29_cells, BT474_cells, CALU6_cells
105619	AA280810	Hs.24003	ESTs; Moderately similar to LEYDIG CELL	2.14	Lu_SQ_H520, MB-MDA-435s, LNCaP_cells
128058	AI126617	Hs.132449	ESTs	2.14	HS578T_cells, EB_cells, HMEC (total RNA)
134573	AA442125	Hs.171873	ESTs; Weakly similar to PUTATIVE STEROID	2.14	EB_cells, MB231_cells, Caco2
134863	AA353903	Hs.183373	ATX1 (antioxidant protein 1; yeast) homo	2.14	Lu_SC_H345, HT29_cells, BT474_cells
128811	H17317	Hs.169100	ESTs; Weakly similar to HPBRII-7 protein	2.13	Caco2, Lu_SC_H345, EB_cells
112368	R59371	Hs.26653	EST	2.13	HMEC, HMEC (total RNA), Lu_SQ_H520
108395	AA075144		zm86f6.s1 Stratagene ovarian cancer (#93 gb:X1664 TRANSLATIONALLY CONTROLLED TUM	2.13	HMEC (total RNA), HMEC, OVCAR_cells
129611	D45680	Hs.11614	ESTs	2.13	HMEC, HS578T_cells, Caco2
101253	L34355	Hs.99931	sarcoglycan; alpha (50kD dystrophin-asso	2.12	HS578T_cells, OVCAR_cells, CALU6_cells
126701	AA515212	Hs.202590	ESTs; Weakly similar to mucin glycoprote	2.12	EB_cells, Lu_AD_H23, Lu_AD_H23
111628	R15825	Hs.4014	KIAA0946 protein; Huntingtin interacting	2.12	A549_cells, BT474_cells, MB-MDA-435s
108675	AA115240	Hs.61816	ESTs	2.12	Lu_AD_H23, MB-MDA-453, PRSC_con
127131	Z44658	Hs.105460	DKFZP564O0823 protein	2.12	EB_cells, Lu_SC_H69, Lu_SC_H69
109590	F02465	Hs.27281	ESTs	2.12	HMEC, HS578T_cells, HMEC (total RNA)
116539	D12124	Hs.242890	EST	2.12	Lu_AD_H23, Caco2, BT474_cells
112117	R45402	Hs.23789	ESTs	2.12	EB_cells, Lu_AD_H23, Lu_SQ_H520

126367	AA477929	Hs.25584	ESTs	2.12	Lu_SC_H69, Lu_AD_H23, Lu_AD_358
135252	U62966	Hs.97207	solute carrier family 28 (sodium-coupled	2.11	MB-MDA-435s, 293T_cells, CALU6_cells
117565	N34301	Hs.248426	EST	2.11	HMEC, HS578T_cells, MB231_cells
129430	AA258842	Hs.197877	H sapiens clone 23777 putative transmemb	2.11	HS578T_cells, Lu_AD_358, MB-MDA-435s
120256	AA169801		sema domain; immunoglobulin domain (Ig);	2.11	HMEC, HMEC (total RNA), EB_cells
134169	D20342	Hs.178137	transducer of ERBB2; 1 (TOB1)	2.11	HMEC (total RNA), 293T_cells, OVCAR_cells
130397	AA487452	Hs.155344	DNA fragmentation factor; 45 kD; alpha s	2.11	293T_cells, Caco2, Lu_AD_H23
132859	D20925	Hs.5842	ESTs	2.11	HMEC (total RNA), Fibroblasts 2, HMEC
117633	N36404	Hs.44807	ESTs	2.11	HMEC, Caco2, HS578T_cells
125003	T59442	Hs.100445	ESTs	2.11	MB-MDA-435s, HMEC (total RNA), HT29_cells
125329	AA825437	Hs.58875	ESTs	2.11	HS578T_cells, PRSC_con, PRSC_log
114065	Z38149	Hs.134015	uronyl 2-sulfotransferase	2.11	MB-MDA-435s, 293T_cells, PRSC_con
120718	AA292747	Hs.97296	ESTs	2.11	HT29_cells, Lu_AD_H23, Lu_SC_H69
133869	T49444	Hs.77031	Sp2 transcription factor	2.1	Lu_LC_H460, Lu_AD_358, RPWE_2
135351	AA430179	Hs.9933	putative Ac-like transposon	2.1	HS578T_cells, EB_cells, HMEC
110973	N51529	Hs.118047	ESTs	2.09	EB_cells, HS578T_cells, MCF7
131879	AA017161	Hs.33792	ESTs	2.09	HMEC (total RNA), MB231_cells, BT474_cells
116656	F03935	Hs.241640	EST	2.09	HS578T_cells, Lu_LC_H460, Lu_SC_H69
120311	AA194074	Hs.193401	ESTs	2.09	OVCAR_cells, HMEC (total RNA), HMEC
108024	AA040433	Hs.61898	DKFZP586N2124 protein	2.09	HMEC (total RNA), BT474_cells, HT29_cells
105871	AA399633	Hs.24872	ESTs	2.09	Fibroblasts 2, A549_cells, HS578T_cells
120206	Z40805	Hs.91668	ESTs	2.09	BT474_cells, MB-MDA-453, EB_cells
112333	R56222	Hs.26514	ESTs	2.09	Lu_AD_H23, Fibroblasts 2, Lu_LC_H460
116746	H04811	Hs.79027	ESTs	2.08	MB-MDA-435s, HMEC (total RNA), Lu_SC_H345
121529	AA412257	Hs.98121	ESTs	2.08	HMEC, HMEC (total RNA), HS578T_cells
105592	AA279337	Hs.180549	ESTs; Highly similar to R26660_1; partia	2.08	LNCaP_cells, PRSC_log, PRSC_log
108582	AA088231	Hs.91732	ESTs	2.08	HS578T_cells, Lu_SC_H345, Lu_SC_H69
123197	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	2.08	EB_cells, Lu_SC_H69, Lu_SC_H345
134965	J05480	Hs.92	protein phosphatase 3 (formerly 2B); cat	2.08	LNCaP_cells, MB-MDA-435s, HMEC
123856	AA620814	Hs.144959	ESTs	2.08	HS578T_cells, BT474_cells, BT474_cells
132058	AA251737	Hs.172818	Apg12 (autophagy 12; S. cerevisiae)-like	2.07	HS578T_cells, MCF7, HMEC
126476	R94666	Hs.195155	ESTs; Weakly similar to transporter prot	2.07	PRSC_log, Lu_LC_H460, RPWE_2
106087	AA418740	Hs.21111	ESTs	2.07	OVCAR_cells, A549_cells, Lu_AD_H23
103802	AA122003	Hs.62954	ferritin; heavy polypeptide 1	2.07	HMEC, HMEC (total RNA), HS578T_cells
125633	AA908225	Hs.126841	ESTs	2.07	EB_cells, Fibroblasts 2, Lu_SC_H69
112817	R98491	Hs.14584	ESTs	2.07	HMEC, HMEC (total RNA), Fibroblasts 2
111050	N56984	Hs.74335	heat shock 90kD protein 1; beta	2.07	LNCaP_cells, DU145_cells, 293T_cells
133072	AA425294	Hs.64322	ESTs; Weakly similar to Closely related	2.07	LNCaP_cells, MB-MDA-453, Caco2
118270	N62868	Hs.48653	ESTs	2.07	HMEC (total RNA), HMEC, EB_cells
105035	AA128486	Hs.8859	ESTs	2.07	LNCaP_cells, PC3_cells, EB_cells
102337	U36922		Human fork head domain protein (FKHR) mR	2.07	293T_cells, HMEC, HT29_cells
109687	F09380	Hs.182859	lifeguard	2.06	BT474_cells, BT474_cells, Lu_AD_H23
109802	F10789	Hs.12439	ESTs	2.06	EB_cells, EB_cells, Caco2
128103	AA905960	Hs.48516	ESTs	2.06	HT29_cells, HMEC (total RNA), HMEC
128278	AI018343	Hs.131275	ESTs	2.06	PRSC_con, Lu_SC_H345, HS578T_cells
131873	H39997	Hs.33716	ESTs	2.06	HMEC (total RNA), HMEC, EB_cells
122683	AA455528	Hs.96772	ESTs	2.05	LNCaP_cells, Lu_AD_H23, HS578T_cells
128066	AA884838	Hs.189171	ESTs	2.05	HMEC, HMEC (total RNA), Fibroblasts 2
131451	N28028	Hs.26968	H sapiens mRNA from chromosome 5q21-22;	2.05	MB-MDA-435s, Lu_LC_H460, Lu_SQ_H520
120887	AA365644	Hs.97043	ESTs	2.05	HS578T_cells, PRSC_con, HMEC
103966	AA303166	Hs.127270	ESTs	2.05	HMEC (total RNA), LNCaP_cells, PC3_cells
105861	AA399260	Hs.28454	ESTs	2.05	Fibroblasts 2, HMEC (total RNA), EB_cells
104627	AA001976	Hs.19603	ESTs	2.05	HS578T_cells, HMEC, BT474_cells
108794	AA129468	Hs.203392	ESTs	2.04	HS578T_cells, HMEC, A549_cells
111896	R38936	Hs.24894	H sapiens clone 25248 mRNA seq	2.04	HS578T_cells, PC3_cells, 293T_cells
101849	M94167	Hs.172816	neuregulin 1	2.04	HMEC, HS578T_cells, HMEC (total RNA)
119913	W85931	Hs.58785	ESTs	2.04	HMEC, BT474_cells, MB231_cells
130785	AA242826	Hs.19405	caspase recruitment domain 4	2.04	HMEC, HS578T_cells, BT474_cells
124702	R06984	Hs.7745	ESTs; Weakly similar to TESTIS-SPECIFIC	2.03	Fibroblasts 2, PRSC_con, HMEC
106769	AA478001	Hs.225935	diacylglycerol O-acyltransferase (mouse)	2.03	PC3_cells, EB_cells, HS578T_cells
132219	N48682	Hs.172971	ESTs	2.03	HT29_cells, PC3_cells, A549_cells
122033	AA431334	Hs.109297	ESTs	2.03	OVCAR_cells, A549_cells, Caco2
120461	AA251301		zs10b02.s1 NCI_CGAP_GCB1 H sapiens cDNA contains Alu repetitive element;, mRNA	2.03	HS578T_cells, EB_cells, EB_cells
134959	U90550	Hs.91813	butyrophilin; subfamily 2; member A2	2.03	HMEC, Fibroblasts 2, EB_cells
104909	AA055892	Hs.14543	ESTs	2.03	Lu_SC_H345, PC3_cells, DU145_cells
101950	S79219	Hs.80741	propionyl Coenzyme A carboxylase; alpha	2.03	Lu_SC_H69, EB_cells, CALU6_cells
133878	D78947	Hs.7718	ESTs; Weakly similar to weak similarity	2.02	EB_cells, MCF7, MB231_cells
103459	X99894	Hs.32938	insulin promoter factor 1; homeodomain t	2.02	EB_cells, Lu_AD_H23, Lu_AD_358
125507	AI436377	Hs.258590	tetraspanin TM4-B	2.02	A549_cells, Lu_SQ_H520, Lu_AD_H23
116657	F04014	Hs.65996	ESTs	2.01	HS578T_cells, HMEC, MB231_cells
112920	T10234	Hs.4275	ESTs	2.01	HS578T_cells, EB_cells, PRSC_con
105533	AA258572	Hs.6418	ESTs; Moderately similar to seven transm	2.01	HS578T_cells, HMEC, EB_cells
126762	AA064671		zm13b04.r1 Stratagene pancreas (#937208) similar to TR:G413842 G413842 NONCLASSI	2.01	RPWE_2, Lu_AD_H23, Lu_AD_358
128999	R37808	Hs.107765	ESTs	2.01	HS578T_cells, OVCAR_cells, EB_cells

133902	AA114858	Hs.7745	ESTs; Weakly similar to TESTIS-SPECIFIC	2	Fibroblasts 2, PRSC_con, DU145_cells

Table 2

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Mets/BS	Top 3 expressing cell lines
101447	M21305	Hs.247946	Human alpha satellite and satellite 3 ju	110.98	EB_cells, Fibroblasts 2, A549_cells
105039	AA130349	Hs.36475	ESTs	9.13	EB_cells, OVCAR_cells, Lu_SC_H345
106094	AA419461	Hs.18127	ESTs	8.51	HT29_cells, MB-MDA-453, HS578T_cells
105777	AA348412	Hs.23096	ESTs	8.4	293T_cells, OVCAR_cells, EB_cells
129818	N54841	Hs.172572	ESTs	7.2	Lu_SC_H69, EB_cells, Lu_SC_H345
118475	N66845	Hs.165411	ESTs; Weakly similar to !!!! ALU CLASS B	7	DU145_cells, EB_cells, Caco2
112170	R48744	Hs.192878	ESTs	6.91	293T_cells, DU145_cells, HT29_cells
114918	AA236813	Hs.72324	ESTs; Highly similar to unknown [H.sapie	6.6	EB_cells, 293T_cells, DU145_cells
104590	R79750	Hs.83623	nuclear receptor subfamily 1; group I; m	6.58	293T_cells, OVCAR_cells, HMEC
120625	AA285053	Hs.107168	ESTs	6.55	CALU6_cells, OVCAR_cells, EB_cells
115650	AA404564	Hs.47094	ESTs	6.43	EB_cells, LNCaP_cells, Lu_SC_H345
124568	N67086	Hs.102000	ESTs	6.35	PC3_cells, A549_cells, DU145_cells
134238	R81509	Hs.184571	splicing factor; arginine/serine-rich 11	6.32	293T_cells, Lu_SC_H345, HMEC
114721	AA131450	Hs.103822	ESTs	6.13	Caco2, MB-MDA-435s, PRSC_log
106145	AA424791	Hs.5734	KIAA0679 protein	6	OVCAR_cells, EB_cells, 293T_cells
114610	AA081079		zn32h9.s1 Stratagene endothelial cell 93 IMAGE:549185 3', mRNA seq	5.97	PRSC_con, DU145_cells, HS578T_cells
130281	R12777	Hs.15395	ESTs; Weakly similar to ARGINYL-TRNA SYN		5.94 PRSC_con, HT29_cells, EB_cells
124690	R05818	Hs.173830	ESTs	5.92	LNCaP_cells, EB_cells, OVCAR_cells
113490	T88700	Hs.173374	ESTs	5.81	DU145_cells, PC3_cells, HMEC (total RNA)
104425	H88496	Hs.40583	ESTs	5.77	OVCAR_cells, HS578T_cells, A549_cells
118828	N79496	Hs.50824	EST	5.45	LNCaP_cells, OVCAR_cells, DU145_cells
129076	AA262179	Hs.169343	ESTs	5.35	293T_cells, BT474_cells, MCF7
109684	F09317	Hs.140885	ESTs; Weakly similar to LINE-1 REVERSE T	5.34	Fibroblasts 2, Lu_SC_H69, DU145_cells
104558	R56678	Hs.88959	Human DNA seq from clone 967N21 on chr 2 part of KIAA0172; the gene for a novel	5.32	EB_cells, PC3_cells, Lu_SC_H345
109032	AA158234	Hs.72222	ESTs	5.23	HT29_cells, PC3_cells, Lu_AD_358
129350	U50535	Hs.110630	Human BRCA2 region; mRNA seq CG006	5.2	293T_cells, EB_cells, DU145_cells
112662	R85436	Hs.193150	ESTs	5.2	MB-MDA-435s, PRSC_con, MB-MDA-453
132902	AA490969	Hs.168147	ESTs	5.18	PC3_cells, LNCaP_cells, CALU6_cells
126872	AA136653		ESTs	5.04	EB_cells, Fibroblasts 2, A549_cells
122528	AA449804	Hs.250992	EST	5.04	Lu_SC_H345, PRSC_con, LNCaP_cells
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	5.02	Lu_LC_H460, A549_cells, MB-MDA-435s
121332	AA404384	Hs.97921	ESTs	5.01	EB_cells, Lu_SC_H69, DU145_cells
135357	AA235803	Hs.79572	cathepsin D (lysosomal aspartyl protease	4.96	EB_cells, MCF7, DU145_cells
109141	AA176428	Hs.193380	ESTs	4.86	DU145_cells, PC3_cells, PRSC_log
135324	AA082041	Hs.9873	ESTs	4.83	EB_cells, Lu_SC_H345, HS578T_cells
124875	R70506	Hs.207693	ESTs; Weakly similar to !!!! ALU SUBFAMI	4.75	DU145_cells, OVCAR_cells, LNCaP_cells
102380	U40434	Hs.155981	mesothelin	4.71	OVCAR_cells, Lu_AD_H23, RPWE_2
127956	AA826117	Hs.194013	ESTs	4.69	EB_cells, HS578T_cells, DU145_cells
125038	T78089	Hs.168887	ESTs	4.58	OVCAR_cells, 293T_cells, DU145_cells
102515	U52696		Humn adrenal Creb-rp hmlg (Creb-rp), com	4.57	Lu_SC_H345, Lu_SC_H69, HT29_cells
109027	AA157818	Hs.238380	Human endogenous retroviral protease mRN	4.57	PC3_cells, EB_cells, Lu_SQ_H520
115096	AA255991	Hs.175319	ESTs	4.57	OVCAR_cells, 293T_cells, PC3_cells
123470	AA599106	Hs.194208	ESTs	4.55	LNCaP_cells, Lu_SC_H69, 293T_cells
113219	T59257	Hs.194407	ESTs	4.55	A549_cells, 293T_cells, 293T_cells
123433	AA598661	Hs.112478	ESTs	4.55	EB_cells, OVCAR_cells, HT29_cells
135182	M28170	Hs.96023	CD19 antigen	4.53	OVCAR_cells, DU145_cells, EB_cells
121721	AA419470	Hs.199961	ESTs	4.51	DU145_cells, LNCaP_cells, EB_cells
129126	H88486	Hs.108806	ESTs	4.45	LNCaP_cells, Caco2, EB_cells
135232	AA342457	Hs.96800	ESTs; Moderately similar to !!!! ALU SUB	4.43	LNCaP_cells, DU145_cells, OVCAR_cells
124847	R60044	Hs.106706	ESTs; Highly similar to BETA-CATENIN [H.	4.42	OVCAR_cells, CALU6_cells, CALU6_cells
110349	H40988		ESTs; Weakly similar to !!!! ALU SUBFAMI	4.39	DU145_cells, OVCAR_cells, LNCaP_cells
134402	U25165	Hs.82712	fragile X mental retardation; autosomal	4.38	HS578T_cells, OVCAR_cells, DU145_cells
115494	AA290603	Hs.256517	ESTs	4.36	Lu_SC_H345, OVCAR_cells, PC3_cells
119174	R71234		yi54c08.s1 Soares placenta Nb2HP H sapie transcript, (rRNA); gb:S41458 ROD CGMP-BETA-SUBUNIT (HUMAN);contain	4.33	DU145_cells, OVCAR_cells, LNCaP_cells
121943	AA429265	Hs.126759	ESTs	4.3	EB_cells, HT29_cells, Lu_SC_H69
110856	N33063	Hs.23291	ESTs; Weakly similar to S164 [H.sapiens]	4.28	OVCAR_cells, EB_cells, Lu_SC_H69
102474	U49973		Human Tigger1 transposable element, comp	4.28	DU145_cells, LNCaP_cells, OVCAR_cells
123458	AA598963	Hs.112499	KIAA0612 protein	4.27	A549_cells, A549_cells, BT474_cells
116459	AA621399	Hs.64193	ESTs	4.22	Caco2, HS578T_cells, MB-MDA-435s
126301	N62371	Hs.100043	ESTs; Weakly similar to Similar to cutic	4.22	PC3_cells, DU145_cells, Lu_SC_H345
123461	AA598990	Hs.251119	EST	4.22	Lu_SC_H345, Lu_SC_H69, OVCAR_cells

130588	AA287735	Hs.16411	Human DNA seq from clone 1189B24 on chro MLRQ subunit (EC 1.6.5.3; EC 1.6.99.3; Tyrosine-protein Kinase FER (EC 2.7.1.1	4.2	EB_cells, LNCaP_cells, MCF7
125756	W25498	Hs.81634	ATP synthase; H+ transporting; mitochond	4.2	HMEC, EB_cells, DU145_cells
135009	AA040507	Hs.251865	ESTs	4.19	293T_cells, EB_cells, DU145_cells
107001	AA598589	Hs.24492	ESTs	4.18	293T_cells, DU145_cells, EB_cells
124896	R82063	Hs.101594	EST	4.16	OVCAR_cells, Lu_SC_H345, HMEC (total RNA)
119404	T92950		ye27c10.s1 Stratagene lung (#937210) H s	4.15	DU145_cells, PC3_cells, Fibroblasts 2
125090	T91518		ye20f05.s1 Stratagene lung (#937210) H s contains Alu repetitive element;contain	4.14	LNCaP_cells, DU145_cells, OVCAR_cells
117348	N24157	Hs.139615	ESTs	4.1	Lu_SC_H345, Lu_SC_H69, PRSC_log
111389	N95837	Hs.169111	ESTs; Weakly similar to L82A [D.melanoga	4.1	DU145_cells, MCF7, LNCaP_cells
134977	AA464698	Hs.19390	ESTs; Weakly similar to bullous pemphigo	4.09	OVCAR_cells, Fibroblasts 2, Lu_SC_H69
124696	R06273	Hs.186467	ESTs; Moderately similar to !!!! ALU SUB	4.09	OVCAR_cells, Lu_SC_H345, PRSC_con
124090	H09570	Hs.143032	ESTs; Weakly similar to neuronal thread	3.98	DU145_cells, OVCAR_cells, Lu_SC_H345
133992	R46354	Hs.169832	zinc finger protein 42 (myeloid-specific	3.98	HT29_cells, MB231_cells, BT474_cells
126009	H51652	Hs.242985	hemoglobin; gamma G	3.96	Lu_SC_H69, OVCAR_cells, EB_cells
114161	Z38904	Hs.22385	ESTs; Weakly similar to KIAA0970 protein	3.94	HS578T_cells, EB_cells, PRSC_con
109171	AA180356	Hs.73700	EST	3.94	293T_cells, MB-MDA-435s, A549_cells
122007	AA430629	Hs.98564	ESTs	3.93	PC3_cells, A549_cells, OVCAR_cells
131936	AA094865	Hs.179972	interferon; alpha-inducible protein (clo	3.9	CALU6_cells, EB_cells, Lu_SC_H69
128668	AA194849	Hs.103422	ESTs	3.9	Lu_AD_H23, EB_cells, Lu_SC_H69
124977	T33859	Hs.190452	KIAA0365 gene product	3.89	293T_cells, DU145_cells, EB_cells
107048	AA600012	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.89	PC3_cells, HS578T_cells, DU145_cells
105358	AA236034	Hs.25362	ESTs	3.89	Caco2, EB_cells, CALU6_cells
135106	AA599037	Hs.9456	SWI/SNF related; matrix assocd; actin de	3.86	EB_cells, LNCaP_cells, Caco2
106686	AA463215	Hs.29896	ESTs; Weakly similar to proline-rich pro	3.85	OVCAR_cells, DU145_cells, EB_cells
132093	AA400091	Hs.39421	ESTs	3.85	OVCAR_cells, OVCAR_cells, LNCaP_cells
128651	AA446990	Hs.103135	ESTs	3.84	EB_cells, LNCaP_cells, OVCAR_cells
102459	U48936		Human amiloride-sensitive epithelial sod	3.84	HT29_cells, BT474_cells, Lu_SC_H69
113732	T98288	Hs.193295	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.82	DU145_cells, OVCAR_cells, LNCaP_cells
116000	AA448710	Hs.41327	ESTs	3.82	DU145_cells, MB-MDA-453, Lu_SC_H69
120748	AA303153	Hs.237994	EST; Weakly similar to !!!! ALU SUBFAMIL	3.82	DU145_cells, DU145_cells, Lu_SC_H345
116318	AA490830	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	3.79	MB-MDA-453, CALU6_cells, EB_cells
114366	Z41747	Hs.469	succinate dehydrogenase complex; subunit	3.78	DU145_cells, Fibroblasts 2, Caco2
107248	D59894	Hs.34782	ESTs	3.75	LNCaP_cells, DU145_cells, EB_cells
132713	AA286906	Hs.55335	ESTs	3.75	OVCAR_cells, EB_cells, Lu_SC_H345
102222	U24683	Hs.159386	Immunoglobulin heavy variable 4-4	3.73	EB_cells, OVCAR_cells, 293T_cells
108201	AA057518	Hs.63394	ESTs	3.72	293T_cells, DU145_cells, EB_cells
119940	W86779	Hs.171807	DKFZP586B0319 protein	3.71	EB_cells, Caco2, DU145_cells
106508	AA452590	Hs.30348	ESTs	3.67	EB_cells, LNCaP_cells, 293T_cells
114360	Z41592	Hs.22129	hypothetical protein	3.67	HT29_cells, Lu_SQ_H520, Lu_SQ_H520
100991	J03764	Hs.82085	plasminogen activator inhibitor; type I	3.67	Fibroblasts 2, HS578T_cells, MB231_cells
107580	AA002091	Hs.175476	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.67	OVCAR_cells, LNCaP_cells, Lu_SC_H345
111685	R21408	Hs.106095	ESTs	3.66	OVCAR_cells, A549_cells, 293T_cells
128336	AI242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.66	Lu_SC_H345, Caco2, OVCAR_cells
130868	AA004900	Hs.171917	ESTs; Weakly smlr to smlr to glycerophos	3.61	EB_cells, HS578T_cells, LNCaP_cells
116802	H44061	Hs.194026	ESTs	3.6	Lu_SC_H345, OVCAR_cells, DU145_cells
130753	Z46632	Hs.189	phosphodiesterase 4C; cAMP-specific (dun	3.6	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
123074	AA485117	Hs.105653	ESTs	3.6	293T_cells, MB231_cells, Fibroblasts 2
114317	Z41038	Hs.469	succinate dehydrogenase complex; subunit	3.6	DU145_cells, HS578T_cells, CALU6_cells
134194	AA233231	Hs.79828	ESTs	3.59	BT474_cells, MB231_cells, HT29_cells
127752	AA808388	Hs.211167	ESTs	3.59	Lu_SQ_H520, MB-MDA-435s, DU145_cells
123526	AA608657		ESTs; Moderately similar to !!!! ALU SUB	3.59	DU145_cells, OVCAR_cells, LNCaP_cells
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	3.58	Lu_SC_H345, OVCAR_cells, PRSC_con
105941	AA404427	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.58	PC3_cells, DU145_cells, HS578T_cells
124694	R06108	Hs.135258	ESTs	3.56	Lu_AD_H23, Lu_SQ_H520, Lu_AD_358
105656	AA282571	Hs.203772	FSHD region gene 1	3.56	DU145_cells, EB_cells, A549_cells
111168	N66951	Hs.238380	Human endogenous retroviral protease mRN	3.55	PC3_cells, EB_cells, MB231_cells
133254	AA156670	Hs.180780	H sapiens agrin precursor mRNA; partial	3.54	OVCAR_cells, DU145_cells, PC3_cells
132640	U33821		Tax1 (human T-cell leukemia virus type I	3.53	MB231_cells, CALU6_cells, BT474_cells
116562	D25807	Hs.90145	ESTs	3.52	MB231_cells, BT474_cells, Lu_SC_H345
126045	N80361	Hs.14248	ESTs	3.51	DU145_cells, Lu_SC_H345, OVCAR_cells
122878	AA465341	Hs.99640	ESTs	3.47	HT29_cells, OVCAR_cells, HMEC
105220	AA210695	Hs.17212	ESTs	3.47	MB-MDA-435s, HT29_cells, HT29_cells
127001	AA731636	Hs.59319	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.45	LNCaP_cells, DU145_cells, Lu_SC_H345
112693	R88741	Hs.91065	ESTs; Moderately similar to proliferatio	3.44	EB_cells, LNCaP_cells, DU145_cells
104935	AA063280	Hs.35552	ESTs	3.43	LNCaP_cells, CALU6_cells, 293T_cells
128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (niphedi	3.41	HT29_cells, A549_cells, Fibroblasts 2
131996	D86956	Hs.36927	heat shock 105kD	3.4	EB_cells, PC3_cells, Lu_SC_H345
119229	T03229		H sapiens (clone 104) retinoblastoma 1 g	3.4	DU145_cells, Lu_SC_H345, EB_cells
128046	AA873285	Hs.137947	ESTs	3.39	EB_cells, LNCaP_cells, DU145_cells
105175	AA186804	Hs.25740	ESTs; Weakly similar to ubiquitous TPR m	3.39	PC3_cells, MCF7, DU145_cells
132349	Y00705	Hs.181286	serine protease inhibitor; Kazal type 1	3.38	Caco2, EB_cells, Lu_SC_H69
101559	M32053		Human H19 RNA gene, complete cds	3.37	Lu_SC_H69, MCF7, OVCAR_cells
116389	AA599011		troponin T1; skeletal; slow	3.36	DU145_cells, LNCaP_cells, OVCAR_cells

130641	AA182001	Hs.17155	ESTs	3.36	DU145_cells, MB-MDA-435s, HS578T_cells
109362	AA214615	Hs.194348	ESTs	3.33	HT29_cells, Fibroblasts 2, BT474_cells
106278	AA432292	Hs.23388	ESTs; Moderately similar to !!!! ALU SUB	3.33	EB_cells, Fibroblasts 2, BT474_cells
127241	AA321849	Hs.248340	H sapiens mRNA; cDNA DKFZp564J2116 (from	3.32	LNCaP_cells, DU145_cells, EB_cells
133339	N64588	Hs.71252	ESTs	3.32	DU145_cells, EB_cells, Caco2
113260	T64896	Hs.237992	ESTs	3.32	Lu_SC_H345, LNCaP_cells, Lu_SC_H69
133349	N75791	Hs.7153	L-3-hydroxyacyl-Coenzyme A dehydrogenase	3.31	Caco2, EB_cells, OVCAR_cells
107149	AA621159	Hs.23284	ESTs	3.29	HS578T_cells, DU145_cells, PRSC_con
133195	AA350744	Hs.181409	KIAA1007 protein	3.29	EB_cells, Lu_AD_H23, Lu_AD_358
111302	N73838	Hs.15049	ESTs	3.29	DU145_cells, EB_cells, HS578T_cells
106414	AA447971	Hs.28827	ESTs	3.28	A549_cells, OVCAR_cells, PC3_cells
121768	AA421561	Hs.251664	insulin-like growth factor 2 (somatomedi	3.28	Caco2, PRSC_con, PRSC_log
117176	H98670	Hs.49753	ESTs; Weakly similar to hypothetical pro	3.28	PRSC_log, CALU6_cells, OVCAR_cells
131320	AA171948	Hs.145696	splicing factor (CC1.3)	3.28	EB_cells, LNCaP_cells, DU145_cells
100700	HG3227-H		Guanine Nucleotide-Binding Protein Hsr1	3.27	EB_cells, RPWE_2, Lu_AD_H23
134275	AA132328	Hs.3688	acid-inducible phosphoprotein	3.26	EB_cells, DU145_cells, LNCaP_cells
117667	N39214	Hs.44708	Ser-Thr protein kinase related to the my	3.26	LNCaP_cells, DU145_cells, MB-MDA-453
124889	R78604	Hs.101570	ESTs	3.25	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
126631	W95117	Hs.193337	ESTs	3.25	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
105643	AA282069	Hs.173802	KIAA0603 gene product	3.24	Caco2, EB_cells, 293T_cells
132718	AA056731	Hs.554	Sjogren syndrome antigen A2 (60kD; ribon	3.24	CALU6_cells, OVCAR_cells, A549_cells
116417	AA609309	Hs.239302	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.24	A549_cells, CALU6_cells, 293T_cells
108039	AA041341	Hs.46670	ESTs	3.24	293T_cells, EB_cells, Caco2
114116	Z38496	Hs.103283	KIAA0594 protein	3.23	DU145_cells, OVCAR_cells, EB_cells
124514	N58045	Hs.142737	ESTs	3.22	EB_cells, Caco2, Lu_SQ_H520
110802	N26651	Hs.252748	ESTs	3.22	LNCaP_cells, MB-MDA-435s, MB-MDA-453
106920	AA490899	Hs.24462	ESTs	3.22	DU145_cells, EB_cells, OVCAR_cells
123523	AA608588	Hs.193634	ESTs	3.21	DU145_cells, LNCaP_cells, OVCAR_cells
131564	AA491465	Hs.28792	ESTs	3.2	HS578T_cells, HMEC (total RNA), HMEC
119423	T99544	Hs.173734	ESTs; Weakly similar to !!!! ALU CLASS B	3.2	EB_cells, DU145_cells, Caco2
128736	F03934	Hs.104607	ESTs	3.19	PC3_cells, Lu_SQ_H520, Lu_SC_H69
101511	M27826	Hs.238380	Human endogenous retroviral protease mRN	3.18	PC3_cells, DU145_cells, Lu_SQ_H520
114509	AA043551	Hs.95249	ESTs	3.18	EB_cells, Lu_SC_H345, DU145_cells
124196	H52617	Hs.144167	ESTs	3.17	BT474_cells, MB231_cells, HMEC
129095	L12350	Hs.108623	thrombospondin 2	3.17	Fibroblasts 2, PRSC_con, PRSC_log
116457	AA621367	Hs.119683	ESTs	3.17	293T_cells, Lu_SC_H345, CALU6_cells
117040	H89112		yw25e5.s1 Morton Fetal Cochlea H sapiens	3.16	OVCAR_cells, 293T_cells, EB_cells
129112	N32521	Hs.108738	ESTs	3.16	EB_cells, Fibroblasts 2, MB231_cells
130418	J03242	Hs.251664	insulin-like growth factor 2 (somatomedi	3.16	Caco2, PRSC_con, PRSC_log
131199	R80048	Hs.234433	ESTs; Weakly similar to transporter prot	3.15	PC3_cells, EB_cells, OVCAR_cells
110357	H41529	Hs.33549	ESTs; Highly similar to sulfonylurea rec	3.15	Lu_SC_H345, PRSC_con, Lu_AD_H23
130068	AA608903	Hs.106220	KIAA0336 gene product	3.15	OVCAR_cells, CALU6_cells, HS578T_cells
127423	T47546	Hs.119252	tumor protein; translationally-controlle	3.15	EB_cells, PRSC_con, LNCaP_cells
105028	AA126719	Hs.25282	ESTs	3.14	LNCaP_cells, PC3_cells, EB_cells
102349	U37547	Hs.75263	apoptosis inhibitor 1	3.14	DU145_cells, HS578T_cells, LNCaP_cells
105126	AA157814	Hs.36288	ESTs	3.13	EB_cells, HS578T_cells, LNCaP_cells
115465	AA286941	Hs.43691	ESTs	3.12	EB_cells, DU145_cells, 293T_cells
133246	AA086452	Hs.68731	triadin	3.12	Lu_SQ_H520, Lu_AD_H23, PRSC_log
122698	AA456112	Hs.99410	ESTs	3.12	DU145_cells, OVCAR_cells, A549_cells
123553	AA608841	Hs.111977	ESTs	3.12	EB_cells, Caco2, DU145_cells
133437	R57419	Hs.7370	ESTs	3.11	HS578T_cells, 293T_cells, Caco2
104956	AA074880	Hs.120975	ESTs; Weakly similar to hypothetical pro	3.11	OVCAR_cells, Fibroblasts 2, Caco2
116314	AA490588	Hs.43118	ESTs	3.11	EB_cells, MB-MDA-435s, HT29_cells
120562	AA280036	Hs.173912	eukaryotic translation initiation factor	3.11	LNCaP_cells, DU145_cells, EB_cells
108770	AA127845	Hs.71027	EST	3.11	Lu_LC_H460, Lu_SC_H345, Lu_AD_358
129791	F02778	Hs.173887	KIAA0876 protein	3.1	Lu_SC_H345, Lu_SC_H69, PRSC_log
115783	AA424487	Hs.72289	ESTs; Weakly similar to LIV-1 protein [H	3.09	Lu_AD_358, EB_cells, PC3_cells
107630	AA007218	Hs.60178	ESTs	3.07	Lu_SC_H345, CALU6_cells, Lu_SC_H69
124339	H99093	Hs.6179	H sapiens mRNA; cDNA DKFZp586K2322 (from	3.07	293T_cells, MB-MDA-453, Caco2
122314	AA442257	Hs.192076	ESTs	3.07	293T_cells, LNCaP_cells, PC3_cells
104589	R79299	Hs.241160	ESTs; Moderately similar to !!!! ALU SUB	3.07	293T_cells, DU145_cells, EB_cells
115687	AA410508	Hs.183765	ESTs; Moderately smlr to ORF derived frm	3.06	Caco2, EB_cells, MB231_cells
123796	AA620390	Hs.247444	ESTs	3.06	Lu_SC_H345, LNCaP_cells, DU145_cells
106483	AA451676	Hs.30299	IGF-II mRNA-binding protein 2	3.06	OVCAR_cells, HMEC (total RNA), HMEC
133318	AA256168	Hs.70838	ESTs	3.05	OVCAR_cells, LNCaP_cells, 293T_cells
117244	N20979	Hs.1757	L1 cell adhesion molecule (hydrocephalus thumbs) syndrome; spastic paraplegia 1)	3.05	MB231_cells, MCF7, CALU6_cells
130797	AA430050	Hs.180948	KIAA0729 protein	3.05	EB_cells, DU145_cells, DU145_cells
128959	D79791	Hs.107381	ESTs; Weakly similar to F38A5.1 [C.elega	3.05	LNCaP_cells, HS578T_cells, Lu_SQ_H520
120481	AA252703	Hs.191754	ESTs	3.04	EB_cells, Fibroblasts 2, PRSC_con
126649	AA856990	Hs.125058	ESTs	3.03	OVCAR_cells, LNCaP_cells, 293T_cells
106970	AA504835	Hs.24252	ESTs	3.03	EB_cells, OVCAR_cells, 293T_cells
126488	N34935	Hs.25633	ESTs; Highly similar to ARF GTPase-activ	3.03	Lu_AD_358, MCF7, MB231_cells
119498	W37226	Hs.55573	ESTs	3.01	293T_cells, HS578T_cells, CALU6_cells
129967	H99653	Hs.138618	ESTs	3.01	Lu_SC_H345, Lu_SC_H69, PRSC_log
130698	AA037357	Hs.188212	ESTs	3.01	OVCAR_cells, LNCaP_cells, DU145_cells

111018	N54067	Hs.3628	mitogen-activated protein kinase kinase	3.01	PC3_cells, Caco2, Fibroblasts 2
123196	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	3	Lu_SC_H345, BT474_cells, Lu_SC_H69
133229	AA203433	Hs.6834	KIAA1014 protein	3	OVCAR_cells, 293T_cells, EB_cells
130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	3	PRSC_con, EB_cells, DU145_cells
107881	AA025567	Hs.61273	H sapiens chromosome 19; cosmid R32611	3	Lu_SQ_H520, MCF7, Lu_AD_358
116589	D59570	Hs.17132	ESTs	3	EB_cells, A549_cells, HS578T_cells
105479	AA255546	Hs.23467	ESTs	2.99	Lu_SC_H345, PC3_cells, OVCAR_cells
115560	AA393812	Hs.50575	ESTs; Moderately similar to !!!! ALU SUB	2.99	EB_cells, Lu_SC_H69, Fibroblasts 2
130166	AA350690	Hs.151411	KIAA0916 protein	2.98	LNCaP_cells, EB_cells, 293T_cells
123355	AA504773	Hs.160657	ESTs	2.98	PRSC_con, PRSC_log, PRSC_log
109546	F01449	Hs.26954	ESTs	2.97	Lu_SC_H345, HT29_cells, BT474_cells
129001	AA448946	Hs.107812	ESTs; Weakly similar to proline-rich pro	2.97	EB_cells, Lu_AD_H23, Lu_AD_358
102259	U28369	Hs.82222	sema domain; immunoglobulin domain (Ig);	2.97	EB_cells, MB231_cells, OVCAR_cells
105583	AA278907	Hs.24549	ESTs	2.96	EB_cells, DU145_cells, 293T_cells
131859	M90657	Hs.3337	transmembrane 4 superfamily member 1	2.96	A549_cells, PC3_cells, DU145_cells
114533	AA053401	Hs.177526	ESTs	2.96	293T_cells, Lu_LC_H460, PC3_cells
110220	H23543	Hs.27090	ESTs	2.95	PRSC_log, Lu_SC_H345, MB231_cells
124917	R91241	Hs.75470	hypothetical protein; expressed in osteo	2.95	Lu_SC_H345, Lu_SC_H69, PRSC_log
127111	AA805726	Hs.220509	ESTs	2.94	HS578T_cells, 293T_cells, 293T_cells
134882	N73762	Hs.90638	ESTs	2.94	EB_cells, MB-MDA-453, Fibroblasts 2
121788	AA423968	Hs.178113	ESTs; Moderately similar to kinesin like	2.94	HT29_cells, CALU6_cells, HMEC
128530	AA504343	Hs.183475	H sapiens clone 25061 mRNA seq	2.94	DU145_cells, Lu_SC_H345, Caco2
128435	AI301201	Hs.147112	ESTs	2.93	EB_cells, Lu_SQ_H520, PRSC_con
113782	W15580	Hs.15342	phosphate cytidylyltransferase 1; cholin	2.93	EB_cells, Lu_AD_H23, PRSC_log
127569	AA588536	Hs.191783	ESTs	2.93	EB_cells, HS578T_cells, Lu_AD_358
109642	F04465	Hs.22394	ESTs; Weakly similar to weak similarity protein US)1 [C.elegans]	2.92	PC3_cells, EB_cells, OVCAR_cells
114615	AA083812	Hs.159456	DKFZP566F123 protein	2.92	A549_cells, HS578T_cells, PRSC_con
126808	AA086320		zn52d12.s1 Stratagene muscle 937209 H sa	2.92	Lu_SC_H69, Lu_SC_H345, EB_cells
113947	W84768	Hs.141742	ESTs	2.92	DU145_cells, Fibroblasts 2, MCF7
129455	W27301	Hs.187991	DKFZP564A122 protein	2.91	OVCAR_cells, DU145_cells, CALU6_cells
107772	AA018587	Hs.40515	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.91	OVCAR_cells, EB_cells, PC3_cells
127159	AA284097	Hs.237955	RAB7; member RAS oncogene family	2.91	293T_cells, OVCAR_cells, PC3_cells
124792	R44357	Hs.132784	ESTs; Weakly similar to cDNA EST EMBL:T0	2.91	DU145_cells, DU145_cells, CALU6_cells
109751	F10210	Hs.6679	H sapiens mRNA; cDNA DKFZp586A0424 (from	2.91	EB_cells, Lu_SC_H69, 293T_cells
128926	AA481403	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	2.9	CALU6_cells, EB_cells, OVCAR_cells
106637	AA459961	Hs.250824	ESTs	2.9	EB_cells, Caco2, MB-MDA-435s
132164	U84573	Hs.41270	procollagen-lysine; 2-oxoglutarate 5-dio	2.9	DU145_cells, HS578T_cells, A549_cells
128099	AA905327		ESTs	2.9	MCF7, HMEC (total RNA), 293T_cells
104818	AA034947	Hs.24831	ESTs	2.9	EB_cells, Lu_LC_H460, 293T_cells
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k -Coenzyme A hydratase (trifunctional pro	2.89	LNCaP_cells, DU145_cells, OVCAR_cells
116696	F09780	Hs.66124	EST	2.89	CALU6_cells, 293T_cells, 293T_cells
135204	AA421146	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	2.89	PC3_cells, EB_cells, LNCaP_cells
134946	AA406534	Hs.193053	ESTs; Weakly similar to hiwi [H.sapiens]	2.88	EB_cells, LNCaP_cells, Caco2
114975	AA250850	Hs.13944	adrenergic; beta; receptor kinase 2	2.88	EB_cells, EB_cells, EB_cells
113792	W35212	Hs.17691	ESTs; Weakly similar to env protein [H.s	2.88	MB-MDA-435s, Lu_SC_H69, CALU6_cells
102322	U34962	Hs.54473	cardiac-specific homeo box	2.88	293T_cells, HT29_cells, Lu_AD_H23
125642	AI096849	Hs.25274	ESTs; Moderately similar to putative sev	2.88	PC3_cells, CALU6_cells, 293T_cells
100288	D43951	Hs.153834	Human mRNA for KIAA0099 gene; complete c	2.88	293T_cells, LNCaP_cells, EB_cells
105878	AA400184	Hs.24656	KIAA0907 protein	2.88	OVCAR_cells, DU145_cells, 293T_cells
125262	W88755	Hs.108514	ESTs; Highly similar to Trio [H.sapiens]	2.88	DU145_cells, HS578T_cells, MB231_cells
114419	AA011448	Hs.106532	ESTs; Weakly similar to transposon LRE2	2.88	EB_cells, Lu_AD_H23, Fibroblasts 2
130639	D59711	Hs.17132	ESTs	2.87	EB_cells, A549_cells, OVCAR_cells
130972	AA370302	Hs.21739	H sapiens mRNA; cDNA DKFZp586I1518 (from	2.87	293T_cells, A549_cells, Lu_LC_H460
126906	H66949	Hs.168069	ESTs; Highly similar to CALCIUM-BINDING	2.87	Lu_SC_H345, Lu_SC_H69, LNCaP_cells
121807	AA424507	Hs.247478	H sapiens Mut S homolog 5 gene; partial 1C7; LST-1; lymphotoxin beta; tumor necr	2.87	Lu_SC_H69, HT29_cells, RPWE_2
105474	AA255440	Hs.219614	F-box protein FBL11	2.87	Lu_AD_H23, Caco2, EB_cells
122348	AA443695	Hs.231476	ESTs	2.87	HT29_cells, Lu_SC_H69, BT474_cells
116368	AA521186	Hs.94217	ESTs	2.86	MB-MDA-453, OVCAR_cells, Lu_SC_H69
135143	AA102644	Hs.69559	KIAA1096 protein	2.86	PC3_cells, EB_cells, 293T_cells
106711	AA464741	Hs.143187	Human DNA from chromosome 19-specific co	2.86	EB_cells, Lu_AD_H23, Lu_LC_H460
128583	L32832	Hs.101842	AT-binding transcription factor 1	2.85	LNCaP_cells, Caco2, EB_cells
132139	AA213410	Hs.111554	ADP-ribosylation factor-like 7	2.85	A549_cells, HS578T_cells, Caco2
114484	AA034378	Hs.252351	HERV-H LTR-associating 2	2.85	PC3_cells, Lu_SQ_H520, MB231_cells
124620	N74051	Hs.194092	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.85	Lu_SC_H345, MB231_cells, Fibroblasts 2
100403	D85527		H sapiens mRNA for LIM domain, partial c	2.84	Lu_AD_358, Lu_AD_358, MB231_cells
129795	AA448627	Hs.125163	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.84	Lu_SC_H345, OVCAR_cells, PC3_cells
128258	T70214	Hs.183548	ESTs	2.84	DU145_cells, DU145_cells, OVCAR_cells
102662	U70321	Hs.130227	tumor necrosis factor receptor superfami	2.84	EB_cells, Lu_AD_H23, Fibroblasts 2
132232	AA252030	Hs.42640	ESTs	2.84	EB_cells, OVCAR_cells, Lu_SC_H345
106111	AA421638	Hs.6451	ESTs	2.83	EB_cells, Lu_LC_H460, OVCAR_cells
123963	C13961	Hs.210115	EST	2.83	DU145_cells, LNCaP_cells, Lu_SC_H345
122783	AA459895	Hs.98988	ESTs	2.83	EB_cells, MCF7, Lu_SC_H69
112788	R96586	Hs.163630	ESTs	2.82	DU145_cells, Lu_SC_H345, EB_cells

120823	AA347546	Hs.185780	ESTs	2.82	HT29_cells, HMEC (total RNA), BT474_cells
100378	D80009	Hs.10848	KIAA0187 gene product	2.82	Caco2, PC3_cells, OVCAR_cells
114677	AA114163	Hs.188877	ESTs	2.81	DU145_cells, MCF7, EB_cells
108085	AA045602	Hs.62863	ESTs; Moderately similar to serine/threo	2.81	EB_cells, Lu_AD_H23, HT29_cells
104938	AA064627	Hs.18341	ESTs; Highly similar to CGI-72 protein [	2.81	PC3_cells, HS578T_cells, OVCAR_cells
128743	AA237013	Hs.2730	heterogeneous nuclear ribonucleoprotein	2.8	OVCAR_cells, LNCaP_cells, Caco2
124314	H94877	Hs.215766	GTP-binding protein	2.8	LNCaP_cells, DU145_cells, Caco2
134227	D79986	Hs.80338	KIAA0164 gene product	2.8	LNCaP_cells, A549_cells, EB_cells
122922	AA476268		zw44h1.s1 Soares_total_fetus_Nb2HF8_9w H contains Alu repetitive element;contain	2.79	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
126096	H42968	Hs.155606	paired mesoderm homeo box 1	2.78	Lu_AD_H23, Lu_SC_H69, Lu_LC_H460
129295	AA424782	Hs.110121	SEC7 homolog	2.78	Lu_AD_H23, EB_cells, Lu_SC_H345
116155	AA460957	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.78	EB_cells, OVCAR_cells, 293T_cells
105911	AA401809	Hs.189910	ESTs	2.77	293T_cells, HS578T_cells, DU145_cells
119232	T03475	Hs.258624	EST	2.77	EB_cells, Lu_AD_H23, Lu_AD_358
131168	AA482007	Hs.23788	ESTs; Weakly similar to homology with is	2.77	EB_cells, Lu_LC_H460, MCF7
106048	AA416697	Hs.15330	ESTs	2.76	OVCAR_cells, Lu_SC_H345, 293T_cells
124352	N21626	Hs.102406	ESTs	2.76	MCF7, MB-MDA-453, CALU6_cells
129349	D86974	Hs.110613	KIAA0220 protein	2.76	DU145_cells, HT29_cells, Lu_SC_H69
106120	AA423808	Hs.8765	RNA helicase-related protein	2.76	OVCAR_cells, EB_cells, 293T_cells
100643	HG2755-H		T-Plastin	2.75	293T_cells, PC3_cells, HS578T_cells
128500	U60521	Hs.100641	caspase 9; apoptosis-related cysteine pr	2.75	Lu_AD_358, Lu_SC_H69, Lu_SC_H345
126090	R44789	Hs.119486	ESTs; Weakly similar to rostral cerebell	2.75	Lu_SC_H69, Lu_SC_H345, BT474_cells
127064	Z43709		HSC1JA091 normalized infant brain cDNA H	2.75	Caco2, A549_cells, HT29_cells
132989	AA480074	Hs.394	adrenomedullin	2.75	EB_cells, OVCAR_cells, DU145_cells
108888	AA135606	Hs.189384	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.75	OVCAR_cells, LNCaP_cells, DU145_cells
119579	W42429	Hs.150607	ESTs	2.74	293T_cells, DU145_cells, PC3_cells
100387	D83777	Hs.75137	KIAA0193 gene product	2.74	CALU6_cells, DU145_cells, Caco2
114744	AA135407	Hs.252351	HERV-H LTR-associating 2	2.74	PC3_cells, Lu_SQ_H520, RPWE_2
129092	AA011243	Hs.63525	poly(rC)-binding protein 2	2.74	EB_cells, MCF7, DU145_cells
125360	AA677978	Hs.189741	ESTs	2.74	Lu_AD_358, Lu_AD_358, PRSC_log
107874	AA025305	Hs.25218	ESTs; Weakly similar to reverse transcri	2.74	Lu_SC_H345, Lu_LC_H460, HT29_cells
114086	Z38266	Hs.12770	H sapiens PAC clone DJ0777O23 from 7p14-	2.74	EB_cells, LNCaP_cells, BT474_cells
116180	AA463902	Hs.94964	ESTs	2.73	Lu_SC_H69, PRSC_con, Lu_AD_H23
126027	M61982		ESTs	2.73	LNCaP_cells, DU145_cells, A549_cells
116339	AA496257	Hs.72165	ESTs; Weakly similar to R26984_1 [H.sapi	2.73	EB_cells, DU145_cells, OVCAR_cells
105387	AA236951	Hs.108636	chromosome 1 open reading frame 9	2.72	PC3_cells, EB_cells, Caco2
111359	N91273	Hs.27179	ESTs	2.72	EB_cells, LNCaP_cells, 293T_cells
106680	AA461458	Hs.24789	ESTs	2.72	PC3_cells, Lu_SC_H345, Caco2
118598	N69136	Hs.214343	ESTs	2.72	MB-MDA-453, 293T_cells, BT474_cells
107913	AA027161	Hs.59523	ESTs; Highly similar to G1 TO S PHASE TR	2.71	EB_cells, MCF7, Lu_SC_H345
134315	AA136269	Hs.81648	ESTs; Weakly similar to S164 [H.sapiens]	2.71	EB_cells, DU145_cells, HMEC
135233	AA127463	Hs.9683	protein-kinase; interferon-inducible dou	2.71	EB_cells, OVCAR_cells, Caco2
112932	T15470	Hs.189810	ESTs	2.7	293T_cells, Lu_AD_H23, PC3_cells
119053	R11501		yf28f1.s1 Soares fetal liver spleen 1NFL contains Alu repetitive element;, mRNA	2.7	Lu_SC_H345, Lu_SC_H69, DU145_cells
131206	AA044078	Hs.24210	ESTs	2.7	Caco2, Lu_SC_H345, HS578T_cells
126759	AA063642		ESTs; Highly similar to (defline not ava	2.7	LNCaP_cells, Lu_SC_H345, Lu_SC_H69
131060	AA160890	Hs.22564	myosin VI	2.7	LNCaP_cells, MCF7, HT29_cells
132135	N69101	Hs.40730	ESTs	2.7	EB_cells, 293T_cells, OVCAR_cells
120835	AA348446	Hs.96906	ESTs	2.7	Fibroblasts 2, CALU6_cells, RPWE_2
113815	W45311	Hs.14756	ESTs	2.7	EB_cells, PC3_cells, DU145_cells
133234	T90092	Hs.6853	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.69	Lu_SC_H345, OVCAR_cells, DU145_cells
126819	AA305536	Hs.161489	ESTs	2.69	EB_cells, DU145_cells, Caco2
125198	W69474	Hs.225550	ESTs	2.69	Lu_SC_H345, Lu_AD_H23, Lu_AD_H23
108394	AA075144		zm86f6.s1 Stratagene ovarian cancer (#93 gb:X1664 TRANSLATIONALLY CONTROLLED TUM	2.69	HMEC, HMEC (total RNA), Fibroblasts 2
134456	X59405	Hs.83532	membrane cofactor protein (CD46; trophob	2.69	EB_cells, LNCaP_cells, DU145_cells
111720	R23739	Hs.23585	KIAA1078 protein	2.68	PC3_cells, HMEC (total RNA), OVCAR_cells
114617	AA084148	Hs.110659	ESTs	2.68	DU145_cells, LNCaP_cells, OVCAR_cells
127787	AA731764		ESTs; Weakly similar to !!!! ALU CLASS C	2.68	HT29_cells, Lu_SC_H345, MB231_cells
101437	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.68	Caco2, Lu_LC_H460, Fibroblasts 2
133761	AA477223	Hs.75922	brain protein I3	2.68	EB_cells, Lu_AD_H23, Lu_SC_H345
105869	AA399574	Hs.19086	ESTs	2.68	PC3_cells, MCF7, MB231_cells
125191	W67257	Hs.138871	ESTs; Weakly similar to !!!! ALU CLASS B	2.68	OVCAR_cells, DU145_cells, LNCaP_cells
116238	AA479362	Hs.47144	DKFZP586N0819 protein	2.67	OVCAR_cells, DU145_cells, LNCaP_cells
124770	R40555	Hs.120429	ESTs	2.67	Lu_AD_H23, Lu_SC_H69, PRSC_con
101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium murine placental homolog)	2.67	A549_cells, MB231_cells, OVCAR_cells
130897	AA063428	Hs.21022	adaptor-related protein complex 3; beta	2.67	EB_cells, Lu_AD_H23, HMEC
133303	H61046	Hs.237352	EST	2.66	Lu_SC_H345, Lu_SC_H69, PRSC_con
124724	R12405	Hs.112423	H sapiens mRNA; cDNA DKFZp586I1420 (from	2.66	Lu_SC_H345, BT474_cells, OVCAR_cells
123697	AA609601	Hs.221224	ESTs	2.66	OVCAR_cells, 293T_cells, Lu_SC_H69
111548	R09170	Hs.258707	ESTs	2.66	293T_cells, CALU6_cells, A549_cells
107005	AA598679	Hs.194215	ESTs	2.66	Lu_SC_H345, OVCAR_cells, Lu_AD_H23
105569	AA278399	Hs.20596	ESTs	2.65	MCF7, HT29_cells, BT474_cells

132687	AB002301	Hs.54985	KIAA0303 protein	2.65	HMEC (total RNA), HMEC, LNCaP_cells
104105	AA422123	Hs.42457	ESTs	2.65	Lu_SC_H345, Lu_SC_H69, DU145_cells
121335	AA404418	Hs.144953	ESTs	2.65	EB_cells, Fibroblasts 2, DU145_cells
124853	R61693	Hs.172330	ESTs; Weakly similar to Wiskott-Aldrich	2.64	Lu_SC_H69, 293T_cells, EB_cells
124253	H69742	Hs.102201	ESTs	2.64	DU145_cells, OVCAR_cells, Lu_SC_H345
123044	AA481549	Hs.165694	ESTs	2.64	EB_cells, Lu_SC_H69, Lu_SC_H345
129535	AA608852	Hs.112603	EST	2.64	EB_cells, Lu_AD_H23, Fibroblasts 2
131397	AB002336	Hs.26395	erythrocyte membrane protein band 4.1-li	2.64	EB_cells, DU145_cells, Caco2
130175	X75593	Hs.151536	RAB13; member RAS oncogene family	2.64	Fibroblasts 2, PRSC_con, HS578T_cells
127507	AI188445	Hs.152618	ESTs	2.63	EB_cells, Lu_AD_H23, Lu_LC_H460
105377	AA236702	Hs.24371	ESTs	2.63	Caco2, EB_cells, CALU6_cells
114671	AA112679	Hs.252291	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.63	EB_cells, DU145_cells, Caco2
133726	W19983	Hs.75761	SFRS protein kinase 1	2.63	EB_cells, Lu_AD_H23, Lu_SC_H69
132380	H68018		yr76h05.r1 Soares fetal liver spleen 1NF IMAGE:211257 5', mRNA seq.	2.62	EB_cells, Lu_AD_H23, Lu_SC_H69
127986	AI370418	Hs.192050	ESTs; Weakly similar to !!!! ALU CLASS A	2.62	DU145_cells, OVCAR_cells, LNCaP_cells
116208	AA476333	Hs.42532	ESTs	2.61	DU145_cells, PRSC_con, Fibroblasts 2
130946	AA069456	Hs.21490	KIAA0438 gene product	2.6	LNCaP_cells, DU145_cells, HS578T_cells
106687	AA463234	Hs.119387	KIAA0792 gene product	2.59	EB_cells, MB-MDA-453, Caco2
101551	M31606	Hs.196177	phosphorylase kinase; gamma 2 (testis)	2.59	LNCaP_cells, EB_cells, MB-MDA-453
114479	AA032084	Hs.124841	ESTs; Moderately similar to transformati	2.59	DU145_cells, Caco2, OVCAR_cells
111863	R37495	Hs.23578	ESTs	2.59	HT29_cells, MB231_cells, Lu_SQ_H520
129018	AA029973	Hs.107979	small membrane protein 1	2.59	A549_cells, EB_cells, HS578T_cells
107058	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.58	DU145_cells, Lu_SC_H345, EB_cells
126175	AA056181	Hs.17311	DKFZP434N161 protein	2.58	Lu_SC_H345, DU145_cells, LNCaP_cells
131979	D52154	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.58	DU145_cells, PC3_cells, A549_cells
126122	H80181		ESTs	2.58	DU145_cells, OVCAR_cells, LNCaP_cells
106961	AA504110	Hs.18063	ESTs	2.58	HMEC, DU145_cells, DU145_cells
114730	AA133527	Hs.126925	ESTs; Weakly similar to The KIAA0138 gen	2.58	DU145_cells, LNCaP_cells, MCF7
117342	N24020	Hs.132913	ESTs	2.58	HS578T_cells, DU145_cells, LNCaP_cells
131622	AA424813	Hs.29692	ESTs	2.57	PRSC_con, PRSC_log, HS578T_cells
104904	AA055560	Hs.13179	ESTs; Moderately similar to !!!! ALU SUB	2.57	Lu_SC_H345, Lu_SC_H69, BT474_cells
117359	N24848	Hs.114062	ESTs; Weakly similar to T15B7.2 [C.elega	2.57	HS578T_cells, PRSC_con, EB_cells
123331	AA497013	Hs.188740	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.57	Lu_SC_H69, Caco2, PRSC_con
125324	R07785		yf15c06.r1 Soares fetal liver spleen 1NF contains Alu repetitive element;contain	2.57	EB_cells, Lu_AD_H23, Fibroblasts 2
129813	T33462	Hs.12600	ESTs	2.57	Lu_SC_H345, 293T_cells, Lu_SC_H69
100265	D38521	Hs.75935	KIAA0077 protein	2.57	EB_cells, LNCaP_cells, PC3_cells
134890	T40902	Hs.90786	ATP-binding cassette; sub-family C (CFTR	2.57	A549_cells, DU145_cells, EB_cells
133582	AA421874	Hs.75087	Fas-activated serine/threonine kinase	2.56	EB_cells, Lu_AD_H23, Lu_AD_358
135011	H73161	Hs.92991	ESTs; Weakly similar to C13F10.4 [C.eleg	2.56	EB_cells, LNCaP_cells, MB-MDA-453
107226	D58185	Hs.21945	ESTs	2.56	Lu_SC_H345, Lu_SC_H69, HMEC (total RNA)
126042	H62441	Hs.157082	H sapiens PAC clone DJ0988G15 from 7q33-	2.56	HMEC (total RNA), HMEC, RPWE_2
114472	AA028924	Hs.177407	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.56	Lu_SC_H345, Lu_SC_H69, DU145_cells
126291	N42090		yy05b07.r1 Soares melanocyte 2NbHM H sap	2.56	HMEC, HMEC (total RNA), PC3_cells
113349	T79021	Hs.14438	ESTs; Moderately similar to histamine N-	2.56	HT29_cells, PRSC_log, Lu_SC_H345
105769	AA347485	Hs.25477	ESTs; Moderately similar to rig-1 protei	2.56	Lu_AD_H23, RPWE_2, Lu_SQ_H520
110918	N46423	Hs.24283	ESTs	2.56	EB_cells, CALU6_cells, DU145_cells
117170	H98153	Hs.42500	ADP-ribosylation factor-like 5	2.56	OVCAR_cells, EB_cells, LNCaP_cells
105159	AA173981	Hs.30490	CD2-associated protein	2.55	LNCaP_cells, EB_cells, DU145_cells
105726	AA292328	Hs.9754	activating transcription factor 5	2.55	MCF7, EB_cells, MB-MDA-453
132079	H67964	Hs.38694	ESTs	2.55	EB_cells, DU145_cells, HS578T_cells
131813	X51757	Hs.3268	heat shock 70kD protein 6 (HSP70B')	2.55	Lu_AD_H23, MB231_cells, Fibroblasts 2
133538	L14837	Hs.74614	tight junction protein 1 (zona occludens	2.54	DU145_cells, Caco2, A549_cells
124981	T40849	Hs.114034	maternal G10 transcript	2.54	EB_cells, Caco2, LNCaP_cells
122028	AA431306	Hs.98722	ESTs	2.54	Fibroblasts 2, BT474_cells, HMEC (total RNA)
122487	AA448332	Hs.80598	transcription elongation factor A (SII);	2.54	Lu_SC_H345, MCF7, MB-MDA-453
119315	T41152	Hs.90485	ESTs	2.54	Lu_SC_H345, MB-MDA-435s, PRSC_con
107957	AA031948	Hs.57548	ESTs	2.54	A549_cells, RPWE_2, DU145_cells
122457	AA447780	Hs.96418	ESTs	2.54	DU145_cells, EB_cells, A549_cells
103572	Z25749	Hs.75538	ribosomal protein S7	2.54	EB_cells, CALU6_cells, DU145_cells
124395	N29963	Hs.193977	ESTs	2.54	HMEC (total RNA), HMEC, RPWE_2
116024	AA451748	Hs.83883	Human DNA seq from clone 718J7 on chromo phosphoenolpyruvate carboxykinase 1; ES	2.53	LNCaP_cells, RPWE_2, MB-MDA-453
134361	D43682	Hs.82208	acyl-Coenzyme A dehydrogenase; very long	2.53	LNCaP_cells, CALU6_cells, DU145_cells
130420	U60975		Human hybrid receptor gp25 precursor mRN	2.53	EB_cells, HMEC (total RNA), Caco2
100336	D63478	Hs.8127	KIAA0144 gene product	2.53	BT474_cells, HT29_cells, Lu_AD_358
105519	AA258063	Hs.23438	ESTs	2.53	EB_cells, Caco2, MB-MDA-435s
124684	R02401	Hs.221078	ESTs	2.53	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
105852	AA398933	Hs.172613	solute carrier family 12 (potassium/chlo	2.52	LNCaP_cells, DU145_cells, EB_cells
105012	AA116036	Hs.9329	chromosome 20 open reading frame 1	2.52	CALU6_cells, Caco2, DU145_cells
126534	W39128	Hs.247901	Human DNA seq from clone 8B1 on chromoso -CELL MEMBRANE GLYCOPROTEIN PC-1; the ge	2.52	BT474_cells, LNCaP_cells, Lu_AD_H23
135334	AA053134	Hs.241558	ariadne-2 (D. melanogaster) homolog (all	2.52	293T_cells, CALU6_cells, DU145_cells
128538	R44214	Hs.101189	ESTs	2.52	EB_cells, Lu_AD_H23, Lu_SC_H345
109865	H02566	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.52	DU145_cells, LNCaP_cells, OVCAR_cells

118579	N68905		small inducible cytokine A5 (RANTES)	2.51	Lu_SC_H345, LNCaP_cells, Lu_SC_H69
117590	N34904		ESTs; Moderately similar to !!!! ALU SUB	2.51	Lu_SC_H345, DU145_cells, Lu_SC_H69
104340	F15201		ESTs	2.51	Lu_SC_H345, PRSC_con, PRSC_log
122455	AA447744	Hs.99141	EST	2.51	Caco2, Lu_SC_H69, 293T_cells
109339	AA211901	Hs.86430	ESTs	2.51	EB_cells, DU145_cells, CALU6_cells
123258	AA490929	Hs.105274	ESTs	2.51	EB_cells, Lu_AD_H23, Lu_SC_H69
118467	N66763	Hs.43080	ESTs	2.51	CALU6_cells, HS578T_cells, OVCAR_cells
106044	AA416546	Hs.149436	kinesin family member 5B	2.51	EB_cells, Caco2, DU145_cells
107480	W58057	Hs.74304	periplakin	2.5	Caco2, OVCAR_cells, HMEC (total RNA)
111760	R26892	Hs.221434	ESTs	2.5	Lu_AD_H23, EB_cells, Lu_AD_358
132474	N68018	Hs.180930	TBP-associated factor 172	2.5	LNCaP_cells, EB_cells, DU145_cells
103423	X97249	Hs.123122	FSH primary response (LRPR1; rat) homolo	2.5	HS578T_cells, Lu_SC_H345, PC3_cells
123488	AA599708	Hs.187764	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.49	OVCAR_cells, Lu_SC_H345, DU145_cells
100475	D90276	Hs.12	carcinoembryonic antigen-related cell ad	2.49	MB-MDA-453, 293T_cells, CALU6_cells
112003	R42547	Hs.172551	ESTs	2.49	EB_cells, Lu_AD_H23, Lu_SC_H345
114315	Z41027	Hs.26297	ESTs	2.49	Lu_SC_H69, OVCAR_cells, Lu_AD_H23
105291	AA233311	Hs.28752	ESTs	2.49	EB_cells, CALU6_cells, DU145_cells
135354	AA188934	Hs.99367	ESTs	2.49	MB-MDA-453, Lu_SC_H69, 293T_cells
107521	X78262		H.sapiens mRNA for TRE5	2.49	Lu_SC_H345, Lu_SC_H69, PRSC_con
108373	AA074393	Hs.61950	ESTs; Weakly similar to nuclear protein	2.49	MCF7, MB-MDA-453, Lu_SC_H345
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	2.48	DU145_cells, Lu_SC_H345, Lu_SC_H345
110386	H45516	Hs.33268	ESTs	2.48	PC3_cells, OVCAR_cells, Lu_SQ_H520
129658	M22348	Hs.131255	ubiquinol-cytochrome c reductase binding	2.48	LNCaP_cells, CALU6_cells, PC3_cells
134283	H12661	Hs.8107	H sapiens mRNA; cDNA DKFZp586B0918 (from	2.48	HMEC (total RNA), HS578T_cells, HMEC
101844	M93425	Hs.62	protein tyrosine phosphatase; non-recept	2.48	DU145_cells, EB_cells, CALU6_cells
133461	M33318	Hs.183584	cytochrome P450; subfamily IIA (phenobar	2.48	EB_cells, Lu_AD_H23, Lu_AD_358
103545	Z14000	Hs.35384	ring finger protein 1	2.47	HT29_cells, Lu_SQ_H520, BT474_cells
128440	N76763		ESTs	2.47	EB_cells, Lu_AD_H23, Lu_AD_358
134992	H05625	Hs.92414	ESTs	2.47	Lu_SC_H345, CALU6_cells, Lu_SC_H69
116295	AA489016	Hs.91216	ESTs; Highly similar to partial CDS; hum	2.47	MB-MDA-453, 293T_cells, MB-MDA-435s
107004	AA598675	Hs.239475	ESTs	2.47	LNCaP_cells, Caco2, OVCAR_cells
132137	AA282312	Hs.4076	CTD (carboxy-terminal domain; RNA polyme	2.46	Lu_SC_H69, HMEC, EB_cells
126390	W28286	Hs.100090	tetraspan 3	2.46	EB_cells, DU145_cells, LNCaP_cells
113050	T26366	Hs.22711	EST; Weakly similar to 60S RIBOSOMAL PRO	2.46	Lu_LC_H460, EB_cells, Lu_AD_358
101667	M60858	Hs.79110	nucleolin	2.46	PC3_cells, 293T_cells, A549_cells
108569	AA085398		zn7e3.s1 Stratagene hNT neuron (#937233) IMAGE:546748 3', mRNA seq	2.45	HT29_cells, BT474_cells, Lu_SQ_H520
117186	H98988	Hs.42612	ESTs	2.45	EB_cells, Lu_AD_H23, Lu_AD_358
129091	AA044622	Hs.183755	Human Chromosome 16 BAC clone CIT987SK-A	2.45	EB_cells, Lu_AD_H23, Lu_AD_H23
128468	T23625	Hs.258674	EST	2.45	Lu_AD_H23, EB_cells, Lu_SC_H69
117498	N31726	Hs.44268	ESTs; Highly similar to myelin gene expr	2.45	Lu_SC_H69, DU145_cells, OVCAR_cells
105407	AA243478	Hs.5206	ESTs	2.45	EB_cells, 293T_cells, PC3_cells
128941	R55763	Hs.107287	ESTs	2.44	EB_cells, LNCaP_cells, A549_cells
116486	C14128	Hs.251980	EST	2.44	MB-MDA-435s, HS578T_cells, 293T_cells
134869	T35288	Hs.90421	ESTs; Moderately similar to !!!! ALU SUB	2.44	EB_cells, Lu_AD_H23, Lu_AD_358
130664	R09049	Hs.17625	ESTs	2.44	PC3_cells, EB_cells, A549_cells
107985	AA035638	Hs.71968	H sapiens mRNA; cDNA DKFZp564F053 (from	2.44	PRSC_con, PRSC_log, Caco2
110300	H37820	Hs.124147	ESTs	2.44	MB-MDA-453, Caco2, OVCAR_cells
113471	T87174	Hs.16341	ESTs; Moderately similar to !!!! ALU SUB	2.44	Caco2, OVCAR_cells, LNCaP_cells
131474	U28749	Hs.2726	high-mobility group (nonhistone chromoso	2.44	CALU6_cells, OVCAR_cells, 293T_cells
120791	AA342802	Hs.194031	ESTs	2.44	Lu_AD_H23, Lu_SQ_H520, PRSC_con
133733	AA416973	Hs.75798	Human DNA seq from clone 1183I21 on chro to predicted fly and worm proteins. Con	2.43	EB_cells, Caco2, DU145_cells
119977	W88579	Hs.124744	ESTs	2.43	HT29_cells, HMEC (total RNA), HMEC
134921	W60186	Hs.169487	Kreisler (mouse) maf-related leucine zip	2.43	LNCaP_cells, HS578T_cells, MB-MDA-453
132295	H66351	Hs.181042	Dmx-like 1	2.43	Lu_SC_H69, BT474_cells, Lu_SQ_H520
133395	AA491296	Hs.72805	ESTs	2.43	EB_cells, LNCaP_cells, OVCAR_cells
106728	AA465355	Hs.153768	U3 snoRNP-associated 55-kDa protein	2.43	EB_cells, Lu_AD_H23, PC3_cells
116370	AA521256	Hs.236204	ESTs; Moderately similar to NUCLEAR PORE	2.43	EB_cells, A549_cells, 293T_cells
113936	W81552	Hs.83623	nuclear receptor subfamily 1; group I; m	2.43	293T_cells, OVCAR_cells, Fibroblasts 2
128862	R61297	Hs.106673	eukaryotic translation initiation factor	2.43	EB_cells, DU145_cells, DU145_cells
111614	R12581	Hs.191146	ESTs	2.43	HMEC (total RNA), Fibroblasts 2, MB-MDA-435s
111993	R42241	Hs.106359	ESTs	2.43	A549_cells, DU145_cells, CALU6_cells
131554	AA100026	Hs.28669	ESTs; Weakly similar to PROTEIN-TYROSINE	2.43	EB_cells, LNCaP_cells, Caco2
130983	N71215	Hs.21862	NCK-associated protein 1	2.42	EB_cells, Caco2, A549_cells
131654	AA497050	Hs.30204	ESTs	2.42	MCF7, MB-MDA-435s, Lu_SC_H345
105014	AA121123	Hs.191374	ESTs	2.42	EB_cells, Lu_AD_H23, Lu_LC_H460
106300	AA435840	Hs.19114	high-mobility group (nonhistone chromoso	2.42	EB_cells, Lu_SC_H345, A549_cells
102386	U40998	Hs.81728	unc119 (C.elegans) homolog	2.42	OVCAR_cells, EB_cells, DU145_cells
112517	R68589	Hs.23721	ESTs	2.42	Caco2, MCF7, DU145_cells
125375	H72971		KIAA0277 gene product	2.42	Lu_SC_H345, OVCAR_cells, Lu_SC_H69
123808	AA620552	Hs.25682	ESTs; Weakly similar to PHOSPHATIDYLETHA	2.42	EB_cells, Lu_AD_H23, Lu_SC_H69
114950	AA243503	Hs.11801	adenosine A2b receptor pseudogene	2.42	MB-MDA-453, HT29_cells, Lu_LC_H460
129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	2.41	Lu_SC_H345, .Fibroblasts 2, DU145_cells
103408	X95876	Hs.198252	G protein-coupled receptor 9	2.41	RPWE_2, PRSC_log, Lu_SC_H345
129703	AA401348	Hs.179999	ESTs	2.41	EB_cells, 293T_cells, DU145_cells

105693	AA287104	Hs.181368	U5 snRNP-specific protein (220 kD); orth	2.41	293T_cells, CALU6_cells, A549_cells
106532	AA453628	Hs.37443	ESTs	2.41	EB_cells, OVCAR_cells, Caco2
132132	AA010933	Hs.4055	core promoter element binding protein	2.41	HMEC, HMEC (total RNA), EB_cells
111409	R00311	Hs.18798	EST; Weakly similar to !!!! ALU SUBFAMIL	2.41	Lu_SC_H345, Lu_SC_H69, PRSC_con
133813	M26657	Hs.250711	dipeptidyl carboxypeptidase 1 (angiotens	2.41	HT29_cells, BT474_cells, MB231_cells
127240	AA888387	Hs.243845	ESTs; Moderately similar to !!!! ALU SUB	2.41	Lu_SC_H345, DU145_cells, LNCaP_cells
104975	AA086071	Hs.50758	chromosome-associated polypeptide C	2.41	OVCAR_cells, DU145_cells, PC3_cells
118078	N54321	Hs.47790	EST	2.41	EB_cells, Fibroblasts 2, HMEC (total RNA)
115840	AA429253	Hs.58103	A kinase (PRKA) anchor protein 9	2.41	OVCAR_cells, EB_cells, PC3_cells
101186	L20298	Hs.179881	core-binding factor; beta subunit	2.4	EB_cells, DU145_cells, CALU6_cells
113098	T40936	Hs.8349	ESTs	2.4	Caco2, HT29_cells, EB_cells
115185	AA259140	Hs.60238	ESTs	2.4	Lu_SC_H69, EB_cells, Caco2
113778	W15263	Hs.5422	ESTs	2.4	Caco2, MB-MDA-435s, LNCaP_cells
128261	AI061213	Hs.13179	ESTs; Moderately similar to !!!! ALU SUB	2.4	DU145_cells, LNCaP_cells, OVCAR_cells
132210	AA235013	Hs.42322	A kinase (PRKA) anchor protein 2	2.4	Caco2, DU145_cells, PRSC_log
112561	R72427	Hs.129873	ESTs; Weakly similar to CYTOCHROME P450	2.4	Lu_SQ_H520, Lu_AD_H23, EB_cells
127598	AA610677	Hs.168851	ESTs	2.4	LNCaP_cells, DU145_cells, OVCAR_cells
106664	AA460969	Hs.7510	mitogen-activated protein kinase kinase	2.4	OVCAR_cells, 293T_cells, A549_cells
131367	AA456687	Hs.26057	ESTs	2.4	EB_cells, MB-MDA-453, 293T_cells
103163	X67683		H.sapiens mRNA for keratin 4	2.39	EB_cells, Lu_AD_H23, Lu_AD_358
109639	F04444	Hs.6217	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.39	EB_cells, Lu_SC_H345, Lu_SC_H69
112007	R42671	Hs.140853	EST; Weakly similar to !!!! ALU SUBFAMIL	2.39	MB-MDA-435s, Lu_SC_H345, Lu_AD_H23
100023			AFFX control: BioC-3	2.39	Caco2, Lu_AD_358, LNCaP_cells
119923	W86214	Hs.184642	ESTs	2.39	EB_cells, HS578T_cells, DU145_cells
127705	AJ003307		AJ003307 Selected chr 21 cDNA library H	2.39	Lu_AD_H23, Lu_SC_H345, Lu_LC_H460
130362	AA182658	Hs.179817	DKFZP586F0222 protein	2.39	EB_cells, DU145_cells, PC3_cells
100168	D14874	Hs.394	adrenomedullin	2.39	Fibroblasts 2, Caco2, HS578T_cells
134261	AA227678	Hs.8084	Human DNA seq from clone 465N24 on chr 1 Contains two novel genes; ESTs; GSSs an	2.39	PRSC_con, MB-MDA-453, LNCaP_cells
103392	X94563		H.sapiens dbi/acbp gene exon 1 & 2	2.38	EB_cells, Lu_AD_H23, Lu_SC_H69
129888	U81001	Hs.131891	Human SNRPN mRNA; 3' UTR; partial seq	2.38	LNCaP_cells, Lu_SC_H69, Lu_LC_H460
130119	T12649	Hs.251653	tubulin; beta; 2	2.38	Lu_AD_H23, Lu_LC_H460, Lu_LC_H460
118136	N57710	Hs.233952	proteasome (prosome; macropain) subunit;	2.38	293T_cells, OVCAR_cells, HS578T_cells
131163	H80107	Hs.23754	ESTs	2.38	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
115964	AA446622	Hs.74313	ESTs	2.38	EB_cells, LNCaP_cells, DU145_cells
135026	H59730	Hs.93231	ESTs	2.37	EB_cells, 293T_cells, Lu_SC_H69
133300	D51401	Hs.70333	ESTs	2.37	OVCAR_cells, Caco2, CALU6_cells
129948	H69281	Hs.13643	ESTs	2.37	EB_cells, Lu_AD_H23, Lu_SC_H345
112505	R67923	Hs.23368	ESTs	2.37	DU145_cells, OVCAR_cells, 293T_cells
130715	T98227	Hs.171952	occludin	2.37	Caco2, LNCaP_cells, DU145_cells
120301	AA192163	Hs.104085	EST	2.37	Lu_AD_H23, EB_cells, PRSC_con
128062	AA379500	Hs.193155	ESTs	2.37	EB_cells, LNCaP_cells, DU145_cells
127154	AA789101	Hs.198860	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.37	HS578T_cells, MCF7, Lu_SC_H69
102814	U90716	Hs.79187	coxsackie virus and adenovirus receptor	2.37	OVCAR_cells, DU145_cells, Lu_SC_H345
120239	Z41691	Hs.65919	ESTs	2.37	EB_cells, DU145_cells, LNCaP_cells
106829	AA481883	Hs.31236	ESTs; Weakly similar to Unknown [H.sapie	2.37	EB_cells, DU145_cells, OVCAR_cells
132681	AA435762	Hs.54894	ESTs; Highly similar to unknown [H.sapie	2.37	EB_cells, LNCaP_cells, PRSC_con
108845	AA132946	Hs.68864	ESTs	2.36	Lu_AD_H23, Lu_AD_358, Lu_SQ_H520
133226	T85327	Hs.169552	ESTs	2.36	Caco2, MB-MDA-453, MCF7
106789	AA478726	Hs.26373	ESTs; Moderately similar to !!!! ALU SUB	2.36	MB-MDA-453, Caco2, OVCAR_cells
119236	T10166	Hs.237297	ESTs	2.36	EB_cells, 293T_cells, LNCaP_cells
106619	AA459255	Hs.23956	ESTs	2.36	LNCaP_cells, A549_cells, Caco2
109178	AA181600	Hs.62741	ESTs	2.36	Lu_SC_H345, LNCaP_cells, EB_cells
112724	R91753	Hs.17757	ESTs	2.36	Caco2, EB_cells, DU145_cells
112655	R85069	Hs.141139	ESTs	2.36	Fibroblasts 2, Lu_AD_H23, Lu_LC_H460
132820	AA454988	Hs.57621	ESTs	2.36	EB_cells, OVCAR_cells, HS578T_cells
106155	AA425309	Hs.33287	nuclear factor I/B	2.36	OVCAR_cells, Lu_SC_H345, MB-MDA-453
114632	AA084742	Hs.194380	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.35	Lu_SC_H345, Lu_LC_H460, Lu_AD_H23
134776	J05582	Hs.89603	mucin 1; transmembrane	2.35	DU145_cells, Lu_AD_H23, Lu_AD_358
101192	L20859	Hs.78452	solute carrier family 20 (phosphate tran	2.35	PC3_cells, CALU6_cells, MB-MDA-435s
130349	W16686	Hs.171825	basic helix-loop-helix domain containing	2.35	A549_cells, DU145_cells, HT29_cells
106389	AA446949	Hs.6236	ESTs	2.35	LNCaP_cells, PC3_cells, DU145_cells
109637	F04426	Hs.23131	kinesin family member C3	2.35	MB-MDA-435s, A549_cells, Lu_LC_H460
101483	M24486	Hs.76768	procollagen-proline; 2-oxoglutarate 4-di	2.35	PC3_cells, HS578T_cells, EB_cells
131751	H18335	Hs.31562	ESTs	2.35	DU145_cells, MB231_cells, HMEC
131050	X13967	Hs.2250	leukemia inhibitory factor (cholinergic	2.35	Lu_AD_H23, PC3_cells, PRSC_log
130097	N21159	Hs.14845	forkhead box O3A	2.34	EB_cells, LNCaP_cells, LNCaP_cells
134533	AA013468	Hs.241493	natural killer-tumor recognition seq	2.34	EB_cells, HT29_cells, HMEC
134839	D63479	Hs.115907	diacylglycerol kinase; delta (130kD)	2.34	Lu_LC_H460, Caco2, DU145_cells
115690	AA410894	Hs.44159	ESTs	2.34	PC3_cells, EB_cells, OVCAR_cells
129079	N91011	Hs.108502	ESTs	2.34	Lu_AD_H23, Lu_SC_H69, Lu_AD_358
123517	AA608525	Hs.243059	EST	2.34	Lu_SC_H345, PC3_cells, MB-MDA-435s
126239	AA527215	Hs.75879	ribosomal protein L19	2.34	BT474_cells, Lu_LC_H460, Lu_AD_H23
124440	N46435		ESTs	2.34	Lu_SC_H69, HT29_cells, MB-MDA-435s
111468	R05809	Hs.205481	ESTs	2.34	Lu_AD_H23, PRSC_log, Lu_SQ_H520
129560	H18428	Hs.113613	ESTs; Moderately similar to !!!! ALU SUB	2.34	Lu_SC_H69, Lu_SC_H345, LNCaP_cells

104857	AA043219	Hs.19058	ESTs	2.34	Lu_AD_H23, Lu_SC_H345, Lu_SC_H345
109647	F04587	Hs.28241	ESTs	2.34	HS578T_cells, A549_cells, CALU6_cells
117160	H97817	Hs.183302	ESTs	2.34	EB_cells, Fibroblasts 2, Lu_SC_H69
112352	R58974	Hs.167343	ESTs	2.34	EB_cells, Lu_SC_H345, HT29_cells
113653	T95745	Hs.187433	ESTs	2.34	MB-MDA-435s, MB-MDA-453, Lu_SC_H345
131606	W56804	Hs.29385	AFG3 (ATPase family gene 3; yeast)-like	2.34	OVCAR_cells, Fibroblasts 2, MB-MDA-435s
101525	M29536	Hs.12163	eukaryotic translation initiation factor	2.34	EB_cells, Caco2, DU145_cells
125921	AA775029	Hs.122591	ESTs	2.33	293T_cells, PRSC_log, Lu_SC_H345
125775	AA213555	Hs.29205	alpha integrin binding protein 63	2.33	EB_cells, DU145_cells, LNCaP_cells
108743	AA126917	Hs.71074	ESTs	2.33	Lu_AD_H23, Lu_AD_358, Lu_LC_H460
133735	AC002045	Hs.251928	nuclear pore complex interacting protein	2.33	LNCaP_cells, Lu_SC_H69, DU145_cells
120403	AA234916	Hs.243851	ESTs	2.33	MB231_cells, Lu_SC_H345, Lu_SC_H69
134998	R02207	Hs.92679	ESTs; Weakly similar to microtubule-base	2.33	LNCaP_cells, BT474_cells, MCF7
108456	AA079326	Hs.143654	ESTs	2.33	HT29_cells, Lu_AD_H23, RPWE_2
130552	M86667	Hs.179662	nucleosome assembly protein 1-like 1	2.33	EB_cells, A549_cells, DU145_cells
111114	N63391	Hs.9238	ESTs	2.33	Caco2, EB_cells, MB-MDA-453
127767	AI269498	Hs.125543	ESTs; Moderately similar to TADA1 protei	2.33	CALU6_cells, 293T_cells, PC3_cells
106546	AA454725	Hs.21056	H sapiens mRNA from chromosome 5q21-22;	2.33	OVCAR_cells, Caco2, LNCaP_cells
122379	AA446110	Hs.250989	EST	2.33	BT474_cells, Fibroblasts 2, MB-MDA-435s
133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	2.33	Lu_SC_H345, EB_cells, EB_cells
106434	AA449099	Hs.8151	ESTs; Weakly similar to atopy related au	2.33	EB_cells, LNCaP_cells, Caco2
105297	AA233451	Hs.183858	transcriptional intermediary factor 1	2.33	EB_cells, LNCaP_cells, Caco2
115976	AA447442	Hs.86327	ESTs	2.33	EB_cells, 293T_cells, Lu_SC_H69
105788	AA351031	Hs.23965	solute carrier family 22 (organic anion	2.33	EB_cells, Lu_AD_H23, Lu_SC_H345
113774	W04550	Hs.9927	H sapiens mRNA; cDNA DKFZp564D156 (from	2.32	OVCAR_cells, EB_cells, Lu_SC_H69
110617	H68772	Hs.35820	ESTs; Weakly similar to b34I8.1 [H.sapie	2.32	Lu_SC_H345, Lu_AD_H23, PRSC_con
102234	U26312	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	2.32	CALU6_cells, LNCaP_cells, A549_cells
114777	AA151699	Hs.184519	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.32	HT29_cells, Fibroblasts 2, Lu_SC_H345
125518	R20148	Hs.193851	ESTs	2.32	HT29_cells, HMEC (total RNA), MB231_cells
130814	AA256695	Hs.19813	ESTs	2.32	MB-MDA-435s, Lu_SC_H69, PRSC_log
123473	AA599143		ESTs; Moderately similar to !!!! ALU SUB	2.32	LNCaP_cells, DU145_cells, Lu_SC_H345
134310	AA313414	Hs.8148	H sapiens clone 24856 mRNA seq; complete	2.32	PC3_cells, LNCaP_cells, OVCAR_cells
119192	R85375	Hs.237262	EST	2.32	Lu_SC_H69, PRSC_log, PRSC_con
114391	AA004876	Hs.133100	ESTs	2.32	PC3_cells, 293T_cells, 293T_cells
119133	R49144	Hs.119756	ESTs	2.32	PRSC_log, 293T_cells, 293T_cells
109710	F09792	Hs.12929	ESTs	2.32	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
116726	F13681	Hs.42309	ESTs	2.32	MCF7, BT474_cells, MB-MDA-453
133206	R32993	Hs.6762	ESTs; Weakly similar to similar to leucy	2.31	DU145_cells, 293T_cells, EB_cells
135163	AA125988	Hs.199955	ESTs	2.31	Lu_SC_H345, LNCaP_cells, DU145_cells
111219	N68836	Hs.19247	ESTs	2.31	OVCAR_cells, LNCaP_cells, 293T_cells
110283	H29565	Hs.12271	ESTs	2.31	BT474_cells, MB231_cells, MB-MDA-453
103772	AA092473	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamm	2.31	CALU6_cells, MCF7, DU145_cells
122766	AA459386	Hs.194058	ESTs; Weakly similar to atypical PKC spe	2.31	HT29_cells, BT474_cells, HMEC
120886	AA365566	Hs.132736	ESTs; Weakly similar to allograft inflam	2.31	DU145_cells, A549_cells, Lu_LC_H460
123512	AA600248	Hs.142245	HERV-H LTR-associating 3	2.31	PC3_cells, 293T_cells, DU145_cells
106644	AA460239	Hs.12680	ESTs	2.31	HS578T_cells, MB231_cells, Lu_SQ_H520
127359	H72971		KIAA0277 gene product	2.31	Lu_SC_H345, DU145_cells, OVCAR_cells
105919	AA402494	Hs.3990	ESTs	2.31	HS578T_cells, DU145_cells, LNCaP_cells
125241	W86291	Hs.121593	ESTs	2.3	HMEC, HMEC (total RNA), EB_cells
104624	AA001936	Hs.184721	ESTs	2.3	DU145_cells, PC3_cells, PRSC_log
128765	AA101767	Hs.10494	ESTs	2.3	EB_cells, HMEC (total RNA), Lu_LC_H460
108360	AA071539		zm74b6.s1 Stratagene neuroepithelium (#9 HYDROXYSTEROID DEHYDROGENASE/DELTA-5-DEL	2.3	HT29_cells, RPWE_2, Lu_AD_H23
115682	AA410300	Hs.44618	ESTs	2.3	HT29_cells, Lu_SQ_H520, Lu_AD_H23
134528	M23161	Hs.84775	Human transposon-like element mRNA	2.3	EB_cells, CALU6_cells, A549_cells
111091	N59858	Hs.33032	H sapiens mRNA; cDNA DKFZp434N185 (from	2.3	LNCaP_cells, DU145_cells, PRSC_log
134044	AA262475	Hs.78746	phosphodiesterase 8A	2.29	DU145_cells, A549_cells, MCF7
118229	N62339	Hs.180532	heat shock 90kD protein 1; alpha	2.29	MCF7, DU145_cells, EB_cells
110188	H20522	Hs.20969	ESTs	2.29	Fibroblasts 2, MB-MDA-435s, Lu_LC_H460
125073	T87185	Hs.193638	ESTs; Weakly similar to !!!! ALU CLASS C	2.29	EB_cells, Lu_SC_H345, Lu_SC_H69
111495	R07210	Hs.19913	ESTs	2.29	CALU6_cells, EB_cells, MCF7
124024	F03077	Hs.106672	ESTs	2.29	HS578T_cells, RPWE_2, Lu_AD_358
128230	AA984074	Hs.176757	ESTs	2.29	LNCaP_cells, DU145_cells, OVCAR_cells
125471	AA477571	Hs.152601	UDP-glucose ceramide glucosyltransferase	2.29	DU145_cells, PRSC_con, PRSC_log
120734	AA299949		EST12545 Uterus tumor I H sapiens cDNA 3	2.28	Lu_AD_H23, Lu_SC_H345, Lu_SC_H69
134349	AA406373	Hs.8208	ESTs	2.28	DU145_cells, PC3_cells, LNCaP_cells
123412	AA521443	Hs.187763	ESTs	2.28	BT474_cells, BT474_cells, Lu_SC_H69
116297	AA489042	Hs.59498	ESTs	2.28	EB_cells, 293T_cells, MB-MDA-453
104476	N33807	Hs.223014	protease; serine; 15	2.28	LNCaP_cells, MCF7, PC3_cells
101004	J04101	Hs.248109	v-ets avian erythroblastosis virus E26 o	2.28	HT29_cells, MB-MDA-435s, HMEC (total RNA)
109991	H09813	Hs.12896	KIAA1034 protein	2.28	EB_cells, CALU6_cells, 293T_cells
118934	N92571	Hs.54808	ESTs	2.28	HS578T_cells, 293T_cells, A549_cells
125096	T94328	Hs.194533	ESTs	2.28	Lu_SC_H345, Lu_SC_H69, 293T_cells
117514	N32226	Hs.124058	ESTs	2.28	CALU6_cells, HMEC, Lu_AD_H23
132792	AA401903	Hs.242985	hemoglobin; gamma G	2.28	OVCAR_cells, Lu_SC_H69, MCF7
129009	AA131421	Hs.107884	ESTs	2.28	HS578T_cells, CALU6_cells, Caco2

111658	R16981	Hs.15276	ESTs	2.28	MB-MDA-435s, 293T_cells, A549_cells
112322	R55757	Hs.26457	EST	2.28	Lu_SC_H345, Lu_SC_H69, Lu_AD_358
133477	W69310	Hs.740	PTK2 protein tyrosine kinase 2	2.28	EB_cells, PC3_cells, DU145_cells
132149	T10822	Hs.4095	ESTs	2.28	LNCaP_cells, EB_cells, PC3_cells
115119	AA256524	Hs.46847	Human DNA seq from clone 30M3 on chromos yeast and archaea bacterial genes; and	2.27	A549_cells, EB_cells, LNCaP_cells
102130	U15009	Hs.1575	small nuclear ribonucleoprotein D3 polyp	2.27	LNCaP_cells, Caco2, EB_cells
114343	Z41424	Hs.21259	ESTs	2.27	HT29_cells, OVCAR_cells, Fibroblasts 2
106746	AA476436	Hs.7991	ESTs	2.27	Lu_AD_358, RPWE_2, Lu_AD_H23
119359	T71021	Hs.93334	ESTs; Highly similar to WS basic-helix-l	2.27	Lu_SC_H69, 293T_cells, DU145_cells
106301	AA435867	Hs.168212	kinesin family member 3B	2.27	OVCAR_cells, LNCaP_cells, EB_cells
130280	L13738	Hs.153937	activated p21cdc42Hs kinase	2.27	MB-MDA-453, DU145_cells, DU145_cells
119724	W69468	Hs.47622	ESTs	2.27	PC3_cells, HT29_cells, A549_cells
108960	AA150199	Hs.49378	DKFZP586D0919 protein	2.27	EB_cells, HS578T_cells, Lu_AD_358
103489	Y08614	Hs.79090	exportin 1 (CRM1; yeast; homolog)	2.26	EB_cells, CALU6_cells, DU145_cells
107711	AA015736	Hs.220687	ESTs	2.26	EB_cells, Lu_AD_H23, Lu_AD_358
131950	W84704	Hs.35380	ESTs	2.26	HS578T_cells, OVCAR_cells, MB-MDA-435s
107093	AA609600	Hs.10018	ESTs	2.26	LNCaP_cells, OVCAR_cells, DU145_cells
113649	T95641	Hs.16400	ESTs; Weakly similar to Hrs [H.sapiens]	2.26	Lu_AD_H23, Lu_SC_H69, PRSC_log
105255	AA227498	Hs.3623	ESTs	2.26	HS578T_cells, 293T_cells, Lu_SC_H345
130094	H43286	Hs.167017	gamma-aminobutyric acid (GABA) B recepto	2.26	Fibroblasts 2, MB231_cells, 293T_cells
111874	R37959	Hs.13358	ESTs	2.26	CALU6_cells, Lu_SQ_H520, 293T_cells
107890	AA026030	Hs.61311	ESTs; Weakly similar to CALPAIN 2; LARGE	2.26	HT29_cells, MB-MDA-453, PC3_cells
124628	N74702	Hs.102834	ESTs	2.26	293T_cells, CALU6_cells, CALU6_cells
119707	W67569	Hs.44143	ESTs; Weakly similar to SNF2alpha protei	2.26	293T_cells, OVCAR_cells, Lu_SC_H345
106737	AA470080	Hs.36237	ESTs; Moderately similar to CGI-34 prote	2.26	LNCaP_cells, DU145_cells, MB-MDA-435s
117305	N22798	Hs.43248	EST	2.26	HT29_cells, BT474_cells, Fibroblasts 2
134470	X54942	Hs.83758	CDC28 protein kinase 2	2.26	DU145_cells, CALU6_cells, LNCaP_cells
130734	T99337	Hs.18624	KIAA1052 protein	2.26	Lu_AD_H23, Lu_SC_H345, Lu_SC_H69
128561	R69227	Hs.101489	ESTs	2.26	Lu_SC_H345, DU145_cells, OVCAR_cells
100670	HG2992-H		Beta-Hexosaminidase, Alpha Polypeptide,	2.26	HT29_cells, BT474_cells, Lu_SC_H345
115953	AA443958	Hs.90960	ESTs	2.26	Caco2, 293T_cells, DU145_cells
129612	H17476	Hs.11615	ESTs; Highly similar to map kinase phosp	2.25	CALU6_cells, LNCaP_cells, PC3_cells
111362	N91973	Hs.23595	deoxyribonuclease III; dnaQ/mutD (E. col	2.25	Lu_SQ_H520, Lu_AD_H23, RPWE_2
116275	AA485453	Hs.250911	interleukin 13 receptor; alpha 1	2.25	OVCAR_cells, 293T_cells, DU145_cells
114461	AA024848	Hs.126705	ESTs	2.25	EB_cells, Lu_AD_H23, Lu_AD_H23
134083	AA278393	Hs.79013	ESTs	2.25	293T_cells, EB_cells, OVCAR_cells
132470	Z24724	Hs.4934	H.sapiens polyA site DNA	2.25	EB_cells, HS578T_cells, Caco2
114718	AA131328		zo8d1.s1 Stratagene neuroepithelium NT2R SW:COX2_MOUSE P45 CYTOCHROME C OXIDASE P	2.25	MB-MDA-435s, HT29_cells, Lu_SC_H69
129499	R40395	Hs.242908	lecithin-cholesterol acyltransferase	2.25	HMEC (total RNA), Fibroblasts 2, HMEC
124758	R38422	Hs.169168	ESTs	2.25	293T_cells, RPWE_2, Lu_LC_H460
130301	X83127	Hs.172471	potassium voltage-gated channel; shaker-	2.25	EB_cells, OVCAR_cells, A549_cells
131263	R38334	Hs.24950	regulator of G-protein signalling 5	2.25	Lu_AD_H23, EB_cells, Lu_SC_H69
107159	AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	2.25	LNCaP_cells, HMEC, EB_cells
133262	N72009	Hs.206710	ESTs	2.24	Lu_SC_H345, DU145_cells, LNCaP_cells
132985	AA093619	Hs.62113	KIAA0717 protein	2.24	EB_cells, Lu_AD_H23, Lu_AD_358
114172	Z39043	Hs.21421	ESTs; Weakly similar to cysteine desulfu	2.24	293T_cells, CALU6_cells, Lu_SQ_H520
127847	AA913387	Hs.126717	ESTs	2.24	LNCaP_cells, DU145_cells, Lu_SC_H69
106499	AA452244	Hs.16727	ESTs	2.24	Lu_SC_H345, MB-MDA-453, Lu_SC_H69
105095	AA150088	Hs.27023	KIAA0917 protein	2.24	DU145_cells, LNCaP_cells, CALU6_cells
108876	AA134361	Hs.191453	ESTs	2.24	EB_cells, Lu_SC_H345, Lu_AD_H23
121971	AA429667	Hs.120405	ESTs	2.24	Lu_AD_H23, 293T_cells, CALU6_cells
114334	Z41342	Hs.22941	ESTs	2.24	DU145_cells, PC3_cells, EB_cells
114565	AA063001	Hs.103527	SH2 domain protein 2A	2.24	Lu_LC_H460, MCF7, HMEC (total RNA)
115766	AA421761	Hs.77603	ESTs	2.24	Fibroblasts 2, MB-MDA-435s, MB231_cells
130989	AA608546	Hs.21906	ESTs	2.24	PC3_cells, LNCaP_cells, DU145_cells
116304	AA489461	Hs.64742	H sapiens mRNA for KIAA0540 protein; par	2.24	BT474_cells, EB_cells, LNCaP_cells
111154	N66545	Hs.29169	ESTs	2.24	OVCAR_cells, MB-MDA-435s, HMEC
105561	AA262881	Hs.16029	ESTs; Weakly similar to alternatively sp	2.23	HS578T_cells, A549_cells, HMEC
105939	AA404421	Hs.12258	ESTs	2.23	EB_cells, LNCaP_cells, DU145_cells
126379	AI085342	Hs.166146	Homer; neuronal immediate early gene; 3	2.23	HS578T_cells, PC3_cells, RPWE_2
106610	AA458882	Hs.4832	ESTs; Moderately similar to Lasp-1 prote	2.23	DU145_cells, MCF7, Lu_SC_H345
132786	AA424545	Hs.56851	H sapiens mRNA expressed in placenta	2.23	EB_cells, Lu_AD_H23, Fibroblasts 2
107206	D20728	Hs.30767	ESTs	2.23	BT474_cells, Fibroblasts 2, MB-MDA-435s
133708	R42172	Hs.75667	synaptophysin	2.23	Lu_SC_H345, CALU6_cells, Lu_SC_H69
135123	AA227567	Hs.9482	target of myb1 (chicken) homolog	2.23	BT474_cells, MB231_cells, EB_cells
132156	AA157401	Hs.4113	S-adenosylhomocysteine hydrolase-like 1	2.23	DU145_cells, 293T_cells, LNCaP_cells
116934	H75624	Hs.39662	ESTs	2.23	CALU6_cells, Lu_SC_H345, Lu_LC_H460
133660	R87373		ym88e05.r1 Soares adult brain N2b4HB55Y IMAGE:166016 5', mRNA seq.	2.23	DU145_cells, A549_cells, PC3_cells
119468	W23633	Hs.125043	ESTs	2.23	293T_cells, MB-MDA-453, OVCAR_cells
101247	L33801	Hs.78802	glycogen synthase kinase 3 beta	2.23	LNCaP_cells, EB_cells, MB-MDA-435s
126008	AA253460		zs06f04.s1 NCI_CGAP_GCB1 H sapiens cDNA	2.23	HT29_cells, PRSC_log, Fibroblasts 2
122938	AA477119		zu37c7.s1 Soares ovary tumor NbHOT H sap TR:G288289 G288289 MITOCHONDRIAL D-LOOP	2.23	PC3_cells, MCF7, MB-MDA-435s

114148	Z38804	Hs.184777	ESTs; Moderately similar to OPIOID BINDI MOLECULE PRECURSOR [H.sapiens]	2.23	HS578T_cells, Fibroblasts 2, Lu_SC_H345
103433	X98001	Hs.78948	Rab geranylgeranyltransferase; beta subu	2.22	LNCaP_cells, EB_cells, 293T_cells
132954	AA027112	Hs.216194	ESTs	2.22	EB_cells, Lu_AD_H23, Fibroblasts 2
133228	N90029	Hs.6831	H sapiens clone 1400 unknown protein mRN	2.22	293T_cells, PC3_cells, DU145_cells
103891	AA242887	Hs.124186	ring finger protein 2	2.22	EB_cells, Lu_SC_H69, Lu_SC_H345
124883	R75630	Hs.177242	ESTs	2.22	EB_cells, Lu_AD_H23, Lu_SC_H345
109921	H05734	Hs.30559	ESTs	2.22	Lu_SQ_H520, 293T_cells, RPWE_2
127306	AI305162	Hs.193687	ESTs	2.22	MCF7, HT29_cells, MB-MDA-453
102707	U77456	Hs.78103	nucleosome assembly protein 1-like 4	2.22	Caco2, EB_cells, CALU6_cells
106193	AA427625	Hs.23272	ESTs	2.22	293T_cells, EB_cells, A549_cells
118819	N79045	Hs.50800	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.22	Lu_SC_H345, Lu_SC_H69, DU145_cells
134326	U16306	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.22	HS578T_cells, PRSC_log, CALU6_cells
112241	R51248	Hs.16027	ESTs	2.22	293T_cells, HMEC (total RNA), HMEC (total RNA)
123693	AA609591	Hs.112728	ESTs	2.22	HT29_cells, HMEC (total RNA), BT474_cells
129052	AA496297	Hs.182740	ribosomal protein S11	2.22	EB_cells, Lu_AD_H23, Lu_AD_358
122481	AA448271	Hs.99126	ESTs	2.21	Lu_AD_H23, HT29_cells, Lu_AD_358
128895	R37753	Hs.106985	ESTs	2.21	EB_cells, Lu_AD_H23, Lu_SC_H345
124691	R05835	Hs.110153	ESTs; Weakly similar to B-CELL GROWTH FA	2.21	EB_cells, Lu_AD_H23, Lu_AD_358
131556	AA442853	Hs.2869	cyclin-dependent kinase 5; regulatory su	2.21	HT29_cells, Lu_LC_H460, Lu_SC_H69
128869	AA424570	Hs.106736	ESTs	2.21	EB_cells, Lu_AD_H23, Lu_SC_H69
107114	AA610089	Hs.11776	U4/U6-associated RNA splicing factor	2.21	MCF7, Lu_SC_H345, DU145_cells
106255	AA431191	Hs.161489	ESTs	2.21	EB_cells, Caco2, DU145_cells
130724	AA370091	Hs.179680	ESTs	2.2	EB_cells, Lu_AD_H23, Lu_SC_H69
105483	AA255874	Hs.23458	ESTs	2.2	LNCaP_cells, DU145_cells, PC3_cells
118970	N93503	Hs.54961	stoned B/TFIIA-alpha/beta-like factor	2.2	293T_cells, HS578T_cells, OVCAR_cells
120805	AA346041	Hs.96844	ESTs	2.2	HT29_cells, HS578T_cells, 293T_cells
106158	AA425382	Hs.6553	ESTs	2.2	CALU6_cells, PC3_cells, EB_cells
102121	U14391	Hs.82251	myosin IC	2.2	A549_cells, EB_cells, Caco2
109446	AA232125	Hs.87062	ESTs	2.2	HT29_cells, Lu_LC_H460, CALU6_cells
129515	AA490882	Hs.112227	ESTs	2.2	Lu_SC_H345, BT474_cells, Caco2
113128	T49325	Hs.8977	ESTs	2.2	Lu_SQ_H520, Lu_AD_H23, Lu_AD_358
127289	AI041014	Hs.220752	ESTs	2.2	EB_cells, Lu_AD_H23, Lu_AD_H23
129912	AA047344	Hs.107213	ESTs; Highly similar to NY-REN-6 antigen	2.2	CALU6_cells, A549_cells, EB_cells
115700	AA411685	Hs.67709	ESTs	2.2	OVCAR_cells, EB_cells, Caco2
106267	AA431873	Hs.4988	H sapiens clone 24711 mRNA seq	2.2	Lu_SQ_H520, EB_cells, PC3_cells
112881	T03593	Hs.182814	ESTs	2.19	A549_cells, OVCAR_cells, 293T_cells
116902	H70739		yu69f11.s1 Weizmann Olfactory Epithelium IMAGE:239085 3' similar to contains LTR	2.19	LNCaP_cells, DU145_cells, PC3_cells
105621	AA280865	Hs.6375	H sapiens mRNA; cDNA DKFZp564K0222 (from	2.19	HMEC, Caco2, HMEC (total RNA)
126991	R31652	Hs.821	biglycan	2.19	Fibroblasts 2, Lu_SC_H69, HS578T_cells
125466	R08234	Hs.180461	ESTs	2.19	Lu_AD_358, Lu_AD_H23, Lu_SQ_H520
108491	AA082973		zn7g1.s1 Stratagene hNT neuron (#937233) to gb:M3672 6S RIBOSOMAL PROTEIN L7A (H	2.19	Lu_AD_358, RPWE_2, Lu_LC_H460
109978	H09356	Hs.22528	ESTs	2.19	PRSC_log, Lu_SC_H345, Lu_SC_H69
106990	AA521354	Hs.24758	ESTs	2.19	EB_cells, LNCaP_cells, OVCAR_cells
122362	AA443919	Hs.96840	ESTs	2.19	EB_cells, Lu_AD_358, PRSC_con
125367	AI016490	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.19	HT29_cells, Lu_SC_H69, Lu_AD_H23
110716	H97188	Hs.35096	ESTs	2.19	DU145_cells, Fibroblasts 2, PRSC_con
129297	R11267	Hs.180570	H sapiens chromosome 19; cosmid F22329	2.19	293T_cells, MB-MDA-435s, A549_cells
104992	AA102652	Hs.22753	ESTs; Weakly similar to coded for by C.	2.18	MCF7, MB-MDA-453, Lu_SQ_H520
119896	W84738	Hs.137319	ESTs	2.18	293T_cells, 293T_cells, OVCAR_cells
118594	N69022	Hs.49599	ESTs	2.18	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
129786	H98977	Hs.246109	ESTs	2.18	293T_cells, 293T_cells, 293T_cells
104325	D81608	Hs.150675	polymerase (RNA) II (DNA directed) polyp	2.18	PC3_cells, Lu_SC_H345, LNCaP_cells
123022	AA480909		aa28f10.s1 NCI_CGAP_GCB1 H sapiens cDNA Alu repetitive element;contains element	2.18	OVCAR_cells, DU145_cells, LNCaP_cells
133572	W94333	Hs.7499	translocase of inner mitochondrial membr	2.18	Caco2, LNCaP_cells, Lu_SQ_H520
133363	AA479713	Hs.71962	ESTs	2.18	EB_cells, Lu_AD_H23, Fibroblasts 2
135361	AA053319	Hs.167700	ESTs	2.18	EB_cells, 293T_cells, Caco2
128319	AA808904	Hs.115095	ESTs; Weakly similar to RHO-RELATED GTP-	2.18	Lu_SC_H345, OVCAR_cells, DU145_cells
128660	AA011597	Hs.177398	ESTs	2.18	EB_cells, Lu_AD_H23, Lu_SQ_H520
114877	AA235618	Hs.205125	ESTs	2.18	DU145_cells, 293T_cells, OVCAR_cells
125925	H28737		ESTs; Moderately similar to !!!! ALU SUB	2.18	Lu_SC_H69, Lu_SC_H345, HS578T_cells
113427	T85105	Hs.15471	ESTs	2.18	EB_cells, Lu_AD_H23, Lu_SC_H69
117500	N31909	Hs.44278	ESTs	2.18	PRSC_con, Lu_SC_H345, PRSC_log
131384	F13608	Hs.26226	ESTs	2.18	293T_cells, LNCaP_cells, OVCAR_cells
134499	U70370	Hs.84136	paired-like homeodomain transcription fa	2.18	Caco2, BT474_cells, MB231_cells
128154	AA922969	Hs.127100	ESTs	2.17	MB-MDA-453, MB-MDA-453, Lu_SC_H345
134585	T48154	Hs.168655	H sapiens mRNA for H-2K binding factor-2	2.17	LNCaP_cells, 293T_cells, PRSC_log
104987	AA101723	Hs.16683	ESTs	2.17	EB_cells, MCF7, DU145_cells
132992	AA091017	Hs.6226	ESTs	2.17	Caco2, LNCaP_cells, DU145_cells
135311	M36089	Hs.98493	X-ray repair complementing defective rep	2.17	HMEC (total RNA), Fibroblasts 2, HMEC
113171	T54613	Hs.9761	EST	2.17	HT29_cells, PRSC_con, Lu_SQ_H520
117736	N46999	Hs.46648	ESTs	2.16	PRSC_log, OVCAR_cells, A549_cells

125181	W58461	Hs.12396	ESTs	2.16	LNCaP_cells, DU145_cells, 293T_cells
120187	Z40251	Hs.56974	ESTs	2.16	LNCaP_cells, MB-MDA-453, HMEC (total RNA)
100308	D50532	Hs.54403	macrophage lectin 2 (calcium dependent)	2.16	HT29_cells, Lu_AD_H23, Lu_AD_H23
110960	N50887	Hs.26549	ESTs; Weakly similar to KIAA0449 protein	2.16	Caco2, A549_cells, LNCaP_cells
113608	T93113		ESTs; Moderately similar to !!!! ALU SUB	2.16	Lu_SC_H69, CALU6_cells, 293T_cells
107538	Z21089	Hs.50094	ESTs; Weakly similar to KALIRIN [R.norve	2.16	HS578T_cells, 293T_cells, DU145_cells
128703	S76992	Hs.104005	vav 2 oncogene	2.16	RPWE_2, Lu_SC_H69, HT29_cells
126065	AI366484		ESTs	2.16	293T_cells, CALU6_cells, A549_cells
130000	AA465727	Hs.124084	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.16	DU145_cells, LNCaP_cells, OVCAR_cells
120407	AA235040	Hs.107283	ESTs	2.16	EB_cells, 293T_cells, A549_cells
121199	AA400371	Hs.97792	ESTs	2.16	Lu_AD_358, Lu_AD_H23, A549_cells
114963	AA243867	Hs.193055	ESTs	2.16	DU145_cells, PRSC_con, LNCaP_cells
100343	D63874	Hs.189509	high-mobility group (nonhistone chromoso	2.15	CALU6_cells, MB-MDA-453, Caco2
125077	T88822		yd32f5.s1 Soares fetal liver spleen 1NFL	2.15	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
117286	N22181		yw36d12.s1 Morton Fetal Cochlea H sapien	2.15	293T_cells, Lu_SC_H345, Lu_SC_H69
132876	AA130603	Hs.169683	ESTs; Moderately similar to !!!! ALU SUB	2.15	EB_cells, LNCaP_cells, HS578T_cells
133834	AA147510	Hs.154737	serine protease; umbilical endothelium	2.15	DU145_cells, EB_cells, Caco2
126908	AA169866		ESTs; Weakly similar to !!!! ALU SUBFAMI	2.15	DU145_cells, LNCaP_cells, OVCAR_cells
106900	AA490142	Hs.6193	ESTs	2.15	Fibroblasts 2, Lu_AD_H23, PRSC_con
129398	AA437374	Hs.234573	H sapiens mRNA for TL132	2.15	MCF7, DU145_cells, LNCaP_cells
114512	AA044274	Hs.165215	ESTs	2.15	Lu_AD_358, MB-MDA-453, HS578T_cells
134381	U56637	Hs.184270	capping protein (actin filament) muscle	2.15	LNCaP_cells, EB_cells, PC3_cells
118848	N80671	Hs.220255	ESTs	2.14	EB_cells, DU145_cells, MCF7
115526	AA342049	Hs.69606	ESTs	2.14	293T_cells, Caco2, Lu_SC_H69
123460	AA598981	Hs.251122	EST	2.14	Lu_SC_H345, DU145_cells, MCF7
119812	W73951	Hs.58348	ESTs; Weakly similar to CORNIFIN A [H.sa	2.14	293T_cells, HS578T_cells, CALU6_cells
105263	AA227926	Hs.6682	ESTs	2.14	A549_cells, HMEC (total RNA), EB_cells
129242	W81679	Hs.5174	ribosomal protein S17	2.14	293T_cells, CALU6_cells, HMEC (total RNA)
132348	AA037285	Hs.170311	heterogeneous nuclear ribonucleoprotein	2.14	A549_cells, HT29_cells, Lu_SQ_H520
114425	AA015763	Hs.132812	ESTs	2.14	293T_cells, HS578T_cells, PRSC_con
127759	AI369384		arylsulfatase D	2.14	DU145_cells, LNCaP_cells, EB_cells
134069	U29607	Hs.78935	methionine aminopeptidase; eIF-2-associa	2.14	Lu_SC_H345, DU145_cells, MCF7
116158	AA461187	Hs.61762	ESTs	2.14	Lu_SC_H69, MCF7, MB-MDA-453
125627	R35166	Hs.14881	ESTs	2.14	HT29_cells, Fibroblasts 2, BT474_cells
118684	N71364	Hs.109510	ESTs	2.14	OVCAR_cells, PRSC_con, HS578T_cells
119419	T97977	Hs.60260	ESTs	2.14	Lu_AD_H23, Lu_SQ_H520, Lu_SQ_H520
133097	N67515	Hs.6479	ESTs; Weakly similar to KIAA0872 protein	2.14	EB_cells, Lu_AD_H23, Lu_AD_358
112121	R45445	Hs.252723	H sapiens mRNA; cDNA DKFZp434D115 (from	2.13	Lu_AD_H23, Lu_AD_358, BT474_cells
114894	AA236019	Hs.188803	ESTs	2.13	MB-MDA-453, MCF7, Lu_SQ_H520
124087	H08773		yl94d5.s1 Soares infant brain 1NIB H sap	2.13	Lu_SC_H69, Fibroblasts 2, HMEC (total RNA)
111902	R39191	Hs.109445	KIAA1020 protein	2.13	Caco2, 293T_cells, Lu_SC_H69
119943	W86835	Hs.14158	copine III	2.13	LNCaP_cells, PC3_cells, HS578T_cells
109276	AA196306	Hs.86045	ESTs	2.13	Lu_SC_H345, Lu_SC_H69, Lu_LC_H460
117351	N24581	Hs.43230	ESTs	2.13	HS578T_cells, CALU6_cells, PRSC_con
116046	AA453461	Hs.94491	H sapiens clone 23585 mRNA seq	2.13	LNCaP_cells, Caco2, EB_cells
112785	R96478	Hs.16586	ESTs	2.13	EB_cells, Lu_AD_H23, Lu_SC_H69
115835	AA428576	Hs.41371	ESTs	2.13	EB_cells, Lu_SC_H345, OVCAR_cells
127499	T49891	Hs.119252	tumor protein; translationally-controlle	2.13	EB_cells, PRSC_con, LNCaP_cells
129951	AA019475	Hs.74615	platelet-derived growth factor receptor;	2.13	EB_cells, Lu_AD_H23, Lu_SC_H69
124270	H79560	Hs.107840	ESTs	2.13	OVCAR_cells, 293T_cells, 293T_cells
133766	D52420	Hs.184326	cell division cycle 10 (homologous to CD	2.12	CALU6_cells, DU145_cells, PC3_cells
109248	AA194720	Hs.189996	ESTs; Highly similar to sec61 homolog [H	2.12	HT29_cells, MB231_cells, HMEC (total RNA)
106724	AA465226	Hs.28631	ESTs	2.12	EB_cells, 293T_cells, DU145_cells
100571	HG2264-H		Atpase, Ca2+ Transporting, Plasma Membra	2.12	EB_cells, Lu_AD_H23, Lu_SC_H69
133017	AA450187	Hs.178518	ESTs	2.12	OVCAR_cells, PC3_cells, 293T_cells
124313	H94650	Hs.108002	ESTs	2.12	MB-MDA-453, Lu_SC_H345, HT29_cells
113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (e	2.12	MB-MDA-453, PC3_cells, LNCaP_cells
113241	T63313	Hs.226136	ESTs; Moderately similar to !!!! ALU SUB	2.12	HMEC (total RNA), BT474_cells, HMEC
111952	R40782	Hs.21296	ESTs	2.12	HT29_cells, PC3_cells, A549_cells
113965	W86519	Hs.19631	ESTs	2.12	PC3_cells, EB_cells, LNCaP_cells
108059	AA043944	Hs.62663	ESTs	2.12	EB_cells, OVCAR_cells, 293T_cells
124235	H63994	Hs.221134	ESTs	2.12	Fibroblasts 2, MB-MDA-453, PRSC_con
106400	AA447621	Hs.31257	ESTs	2.12	DU145_cells, EB_cells, Caco2
119590	W44798	Hs.55876	ESTs	2.12	PRSC_log, Lu_SC_H69, Lu_SC_H345
112434	R63068	Hs.159793	EST	2.11	HS578T_cells, LNCaP_cells, OVCAR_cells
122731	AA457549		aa92b1.s1 Stratagene fetal retina 93722 gb:X5275_ma3 LEUKOSIALIN PRECURSOR (HU	2.11	MB-MDA-453, RPWE_2, MCF7
115348	AA281562	Hs.88860	ESTs	2.11	EB_cells, Lu_AD_H23, Fibroblasts 2
128873	AA226768	Hs.109463	ESTs; Weakly similar to predicted using	2.11	MB-MDA-435s, EB_cells, LNCaP_cells
133742	T54301	Hs.75844	ESTs	2.11	EB_cells, CALU6_cells, DU145_cells
102099	U11870	Hs.194778	interleukin 8 receptor; alpha	2.11	Lu_AD_358, PC3_cells, PRSC_con
125840	H05787	Hs.12064	ubiquitin specific protease 22	2.11	EB_cells, LNCaP_cells, Caco2
105501	AA256604	Hs.31930	ESTs	2.1	Fibroblasts 2, HS578T_cells, MB-MDA-435s
111576	R10334	Hs.15489	ESTs	2.1	Lu_SC_H69, PRSC_log, Lu_SC_H345
104275	C02170	Hs.39387	ESTs; Weakly similar to weak similarity	2.1	HT29_cells, MB231_cells, Lu_SC_H69
117803	N48620	Hs.28483	pregnancy specific beta-1-glycoprotein 9	2.1	HT29_cells, HMEC, RPWE_2

122725	AA457407	Hs.152204	transmembrane protease; serine 2	2.1	Lu_SC_H69, Lu_LC_H460, Lu_SC_H345
120987	AA398233	Hs.111894	KIAA0108 gene product	2.1	Fibroblasts 2, PRSC_con, MCF7
105932	AA403305	Hs.12185	ESTs; Weakly similar to myosin phosphata	2.1	LNCaP_cells, MCF7, OVCAR_cells
118398	N64706	Hs.137282	ESTs	2.1	Lu_SC_H345, HT29_cells, HMEC
103679	Z86000		Human DNA seq from PAC 151B14 on chromos receptor subtype 3 (SSTR3), tRNA, ESTs,	2.1	CALU6_cells, A549_cells, Lu_SC_H345
130303	L40392	Hs.180789	H sapiens (clone S164) mRNA; 3' end of c	2.1	PC3_cells, DU145_cells, LNCaP_cells
122815	AA461080	Hs.139446	ESTs	2.1	HT29_cells, BT474_cells, MB231_cells
105598	AA279439	Hs.20594	ESTs; Weakly similar to misato [D.melano	2.1	EB_cells, Lu_SC_H345, LNCaP_cells
124869	R69088	Hs.28728	ESTs; Weakly similar to F55A12.9 [C.eleg	2.1	HT29_cells, BT474_cells, MB231_cells
129599	F10720	Hs.180804	ESTs	2.1	HS578T_cells, HT29_cells, HT29_cells
110338	H40359	Hs.177256	ESTs	2.09	MCF7, A549_cells, MB-MDA-435s
134092	H17490	Hs.7905	ESTs; Highly similar to sorting nexin 9	2.09	EB_cells, Fibroblasts 2, HS578T_cells
133002	AF006082	Hs.62461	ARP2 (actin-related protein 2; yeast) ho	2.09	EB_cells, HS578T_cells, A549_cells
115570	AA398343	Hs.94943	ESTs	2.09	Lu_SC_H345, PC3_cells, LNCaP_cells
120055	W93299	Hs.59363	ESTs; Weakly similar to cytokeratin 20 [	2.09	HMEC (total RNA), HS578T_cells, HS578T_cells
116332	AA491208	Hs.62620	ESTs	2.09	EB_cells, Lu_AD_H23, Lu_SC_H69
105415	AA243768	Hs.4232	ESTs; Highly similar to match to ESTs Z4	2.09	LNCaP_cells, Lu_AD_H23, MB-MDA-453
116607	D80354	Hs.256321	EST	2.09	LNCaP_cells, DU145_cells, RPWE_2
126731	AA593973	Hs.232217	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.09	MB231_cells, HT29_cells, HMEC
102276	U30999	Hs.10247	activated leucocyte cell adhesion molecu	2.09	PC3_cells, HS578T_cells, DU145_cells
113666	T96077	Hs.17738	EST	2.09	Lu_AD_H23, Lu_AD_H23, Lu_SQ_H520
101183	L19779	Hs.795	H2A histone family; member O	2.09	LNCaP_cells, MCF7, OVCAR_cells
112177	R49025	Hs.22996	ESTs	2.09	Lu_AD_H23, Lu_AD_358, Lu_SC_H69
115038	AA252360	Hs.87968	ESTs	2.08	BT474_cells, MB231_cells, HT29_cells
109638	F04432	Hs.17904	ESTs	2.08	EB_cells, DU145_cells, PC3_cells
109592	F02475	Hs.26370	ESTs	2.08	Lu_AD_H23, Lu_SQ_H520, Lu_LC_H460
133740	U68142	Hs.170160	RAB2; member RAS oncogene family-like	2.08	LNCaP_cells, MB-MDA-453, EB_cells
126716	AA031700	Hs.251962	ESTs	2.08	HS578T_cells, Fibroblasts 2, Lu_SC_H69
124055	F10904	Hs.100516	H sapiens clone 23605 mRNA seq	2.08	Lu_SC_H345, OVCAR_cells, DU145_cells
113283	T66813	Hs.12947	EST	2.08	EB_cells, Lu_SC_H69, Lu_AD_H23
120097	W95068	Hs.59621	ESTs	2.08	HS578T_cells, A549_cells, CALU6_cells
102066	U08471	Hs.352	folate receptor 3 (gamma)	2.08	EB_cells, Lu_AD_H23, Lu_AD_358
108712	AA121993		zm24d11.s1 Stratagene pancreas (#93728) similar to gb:Y433 GLUTATHIONE PEROXIDAS	2.08	Lu_SQ_H520, HT29_cells, BT474_cells
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	2.08	EB_cells, Lu_SC_H345, Lu_SC_H69
103883	AA232836	Hs.87363	ESTs	2.08	HT29_cells, 293T_cells, 293T_cells
105313	AA233856	Hs.16930	ESTs	2.08	DU145_cells, MB-MDA-435s, HS578T_cells
113669	T96148	Hs.17762	ESTs	2.08	EB_cells, Lu_SQ_H520, Fibroblasts 2
120380	AA227904	Hs.104223	ESTs	2.08	293T_cells, CALU6_cells, A549_cells
121045	AA398554	Hs.181012	double-stranded RNA-binding zinc finger	2.08	293T_cells, PC3_cells, OVCAR_cells
104949	AA070735	Hs.146090	ESTs	2.08	Lu_SC_H69, Lu_SC_H345, RPWE_2
118751	N74210	Hs.50454	EST	2.08	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
112399	R60920	Hs.26419	H sapiens clone 24510 mRNA seq	2.08	EB_cells, Lu_AD_H23, Lu_SC_H69
129994	AA599443	Hs.38194	ESTs; Moderately similar to !!!! ALU SUB	2.08	DU145_cells, EB_cells, HS578T_cells
116402	AA600054	Hs.65302	ESTs	2.08	HT29_cells, BT474_cells, Lu_AD_H23
125307	Z40583	Hs.101259	ESTs	2.08	HMEC, HMEC (total RNA), EB_cells
105047	AA132453	Hs.15396	ESTs	2.08	Caco2, HT29_cells, LNCaP_cells
128659	T95280	Hs.103315	trinucleotide repeat containing 1	2.08	EB_cells, Lu_AD_H23, Lu_SC_H69
122301	AA437378	Hs.98791	ESTs	2.08	Lu_SC_H345, Lu_AD_H23, Lu_AD_358
121974	AA429804	Hs.229675	EST	2.08	HS578T_cells, 293T_cells, OVCAR_cells
116905	H71420		ys8c12.s1 Soares fetal liver spleen 1NFL 3' similar to contains Alu repetitive e	2.08	Lu_AD_H23, EB_cells, PRSC_con
106703	AA463979	Hs.21264	KIAA0782 protein	2.08	EB_cells, Caco2, PRSC_con
121908	AA427858	Hs.98534	EST	2.07	293T_cells, Lu_SC_H345, CALU6_cells
135119	T23992	Hs.94769	ESTs; Moderately similar to RAS-RELATED	2.07	HS578T_cells, PRSC_con, OVCAR_cells
103558	Z19574	Hs.2785	keratin 17	2.07	RPWE_2, HMEC (total RNA), HMEC
124209	H57317	Hs.193433	ESTs	2.07	Fibroblasts 2, OVCAR_cells, 293T_cells
133936	AA045083	Hs.77719	gamma-glutamyl carboxylase	2.07	Fibroblasts 2, MB-MDA-453, PRSC_con
116246	AA479961	Hs.42913	ESTs; Highly similar to ubiquitin-conjug	2.07	EB_cells, LNCaP_cells, LNCaP_cells
123230	AA490134	Hs.105308	EST	2.07	Lu_AD_H23, Lu_SC_H69, Lu_SC_H345
127378	AA452696		zx39b05.r1 Soares_total_fetus_Nb2HF8_9w to contains Alu repetitive element;cont	2.07	HS578T_cells, LNCaP_cells, EB_cells
110464	H53013	Hs.221901	ESTs	2.07	Fibroblasts 2, Lu_SQ_H520, Lu_SQ_H520
135191	X07619	Hs.169876	cytochrome P450; subfamily IID (debrisoq polypeptide 7a (pseudogene)	2.07	Lu_AD_H23, Lu_SC_H69, Lu_AD_358
101267	L36818	Hs.75339	inositol polyphosphate phosphatase-like	2.07	Lu_SC_H345, OVCAR_cells, Caco2
105185	AA191495	Hs.189937	ESTs	2.07	Lu_SC_H69, Lu_AD_H23, Lu_SC_H345
125366	H60192	Hs.76853	ESTs; Weakly similar to human homolog of	2.07	DU145_cells, Lu_LC_H460, Lu_AD_358
117472	N30131	Hs.93738	DKFZP434M098 protein	2.07	EB_cells, Lu_SC_H69, 293T_cells
114235	Z39710	Hs.25341	ESTs	2.07	DU145_cells, BT474_cells, Lu_SC_H69
109081	AA165268	Hs.72488	ESTs	2.07	Lu_SC_H69, Lu_SC_H345, PC3_cells
112596	R78212	Hs.163705	ESTs	2.07	MB-MDA-435s, Lu_SQ_H520, MB-MDA-453
109254	AA194940	Hs.85956	ESTs; Weakly similar to line-1 protein O	2.07	HS578T_cells, 293T_cells, OVCAR_cells
105898	AA401144	Hs.27354	ESTs	2.07	EB_cells, 293T_cells, PRSC_con
116290	AA488691	Hs.57969	phenylalanine-tRNA synthetase	2.06	Lu_AD_H23, Lu_SC_H345, PRSC_log

122529	AA449828	Hs.99229	ESTs	2.06	DU145_cells, HS578T_cells, 293T_cells
104612	R99199	Hs.173063	transducin-like enhancer of split 2; hom	2.06	MB-MDA-435s, 293T_cells, 293T_cells
116465	AA621650	Hs.41045	ESTs; Weakly similar to KIAA0734 protein	2.06	MB231_cells, HT29_cells, Lu_AD_358
123155	AA488414	Hs.76127	hect (homologous to the E6-AP (UBE3A) ca domain (RLD) 1	2.06	DU145_cells, CALU6_cells, PC3_cells
126752	AI073373	Hs.183275	ESTs	2.06	LNCaP_cells, EB_cells, DU145_cells
126455	N80749	Hs.111515	ESTs; Weakly similar to predicted using	2.06	CALU6_cells, PRSC_log, OVCAR_cells
129339	R77869	Hs.28506	ESTs	2.06	EB_cells, BT474_cells, Lu_AD_H23
115021	AA252028	Hs.39168	ESTs	2.06	Lu_SQ_H520, Fibroblasts 2, EB_cells
129054	T67231	Hs.168289	succinate dehydrogenase complex; subunit	2.06	Caco2, LNCaP_cells, EB_cells
101261	L35545	Hs.82353	endothelial cell protein C/activated pro	2.06	EB_cells, RPWE_2, DU145_cells
132697	AA281951	Hs.5518	H sapiens mRNA; cDNA DKFZp566J2146 (from	2.06	OVCAR_cells, LNCaP_cells, DU145_cells
124380	N26536	Hs.84999	ATPase; Cu++ transporting; beta polypept	2.06	Caco2, Caco2, 293T_cells
103967	AA303711	Hs.144700	ephrin-B1	2.06	HT29_cells, HMEC (total RNA), HMEC
119403	T92935	Hs.119908	ESTs; Highly similar to nucleolar protei	2.06	HMEC, EB_cells, HMEC (total RNA)
125755	R66080	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.06	LNCaP_cells, DU145_cells, OVCAR_cells
101843	M93405	Hs.170008	methylmalonate-semialdehyde dehydrogenas	2.05	LNCaP_cells, MB-MDA-453, EB_cells
113032	T24024	Hs.7387	DKFZP564B116 protein	2.05	EB_cells, A549_cells, A549_cells
112563	R72632	Hs.29282	ESTs	2.05	MCF7, HS578T_cells, PRSC_con
126432	AA583825	Hs.235860	ESTs	2.05	MB231_cells, HT29_cells, Fibroblasts 2
101636	M57763	Hs.89474	ADP-ribosylation factor 6	2.05	DU145_cells, LNCaP_cells, PC3_cells
125174	W51835	Hs.231082	EST	2.05	EB_cells, Fibroblasts 2, Lu_AD_H23
106168	AA425943	Hs.82208	acyl-Coenzyme A dehydrogenase; very long	2.05	OVCAR_cells, PC3_cells, EB_cells
135343	AA236796	Hs.9914	follistatin	2.05	HMEC (total RNA), PC3_cells, HMEC
105267	AA227956	Hs.25348	follistatin-like 3 (secreted glycoprotei	2.05	HMEC, RPWE_2, HMEC (total RNA)
134331	AA452020	Hs.234156	ESTs; Weakly similar to CGI-128 protein	2.05	EB_cells, CALU6_cells, A549_cells
121634	AA417012	Hs.28921	ESTs	2.05	HS578T_cells, EB_cells, Lu_SC_H345
131394	R72637	Hs.26343	ESTs	2.05	EB_cells, Lu_SC_H69, Lu_AD_H23
111526	R08260	Hs.20131	ESTs	2.05	Lu_AD_H23, Lu_SC_H69, BT474_cells
125049	T79840	Hs.111798	ESTs	2.05	HT29_cells, Lu_AD_H23, Lu_SC_H345
120433	AA237077	Hs.180777	H sapiens mRNA; cDNA DKFZp564M0264 (from	2.05	DU145_cells, CALU6_cells, PC3_cells
129498	AA449789	Hs.75511	connective tissue growth factor	2.05	HS578T_cells, PRSC_log, PRSC_con
127805	AA740921	Hs.1197	heat shock 10kD protein 1 (chaperonin 10	2.05	DU145_cells, LNCaP_cells, OVCAR_cells
109275	AA196287	Hs.20303	ESTs; Moderately similar to !!!! ALU SUB	2.05	EB_cells, MB-MDA-453, Fibroblasts 2
120683	AA290987	Hs.49657	ESTs; Weakly similar to contains similar	2.04	Lu_AD_358, Lu_SQ_H520, Lu_LC_H460
135415	X60655	Hs.99967	even-skipped homeo box 1 (homolog of Dro	2.04	Lu_AD_H23, RPWE_2, Lu_SQ_H520
132925	AA252759	Hs.238296	DKFZP434A033 protein	2.04	293T_cells, HS578T_cells, LNCaP_cells
101875	M97287	Hs.74592	special AT-rich seq binding protein 1 (b	2.04	EB_cells, Lu_SC_H69, 293T_cells
101463	M22490	Hs.68879	bone morphogenetic protein 4	2.04	PRSC_con, HT29_cells, MB231_cells
129177	T95005	Hs.209587	ESTs	2.04	293T_cells, MB-MDA-435s, Lu_SC_H69
130726	W88946	Hs.18508	putative glycine-N-acyltransferase	2.04	HT29_cells, Fibroblasts 2, MB-MDA-435s
105549	AA262417	Hs.5415	ESTs	2.04	DU145_cells, OVCAR_cells, PC3_cells
124543	N63706	Hs.104573	ESTs	2.04	Caco2, 293T_cells, DU145_cells
123062	AA482069	Hs.100847	ESTs	2.04	Lu_AD_358, HT29_cells, HT29_cells
109464	AA232857	Hs.87100	ESTs	2.04	DU145_cells, Lu_AD_H23, LNCaP_cells
129619	AA610116	Hs.11663	tetraspan NET-6 protein	2.04	BT474_cells, Caco2, LNCaP_cells
127545	AA935809	Hs.115899	ESTs	2.04	BT474_cells, MB-MDA-435s, MB-MDA-453
133068	R73427	Hs.235712	ESTs	2.04	Caco2, OVCAR_cells, MCF7
113609	T93263	Hs.16875	ESTs; Weakly similar to hypothetical pro	2.04	EB_cells, Lu_SC_H345, PRSC_con
106645	AA460270	Hs.27695	midline 1 (Opitz/BBB syndrome)	2.04	A549_cells, 293T_cells, Caco2
126256	Z21124		HSAAADNVE TEST1, Human adult Testis tiss	2.04	Fibroblasts 2, Fibroblasts 2, MCF7
129697	R00841	Hs.172069	DKFZP434C212 protein	2.04	HT29_cells, Lu_SQ_H520, BT474_cells
126730	T19477		A1426R Heart H sapiens cDNA clone A1426,	2.04	EB_cells, Lu_AD_H23, Lu_SC_H69
125244	W86466	Hs.132756	ESTs; Weakly similar to KIAA0591 protein	2.04	EB_cells, Lu_AD_H23, Lu_LC_H460
134762	M91036	Hs.242985	hemoglobin; gamma G	2.04	MB231_cells, Lu_AD_358, HT29_cells
119564	W38206		Accession not listed in Genbank	2.04	BT474_cells, HT29_cells, Lu_AD_H23
132523	AB002332	Hs.50722	clock (mouse) homolog	2.04	PC3_cells, OVCAR_cells, PRSC_log
127758	AI337031	Hs.180195	ESTs	2.04	293T_cells, MB-MDA-435s, A549_cells
126471	AA158755	Hs.175652	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.04	EB_cells, Lu_AD_358, Lu_LC_H460
110911	N45120	Hs.22305	ESTs	2.03	Lu_AD_H23, RPWE_2, Lu_LC_H460
122317	AA442742	Hs.8693	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.03	EB_cells, Fibroblasts 2, Lu_SC_H345
100253	D38024	Hs.247951	Humn facioscapulohumeral muscular dystro	2.03	Lu_AD_H23, Lu_AD_358, Lu_SQ_H520
120431	AA236884	Hs.247323	H sapiens mRNA for G4 protein (G4 gene;	2.03	Lu_SC_H69, EB_cells, Lu_SC_H345
122449	AA447638	Hs.104977	ESTs	2.03	Lu_SC_H345, Lu_SC_H345, Lu_SQ_H520
100961	J00148		Accession not listed in Genbank	2.03	HT29_cells, BT474_cells, HMEC
130908	W86389	Hs.21122	ESTs; Moderately similar to KIAA0438 [H.	2.03	293T_cells, Lu_SC_H345, OVCAR_cells
102643	U67849		Human beta-galactoside alpha2,6-sialyltr	2.03	HT29_cells, 293T_cells, Lu_SC_H345
127932	AA398510	Hs.133148	ESTs	2.03	EB_cells, Lu_SC_H345, Lu_SC_H69
109207	AA190906	Hs.204692	ESTs	2.03	Lu_SQ_H520, Lu_SC_H345, Lu_SC_H69
102598	U62962	Hs.106673	eukaryotic translation initiation factor	2.03	EB_cells, DU145_cells, MCF7
124470	N51702	Hs.101392	ESTs	2.03	HT29_cells, Fibroblasts 2, HMEC (total RNA)
104961	AA076672	Hs.33905	ESTs	2.03	Caco2, LNCaP_cells, EB_cells
124164	H30667	Hs.7535	ESTs; Highly similar to COBW-like placen	2.03	CALU6_cells, CALU6_cells, A549_cells
126468	AA242853	Hs.237856	ESTs; Moderately similar to cAMP inducib	2.03	MB231_cells, BT474_cells, Fibroblasts 2
129683	W05348	Hs.158196	DKFZP434B103 protein	2.03	HT29_cells, MB-MDA-435s, Lu_AD_H23
105350	AA235737	Hs.186571	ATPase; Na+/K+ transporting; alpha 3 pol	2.03	MB-MDA-453, Lu_SQ_H520, Lu_AD_358

129794	AA447772	Hs.14520	eukaryotic translation initiation factor	2.03	EB_cells, Lu_AD_358, Lu_AD_H23
115664	AA405974	Hs.54673	tumor necrosis factor (ligand) superfami	2.03	Lu_AD_358, HT29_cells, HT29_cells
119096	R41672	Hs.91471	ATPase type IV; phospholipid transportin	2.03	HT29_cells, MB231_cells, BT474_cells
133866	L36151	Hs.171625	phosphatidylinositol 4-kinase; catalytic	2.03	293T_cells, DU145_cells, LNCaP_cells
132055	N69440	Hs.38132	ESTs	2.03	Lu_SC_H345, MB-MDA-453, MB-MDA-435s
125691	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.03	Lu_SC_H345, LNCaP_cells, DU145_cells
121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND TRANSPORTER 2 [H.sapiens]	2.03	LNCaP_cells, HT29_cells, RPWE_2
105289	AA233178	Hs.103000	KIAA0831 protein	2.02	PC3_cells, Lu_AD_H23, MB231_cells
100967	J02621	Hs.251064	high-mobility group (nonhistone chromoso	2.02	MCF7, DU145_cells, OVCAR_cells
124430	N38913	Hs.221575	ESTs	2.02	MB-MDA-435s, Fibroblasts 2, EB_cells
128322	AI306331	Hs.133296	ESTs	2.02	HT29_cells, MB-MDA-435s, Lu_SC_H345
131077	X91809	Hs.22698	G alpha interacting protein	2.02	Lu_AD_H23, RPWE_2, MCF7
108033	AA040923	Hs.92200	KIAA0480 gene product	2.02	MCF7, Fibroblasts 2, DU145_cells
107550	AA001045	Hs.46783	ESTs	2.02	DU145_cells, PC3_cells, OVCAR_cells
109475	AA233159	Hs.87131	ESTs	2.02	HT29_cells, MB-MDA-435s, Lu_SC_H69
111400	R00144	Hs.189771	ESTs	2.02	HT29_cells, Fibroblasts 2, HMEC
117516	N32495	Hs.151560	ESTs	2.02	HT29_cells, HMEC (total RNA), Fibroblasts 2
120506	AA257955	Hs.173705	ESTs; Weakly similar to !!!! ALU CLASS C	2.02	MCF7, Fibroblasts 2, LNCaP_cells
130850	N39306	Hs.20237	DKFZP566C134 protein	2.02	EB_cells, Lu_AD_H23, Lu_LC_H460
123118	AA486571	Hs.105696	ESTs; Moderately similar to !!!! ALU SUB	2.02	CALU6_cells, 293T_cells, PRSC_log
111285	N71704	Hs.4310	eukaryotic translation initiation factor	2.02	293T_cells, PC3_cells, EB_cells
119106	R42362	Hs.91785	ESTs	2.02	CALU6_cells, MB-MDA-453, PC3_cells
111370	N92915	Hs.94631	brefeldin A-inhibited guanine nucleotide	2.02	EB_cells, OVCAR_cells, LNCaP_cells
125013	T67261	Hs.154431	ESTs; Weakly similar to neuronal thread	2.02	Lu_SC_H345, Lu_SC_H69, PRSC_con
129762	AA460273	Hs.12372	KIAA0517 protein	2.02	EB_cells, MB-MDA-435s, OVCAR_cells
120704	AA291970	Hs.107054	KIAA0821 protein	2.01	Lu_SC_H69, EB_cells, MB-MDA-453
105355	AA235985	Hs.26938	Human DNA seq from clone 126A5 on chromo genes (one with DnaJ domains); the gene family member HKR3. Contains ESTs; STSs;	2.01	Lu_AD_H23, Lu_LC_H460, Lu_SQ_H520
125952	AA017723		small inducible cytokine A5 (RANTES)	2.01	LNCaP_cells, DU145_cells, MB231_cells
103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.01	HMEC (total RNA), HMEC, RPWE_2
133544	T33873	Hs.74624	protein tyrosine phosphatase; receptor t	2.01	Lu_SC_H345, BT474_cells, HT29_cells
112746	R93237		yq11e10.s1 Soares fetal liver spleen 1NF IMAGE:196650 3', mRNA seq.	2.01	PC3_cells, LNCaP_cells, OVCAR_cells
118513	N67504	Hs.40061	ESTs	2.01	Lu_SC_H345, Lu_SC_H69, PRSC_con
123423	AA598484	Hs.238476	EST	2.01	EB_cells, Lu_AD_H23, Lu_SC_H345
127854	AA769520		ESTs; Weakly similar to REGULATOR OF MIT	2.01	HS578T_cells, CALU6_cells,
Lu_SQ_H520					
111843	R36969	Hs.18888	ESTs	2.01	Lu_AD_H23, Lu_AD_358, Lu_SQ_H520
100221	D28383		Human mRNA for ATP synthase B chain, 5'U	2.01	EB_cells, Lu_AD_H23, LNCaP_cells
129966	AA452237	Hs.194443	ESTs; Weakly similar to BC37295_2 [H.sap	2.01	Lu_SC_H345, Lu_SC_H69, DU145_cells
106798	AA478968	Hs.20558	ESTs	2.01	EB_cells, Lu_AD_H23, Lu_LC_H460
114636	AA085374		zn13d5.s1 Stratagene hNT neuron (#937233 gb:L8441 CYTOCHROME C OXIDASE POLYPEPTI	2.01	EB_cells, CALU6_cells, OVCAR_cells
125348	H21585	Hs.191277	ESTs; Moderately similar to ATP binding	2.01	EB_cells, HS578T_cells, PC3_cells
130620	AA233245	Hs.16773	ESTs	2.01	EB_cells, DU145_cells, 293T_cells
106471	AA450118	Hs.25722	ESTs; Weakly similar to ZINC FINGER PROT	2.01	OVCAR_cells, LNCaP_cells, EB_cells
134175	T33128	Hs.7966	ESTs	2	Lu_SC_H345, Fibroblasts 2, Lu_AD_H23
117291	N22289		yw36g08.s1 Morton Fetal Cochlea H sapien	2	MB-MDA-453, OVCAR_cells, CALU6_cells
134199	U47635	Hs.79877	myotubularin related protein 6	2	EB_cells, PC3_cells, LNCaP_cells
128758	AA129545	Hs.181165	eukaryotic translation elongation factor	2	Lu_SC_H69, EB_cells, Lu_SC_H345
112005	R42569	Hs.22444	ESTs	2	Lu_AD_H23, PRSC_log, Lu_AD_358
122521	AA449433	Hs.149227	ESTs; Weakly similar to PROLINE-RICH PRO	2	HT29_cells, RPWE_2, MB231_cells
130356	X84373	Hs.155017	nuclear receptor interacting protein 1	2	DU145_cells, PC3_cells, MCF7
114067	Z38153	Hs.26921	ESTs	2	293T_cells, MB-MDA-435s, HT29_cells
107136	AA620795	Hs.8207	ESTs	2	LNCaP_cells, PC3_cells, EB_cells

Table 3

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UG_ID	Complete_Title	Ratio BS/Met	Top 3 expressing cell lines
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	19.71	EB, NCI-H520, NCI-H23
316304	AI936587	Hs.221599	ESTs	14.49	PRSC_con, RPWE-2, OVCA-R
339196			CH22_FF113D11.GENSCAN.3-1	10.37	NCI-H69, PRSC_con, NCI-H345
336171			CH22_FGENES.708_3	9.45	NCI-H69, NCI-H460, NCI-H23
338895			CH22_DJ32I10.GENSCAN.9-2	9.31	PC3, BT474, OVCA-R
333625			CH22_FGENES.223_2	8.96	NCI-H69, PRSC_con, NCI-H345
333730			CH22_FGENES.258_1	8.82	NCI-H69, BT474, MB-MDA-231
320244	AA296922	Hs.129778	gastrointestinal peptide	8.22	BT474, CALU6, DU145
333643			CH22_FGENES.232_2	7.66	MCF7, NCI-H69, LnCap
333423			CH22_FGENES.147_3	7.57	HT29, MB-MDA-231, EB
302332	AI833168	Hs.184507	H sapiens Chromosome 16 BAC clone CIT987	7.55	MB-MDA-231, HT29, MB-MDA-453
333588			CH22_FGENES.206_2	7.46	HT29, OVCA-R, BT474
322033	AL137507		EST cluster (not in UniGene)	7.35	PRSC_con, PRSC_log, NCI-H345
308601	AI719930		EST singleton (not in UniGene) with exon	6.83	PC3, DU145, DU145
339044			CH22_DA59H18.GENSCAN.27-5	6.46	NCI-H69, NCI-H345, PRSC_log
314516	AA371513	Hs.231748	ESTs	6.41	EB, OVCA-R, Caco2
327805			CH.05_hs gi|5867968	6.28	NCI-H69, NCI-H345, PRSC_con
334239			CH22_FGENES.364_2	6.09	NCI-H520, MB-MDA-435s, MB-MDA-453
332958			CH22_FGENES.48_15	6.04	NCI-H69, PRSC_con, PRSC_log
313386	W85772	Hs.173924	ESTs	5.88	MB-MDA-231, OVCA-R, BT474
314350	AL037927	Hs.190675	ESTs; Moderately similar to !!!! ALU SUB	5.84	OVCA-R, CALU6, EB
337170			CH22_FGENES.564-1	5.67	LnCap, CALU6, NCI-H69
337503			CH22_FGENES.803-1	5.66	NCI-H345, PRSC_con, RPWE-2
337562			CH22_C65E1.GENSCAN.1-2	5.53	HT29, MB-MDA-453, BT474
337219			CH22_FGENES.614-3	5.45	NCI-H69, NCI-H345, PRSC_log
311331	AI679622	Hs.32225	immunoglobulin alpha 1	5.43	NCI-H69, NCI-H23, NCI-H345
314251	AA713589		EST cluster (not in UniGene)	5.41	PC3, EB, LnCap
336246			CH22_FGENES.746_5	5.34	NCI-H69, NCI-H345, PRSC_log
335009			CH22_FGENES.472_13	5.31	EB, EB, NCI-H69
339365			CH22_BA354I12.GENSCAN.34-1	5.25	PRSC_con, NCI-H69, PRSC_log
336088			CH22_FGENES.688_17	5.21	PRSC_con, Caco2, PRSC_log
334966			CH22_FGENES.465_36	5.16	DU145, BT474, MB-MDA-231
334666			CH22_FGENES.418_18	5.15	NCI-H69, NCI-H345, PRSC_log
316830	AW182106	Hs.127821	ESTs	5.12	NCI-H345, PRSC_con, PRSC_log
339413			CH22_DJ579N16.GENSCAN.5-8	5.06	NCI-H69, NCI-H345, PRSC_log
337951			CH22_EM:AC005500.GENSCAN.94-1	5.01	NCI-H345, NCI-H69, PRSC_con
330153			CH.21_p2 gi|4325335	5	PRSC_con, PRSC_log, NCI-H69
333987			CH22_FGENES.310_11	4.96	MB-MDA-231, MB-MDA-453, MB-MDA-453
334304			CH22_FGENES.373_7	4.96	OVCA-R, CALU6, NCI-H23
338990			CH22_DA59H18.GENSCAN.6-6	4.95	PRSC_log, PRSC_con, NCI-H69
333152			CH22_FGENES.89_1	4.89	MB-MDA-435s, OVCA-R, A549
327049			CH.21_hs gi|6531965	4.87	PRSC_con, NCI-H345, PRSC_log
337225			CH22_FGENES.626-3	4.83	DU145, CALU6, EB
333496			CH22_FGENES.168_6	4.81	NCI-H69, NCI-H345, PRSC_con
334451			CH22_FGENES.387_11	4.79	RPWE-2, PRSC_con, NCI-H69
333594			CH22_FGENES.210_3	4.78	OVCA-R, PC3, HT29
333635			CH22_FGENES.228_2	4.78	NCI-H69, PRSC_log, PRSC_con
336796			CH22_FGENES.176-6	4.73	NCI-H69, NCI-H345, PRSC_log
333313			CH22_FGENES.138_5	4.72	NCI-H69, NCI-H345, PRSC_log
336833			CH22_FGENES.242-2	4.7	NCI-H345, NCI-H69, PRSC_con
336090			CH22_FGENES.689_2	4.7	NCI-H69, PRSC_con, PRSC_log
336645			CH22_FGENES.26-1	4.63	HT29, OVCA-R, DU145
334565			CH22_FGENES.405_5	4.62	NCI-H345, PRSC_log, RPWE-2
333242			CH22_FGENES.111_6	4.56	NCI-H345, PRSC_log, PRSC_con
326304			CH.17_hs gi|5867277	4.48	OVCA-R, EB, DU145
337445			CH22_FGENES.769-4	4.47	RPWE-2, NCI-H69, PRSC_log
327413			CH.02_hs gi|5867750	4.46	NCI-H69, PRSC_log, NCI-H345
327990			CH.06_hs gi|5868218	4.44	PRSC_con, PRSC_log, RPWE-2
325038	H38304	Hs.21782	ESTs	4.43	PRSC_con, MB-MDA-231, HT29
314923	AI732489	Hs.136370	ESTs	4.4	HT29, MB-MDA-231, NCI-358
328859			CH.07_hs gi|6381928	4.4	OVCA-R, BT474, A549
334476			CH22_FGENES.394_7	4.38	OVCA-R, PC3, EB
336092			CH22_FGENES.689_6	4.35	PRSC_con, Caco2, PRSC_log
333965			CH22_FGENES.305_3	4.35	NCI-H69, NCI-H345, PRSC_log

336402			CH22_FGENES.823_17	4.34	RPWE-2, HT29, OVCA-R
337947			CH22_EM:AC005500.GENSCAN.90-5	4.33	OVCA-R, DU145, PC3
337504			CH22_FGENES.803-2	4.33	NCI-H345, PRSC_con, PRSC_log
336813			CH22_FGENES.213-6	4.33	DU145, HT29, OVCA-R
338069			CH22_EM:AC005500.GENSCAN.166-14	4.33	NCI-H69, PRSC_con, NCI-H345
318538	N28625	Hs.74034	caveolin 1; caveolae protein; 22kD	4.31	PC3, A549, BT474
333631			CH22_FGENES.227_2	4.3	OVCA-R, PRSC_con, LnCap
302646	M14268		EST	4.27	PRSC_con, PRSC_log, RPWE-2
336049			CH22_FGENES.681_2	4.26	HT29, DU145, DU145
335667			CH22_FGENES.590_18	4.25	NCI-H520, Caco2, MB-MDA-453
320352	Y13323	Hs.145296	disintegrin protease	4.25	MB-MDA-231, DU145, BT474
304480	AA430373		EST singleton (not in UniGene) with exon	4.22	NCI-358, NCI-H460, NCI-H23
327273			CH.01_hs gi|5867466	4.22	NCI-H69, NCI-H345, PRSC_con
334540			CH22_FGENES.403_5	4.17	NCI-H69, NCI-H345, PRSC_log
334719			CH22_FGENES.421_30	4.17	NCI-H69, NCI-H345, RPWE-2
327827			CH.05_hs gi|5867968	4.17	OVCA-R, NCI-H69, CALU6
333599			CH22_FGENES.212_2	4.17	PRSC_log, NCI-H69, PRSC_con
329638			CH.12_p2 gi|3779004	4.16	DU145, MB-MDA-231, HT29
307556	AI281651		EST singleton (not in UniGene) with exon	4.16	BT474, HT29, CALU6
336836			CH22_FGENES.247-11	4.15	PRSC_con, NCI-H345, NCI-H69
323187	AL121180	Hs.240038	ESTs	4.14	NCI-H345, MB-MDA-435s, RPWE-2
336397			CH22_FGENES.823_12	4.13	NCI-H345, PRSC_con, RPWE-2
325007	AA736429		EST cluster (not in UniGene)	4.13	NCI-H69, PRSC_con, NCI-H345
300199	AI304386	Hs.150836	ESTs	4.11	NCI-H345, PRSC_con, PRSC_log
335832			CH22_FGENES.620_6	4.08	NCI-H69, NCI-H345, PRSC_log
312778	AI631655	Hs.197919	ESTs	4.07	NCI-358, NCI-H23, PRSC_con
323164	AA765301	Hs.151858	ESTs	4.06	NCI-H23, A549, HT29
315871	AW135312	Hs.117237	ESTs	4.05	MB-MDA-231, EB, MCF7
337452			CH22_FGENES.775-1	4.02	PRSC_con, PRSC_log, NCI-H345
335265			CH22_FGENES.521_1	4.01	NCI-H69, MCF7, RPWE-2
335200			CH22_FGENES.508_9	4.01	NCI-H69, PRSC_log, PRSC_con
336917			CH22_FGENES.346-4	3.99	PRSC_con, NCI-H345, PRSC_log
336584			CH22_FGENES.847_1	3.98	PRSC_log, PRSC_con, RPWE-2
333382			CH22_FGENES.143_21	3.97	EB, A549, HT29
329436			CH.Y_hs gi|5868883	3.97	BT474, PC3, HT29
336929			CH22_FGENES.349-3	3.94	NCI-H69, NCI-H345, PRSC_log
337238			CH22_FGENES.641-3	3.92	NCI-H69, NCI-H345, PRSC_log
333875			CH22_FGENES.291_11	3.92	PRSC_con, RPWE-2, PRSC_log
337069			CH22_FGENES.448-2	3.9	NCI-H69, LnCap, RPWE-2
332491	M24470	Hs.1435	guanosine monophosphate reductase	3.86	OVCA-R, MB-MDA-435s, CALU6
304623	AA521331		EST singleton (not in UniGene) with exon	3.86	OVCA-R, DU145, PC3
335348			CH22_FGENES.537_4	3.85	HT29, MB-MDA-231, PC3
334568			CH22_FGENES.405_9	3.85	NCI-H69, NCI-H345, PRSC_log
336924			CH22_FGENES.347-9	3.84	NCI-H345, PRSC_log, RPWE-2
301654	H81795		EST	3.84	NCI-H520, LnCap, NCI-358
334677			CH22_FGENES.418_30	3.83	PRSC_con, NCI-H345, NCI-H69
326688			CH.20_hs gi|5867582	3.83	NCI-H345, PRSC_con, PRSC_log
327790			CH.05_hs gi|5867977	3.8	PRSC_con, PRSC_log, NCI-H345
334591			CH22_FGENES.408_1	3.8	NCI-H69, PRSC_log, NCI-H345
337974			CH22_EM:AC005500.GENSCAN.106-3	3.78	PRSC_log, PRSC_con, NCI-H345
311274	AW293128	Hs.197101	ESTs	3.78	NCI-H345, PRSC_con, RPWE-2
326668			CH.20_hs gi|6552455	3.78	NCI-H345, NCI-H69, PRSC_log
304195	N35382		EST singleton (not in UniGene) with exon	3.77	NCI-H69, RPWE-2, PRSC_con
336294			CH22_FGENES.786_4	3.77	PRSC_con, PRSC_log, NCI-H69
311613	AL046311	Hs.252443	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.76	HT29, BT474, MB-MDA-231
338123			CH22_EM:AC005500.GENSCAN.195-5	3.75	MB-MDA-231, HT29, BT474
318230	AA558125		EST cluster (not in UniGene)	3.74	RPWE-2, PRSC_con, NCI-H345
303985	AW514501	Hs.156110	Immunoglobulin kappa variable 1D-8	3.73	MB-MDA-231, BT474, PRSC_con
336502			CH22_FGENES.833_8	3.72	NCI-H345, RPWE-2, PRSC_con
334063			CH22_FGENES.327_17	3.71	NCI-H69, NCI-H345, PRSC_con
333600			CH22_FGENES.213_2	3.7	NCI-H69, OVCA-R, PC3
339424			CH22_DJ579N16.GENSCAN.14-3	3.69	NCI-H69, NCI-H345, PRSC_con
336862			CH22_FGENES.297-2	3.67	NCI-H345, PRSC_con, PRSC_log
334823			CH22_FGENES.437_5	3.67	RPWE-2, PRSC_log, PRSC_con
329940			CH.16_p2 gi|6165199	3.66	CALU6, EB, MCF7
300275	AI632123	Hs.231521	ESTs	3.66	PRSC_con, NCI-H69, RPWE-2
328820			CH.07_hs gi|5868330	3.66	NCI-H69, NCI-H345, PRSC_con
332398	AA446446	Hs.104788	H sapiens clone 24554 unknown mRNA	3.66	PRSC_con, PRSC_log, NCI-H345
325791			CH.14_hs gi|6682476	3.65	NCI-H345, BT474, LnCap
300672	R14469	Hs.256573	ESTs	3.65	MCF7, MB-MDA-453, MB-MDA-435s
338344			CH22_EM:AC005500.GENSCAN.312-8	3.65	NCI-H345, PRSC_log, PRSC_con
333257			CH22_FGENES.118_5	3.65	DU145, EB, OVCA-R
332140	AA620724	Hs.112890	ESTs	3.65	MB-MDA-453, DU145, MCF7
337489			CH22_FGENES.799-2	3.63	NCI-H345, NCI-H69, PRSC_log
305167	AA663080		EST singleton (not in UniGene) with exon	3.63	OVCA-R, MB-MDA-231, MB-MDA-435s
336200			CH22_FGENES.719_4	3.61	NCI-H69, PRSC_log, NCI-H345

339208			CH22_FF113D11.GENSCAN.6-3	3.59	PRSC_con, NCI-H69, PRSC_log
320090	AB002058	Hs.113275	purinergic receptor P2X-like 1; orphan r	3.58	OVCA-R, LnCap, NCI-H69
335999			CH22_FGENES.657_1	3.57	NCI-H345, NCI-H69, PRSC_con
332909			CH22_FGENES.36_13	3.57	NCI-H345, PRSC_con, PRSC_log
306531	AA991423		EST singleton (not in UniGene) with exon	3.56	BT474, MB-MDA-453, MB-MDA-435s
333261			CH22_FGENES.119_1	3.55	HT29, CALU6, MB-MDA-231
303883	AA176396	Hs.169624	ESTs	3.54	NCI-H69, NCI-H345, RPWE-2
335831			CH22_FGENES.620_5	3.53	MCF7, BT474, OVCA-R
333983			CH22_FGENES.310_7	3.52	NCI-H345, PRSC_con, PRSC_log
333623			CH22_FGENES.222_2	3.51	NCI-H69, PRSC_con, PRSC_log
333997			CH22_FGENES.310_22	3.5	NCI-H345, PRSC_con, PRSC_log
325623			CH.14_hs gi|5867000	3.5	CALU6, HT29, BT474
309151	AI935829	Hs.140	immunoglobulin gamma 3 (Gm marker)	3.49	EB, MCF7, MB-MDA-453
305080	AA641485		EST singleton (not in UniGene) with exon	3.49	NCI-H23, NCI-H460, NCI-358
339268			CH22_BA354I12.GENSCAN.10-6	3.47	NCI-H69, NCI-H345, PRSC_con
310048	AI198352	Hs.105077	ESTs	3.47	Caco2, PRSC_con, NCI-H69
314758	AA521458	Hs.192738	ESTs	3.46	NCI-H23, NCI-H23, NCI-H520
334664			CH22_FGENES.418_15	3.45	NCI-H69, PRSC_log, PRSC_con
334661			CH22_FGENES.418_9	3.45	NCI-H69, PRSC_con, PRSC_log
330984	H38678	Hs.32766	H sapiens clone 24803 mRNA seq	3.44	OVCA-R, MCF7, PC3
333464			CH22_FGENES.160_1	3.44	NCI-H69, MB-MDA-231, MCF7
333580			CH22_FGENES.199_2	3.42	PRSC_con, NCI-H69, PRSC_log
313356	AI266254	Hs.132929	ESTs	3.42	RPWE-2, PRSC_con, NCI-H345
334518			CH22_FGENES.400_1	3.41	PRSC_log, PRSC_con, RPWE-2
333627			CH22_FGENES.225_2	3.4	HT29, BT474, BT474
309641	AW194230	Hs.253100	EST	3.4	HT29, MB-MDA-453, MCF7
338221			CH22_EM:AC005500.GENSCAN.246-10	3.4	NCI-H69, PRSC_log, NCI-H345
312993	AI392673	Hs.125230	ESTs	3.4	PRSC_log, NCI-H345, NCI-H345
318336	AI971806	Hs.164158	ESTs	3.38	OVCA-R, EB, CALU6
326218			CH.17_hs gi|5867226	3.38	NCI-H460, NCI-H69, NCI-H345
336231			CH22_FGENES.736_3	3.38	NCI-H69, NCI-H345, PRSC_log
307912	AI382224		EST singleton (not in UniGene) with exon	3.37	NCI-H345, PRSC_con, RPWE-2
336161			CH22_FGENES.707_6	3.37	NCI-H69, NCI-H345, RPWE-2
300875	AW134756	Hs.192477	ESTs	3.37	RPWE-2, PRSC_log, PRSC_con
336593			CH22_FGENES.135_1	3.37	PRSC_con, NCI-H69, RPWE-2
310696	AI431620	Hs.160875	ESTs	3.36	HT29, OVCA-R, BT474
304745	AA577771		EST singleton (not in UniGene) with exon	3.36	NCI-H345, RPWE-2, PRSC_con
308911	AI860287	Hs.156110	Immunoglobulin kappa variable 1D-8	3.36	EB, DU145, CALU6
336347			CH22_FGENES.815_3	3.36	NCI-H69, PRSC_log, PRSC_con
334906			CH22_FGENES.452_21	3.33	Caco2, CALU6, MB-MDA-453
334548			CH22_FGENES.403_13	3.33	NCI-H345, PRSC_con, NCI-H69
336695			CH22_FGENES.48-4	3.32	NCI-H69, PRSC_log, PRSC_con
316684	AA807187	Hs.220783	ESTs; Weakly similar to WNT-1 PROTO-ONCO	3.31	DU145, EB, MB-MDA-231
315901	AI521558	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.3	Caco2, LnCap, NCI-H69
320115	T93574		EST cluster (not in UniGene)	3.3	DU145, HT29, CALU6
307847	AI363993	Hs.157273	EST	3.3	NCI-H345, PRSC_con, PRSC_log
327899			CH.06_hs gi|5868156	3.28	BT474, MB-MDA-231, A549
304612	AA514207		EST singleton (not in UniGene) with exon	3.28	DU145, CALU6, LnCap
330021			CH.16_p2 gi|6671889	3.27	A549, HT29, EB
338132			CH22_EM:AC005500.GENSCAN.200-2	3.27	MB-MDA-231, CALU6, EB
323690	AA317497	Hs.188897	ESTs	3.27	RPWE-2, NCI-H345, MCF7
327362			CH.01_hs gi|6552412	3.26	NCI-H69, RPWE-2, PRSC_log
333488			CH22_FGENES.167_3	3.26	NCI-H69, NCI-H345, PRSC_log
334106			CH22_FGENES.330_5	3.26	NCI-H69, PRSC_con, PRSC_log
306990	AI129298	Hs.146491	EST; Weakly similar to FERRITIN HEAVY CH	3.26	NCI-H345, PRSC_log, PRSC_con
328420			CH.07_hs gi|5868411	3.26	NCI-H69, NCI-H345, PRSC_log
336214			CH22_FGENES.722_8	3.26	MCF7, EB, OVCA-R
330565	U51095	Hs.1545	caudal type homeo box transcription fact	3.25	EB, DU145, HT29
333879			CH22_FGENES.291_15	3.25	PRSC_con, PRSC_log, NCI-H69
300145	AI240850	Hs.232016	ESTs	3.25	NCI-H345, PRSC_con, PRSC_log
327581			CH.03_hs gi|5867825	3.25	EB, DU145, MB-MDA-453
308153	AI500429	Hs.1103	transforming growth factor; beta 1	3.24	MCF7, EB, EB
308337	AI608947		EST singleton (not in UniGene) with exon	3.24	PRSC_log, PRSC_con, NCI-H345
329406			CH.X_hs gi|6682547	3.23	DU145, HT29, MB-MDA-231
325482			CH.12_hs gi|5866957	3.23	NCI-H69, NCI-H345, PRSC_con
337544			CH22_FGENES.833-7	3.22	NCI-H69, NCI-H345, PRSC_con
337204			CH22_FGENES.595-1	3.22	NCI-H69, PRSC_con, PRSC_log
309451	AW105128	Hs.246687	EST	3.22	PRSC_con, RPWE-2, NCI-H345
337259			CH22_FGENES.649-3	3.2	PRSC_con, NCI-H345, NCI-H69
336489			CH22_FGENES.831_10	3.2	CALU6, MB-MDA-435s, Caco2
334804			CH22_FGENES.435_4	3.18	PRSC_log, PRSC_con, RPWE-2
335739			CH22_FGENES.601_10	3.18	NCI-H69, RPWE-2, PRSC_con
306264	AA935305	Hs.179779	ribosomal protein L37	3.17	LnCap, NCI-H69, EB
329386			CH.X_hs gi|6004484	3.17	RPWE-2, NCI-H345, PRSC_log
323479	AA278246		EST cluster (not in UniGene)	3.16	PRSC_con, NCI-H345, RPWE-2
304731	AA576085		EST singleton (not in UniGene) with exon	3.16	NCI-H69, LnCap, DU145

	339419			CH22_DJ579N16.GENSCAN.11-11	3.15	NCI-H69, PRSC_log, RPWE-2
	301202	AI536797	Hs.173155	ESTs	3.15	LnCap, NCI-H69, Caco2
	333608			CH22_FGENES.216_3	3.15	NCI-H345, PRSC_con, PRSC_log
	339193			CH22_FF113D11.GENSCAN.1-5	3.14	NCI-H69, NCI-H345, PRSC_con
5	310527	AW293404	Hs.211986	ESTs	3.14	PRSC_log, PRSC_con, RPWE-2
	321146	AA707443	Hs.183983	ESTs	3.14	PRSC_con, NCI-H69, PRSC_log
	333271			CH22_FGENES.121_2	3.13	NCI-H345, NCI-H69, RPWE-2
	330280			CH.05_p2 gi|6671910	3.13	NCI-H69, NCI-H345, PRSC_log
	309977	AW451663		EST singleton (not in UniGene) with exon	3.13	PRSC_con, PRSC_log, RPWE-2
10	307588	AI285535		EST singleton (not in UniGene) with exon	3.13	MB-MDA-231, BT474, BT474
	330551	U39840	Hs.105440	hepatocyte nuclear factor 3; alpha	3.13	MB-MDA-453, LnCap, Caco2
	314404	AW104203	Hs.157505	ESTs	3.13	DU145, EB, OVCA-R
	334030			CH22_FGENES.320_2	3.13	NCI-H69, NCI-H345, PRSC_con
	309108	AI925949		EST singleton (not in UniGene) with exon	3.13	BT474, MCF7, EB
15	317516	AI733250	Hs.192262	ESTs	3.12	OVCA-R, EB, MB-MDA-453
	304161	H71886		EST singleton (not in UniGene) with exon	3.12	PRSC_con, NCI-H69, RPWE-2
	334590			CH22_FGENES.407_13	3.12	NCI-H69, NCI-H345, PRSC_con
	333408			CH22_FGENES.145_6	3.11	PRSC_log, RPWE-2, PRSC_con
	330387	H14624	Hs.31386	ESTs; Highly similar to secreted apoptos	3.11	DU145, OVCA-R, PC3
20	332567	N23730	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11	EB, MB-MDA-453, MCF7
	333682			CH22_FGENES.247_10	3.1	PRSC_con, PRSC_log, RPWE-2
	323152	AI680562	Hs.246192	ESTs; Weakly similar to REGULATOR OF MIT	3.1	PC3, MB-MDA-453, DU145
	311142	AI638441	Hs.195649	ESTs	3.1	PRSC_con, RPWE-2, PRSC_log
	333441			CH22_FGENES.151_5	3.1	RPWE-2, NCI-H345, PRSC_log
25	326459			CH.19_hs gi|5867400	3.09	EB, CALU6, PC3
	313493	AA910339	Hs.126868	ESTs	3.09	NCI-H345, PRSC_con, RPWE-2
	339356			CH22_BA354I12.GENSCAN.31-1	3.08	NCI-H69, NCI-H345, PRSC_log
	333629			CH22_FGENES.226_5	3.08	NCI-H69, NCI-H345, PRSC_log
	304127	H42981		EST singleton (not in UniGene) with exon	3.07	LnCap, PRSC_con, DU145
30	325691			CH.14_hs gi|5867021	3.07	NCI-H345, PRSC_con, NCI-H69
	333014			CH22_FGENES.61_6	3.07	PRSC_con, PRSC_log, NCI-H345
	327379			CH.02_hs gi|5867795	3.07	PRSC_con, PRSC_log, NCI-H69
	337816			CH22_EM:AC005500.GENSCAN.13-1	3.06	NCI-H69, PRSC_con, PRSC_log
	337954			CH22_EM:AC005500.GENSCAN.96-3	3.06	PRSC_log, NCI-H69, NCI-H345
35	328109			CH.06_hs gi|5868020	3.05	HT29, BT474, MB-MDA-231
	338527			CH22_EM:AC005500.GENSCAN.396-15	3.05	NCI-H69, NCI-H345, PRSC_con
	320083	T87761		EST cluster (not in UniGene)	3.05	BT474, MB-MDA-435s, MCF7
	333466			CH22_FGENES.161_2	3.05	NCI-H345, RPWE-2, PRSC_log
	334788			CH22_FGENES.432_13	3.04	EB, A549, CALU6
40	302681	X97550		EST	3.04	OVCA-R, EB, MB-MDA-453
	336238			CH22_FGENES.743_3	3.03	NCI-H69, PRSC_log, PRSC_con
	337606			CH22_C20H12.GENSCAN.17-2	3.02	HT29, BT474, MB-MDA-231
	333545			CH22_FGENES.180_1	3.02	NCI-H69, NCI-H345, RPWE-2
	309782	AW275156	Hs.156110	Immunoglobulin kappa variable 1D-8	3.02	PRSC_log, PRSC_con, RPWE-2
45	324277	AA429440	Hs.207285	ESTs	3.02	BT474, MB-MDA-231, HT29
	321074	H38098	Hs.32756	ESTs	3.02	PC3, BT474, MB-MDA-231
	337094			CH22_FGENES.465-19	3.01	PRSC_con, PRSC_log, RPWE-2
	313913	AW391342		EST cluster (not in UniGene)	3	NCI-H345, RPWE-2, PRSC_log
	329140			CH.X_hs gi|6017060	3	EB, DU145, PC3
50	335331			CH22_FGENES.535_4	3	MB-MDA-435s, HT29, BT474
	334827			CH22_FGENES.437_9	2.99	CALU6, EB, DU145
	326029			CH.17_hs gi|5867176	2.99	NCI-H345, RPWE-2, PRSC_con
	303100	T09353		EST	2.99	MB-MDA-453, NCI-H345, RPWE-2
	328768			CH.07_hs gi|6017031	2.99	NCI-H345, PRSC_con, NCI-H69
55	329392			CH.X_hs gi|6478815	2.98	NCI-H69, NCI-H345, PRSC_con
	305168	AA663105		EST singleton (not in UniGene) with exon	2.98	LnCap, NCI-H345, MCF7
	300992	AA601213	Hs.191798	ESTs	2.98	Caco2, HT29, NCI-358
	334474			CH22_FGENES.394_5	2.98	NCI-H69, PRSC_con, RPWE-2
	322647	AA007534	Hs.125062	ESTs	2.98	HT29, OVCA-R, A549
60	310620	AI341328	Hs.178953	ESTs	2.97	PRSC_con, RPWE-2, PRSC_log
	328276			CH.07_hs gi|6004471	2.97	NCI-H345, NCI-H69, RPWE-2
	331018	N26904	Hs.24048	ESTs; Weakly similar to FK506/rapamycin-	2.96	Caco2, NCI-H460, A549
	321523	H78472	Hs.191325	ESTs; Weakly similar to cDNA EST yk414c9	2.96	PRSC_con, PRSC_log, NCI-H345
	339280			CH22_BA354I12.GENSCAN.14-12	2.96	NCI-H69, PRSC_log, NCI-H345
65	305967	AA886428		EST singleton (not in UniGene) with exon	2.96	NCI-H520, NCI-358, MB-MDA-453
	335755			CH22_FGENES.604_4	2.95	EB, A549, MB-MDA-453
	323907	AL043098	Hs.165387	ESTs	2.95	PRSC_con, NCI-H345, PRSC_log
	330370			CH.X_p2 gi|6580495	2.95	EB, DU145, MB-MDA-435s
	334529			CH22_FGENES.402_9	2.94	EB, MCF7, DU145
70	339256			CH22_BA354I12.GENSCAN.7-11	2.94	NCI-H69, NCI-H345, PRSC_con
	334783			CH22_FGENES.432_8	2.94	A549, Caco2, PC3
	335266			CH22_FGENES.521_2	2.94	NCI-H69, PRSC_con, PRSC_con
	323707	AA845957	Hs.128385	ESTs	2.94	NCI-H345, PRSC_con, PRSC_log
	336199			CH22_FGENES.719_3	2.93	NCI-H69, NCI-H345, PRSC_log
75	338326			CH22_EM:AC005500.GENSCAN.308-2	2.93	NCI-H69, NCI-H345, NCI-358
	333652			CH22_FGENES.239_1	2.93	PC3, OVCA-R, BT474

336479			CH22_FGENES.829_39	2.92	NCI-H69, PRSC_con, PRSC_log
336086			CH22_FGENES.688_15	2.92	PRSC_con, Caco2, CALU6
338516			CH22_EM:AC005500.GENSCAN.392-6	2.92	NCI-H69, NCI-H345, PRSC_con
320121	T93657		EST cluster (not in UniGene)	2.92	EB, BT474, HT29
305782	AA844730		EST singleton (not in UniGene) with exon	2.92	MB-MDA-453, MCF7, DU145
339304			CH22_BA354I12.GENSCAN.20-16	2.91	PRSC_con, PRSC_log, NCI-H69
327472			CH.02_hs gi|5867775	2.91	PRSC_log, PRSC_con, RPWE-2
311458	AW139426	Hs.244718	ESTs	2.91	PRSC_con, PRSC_log, RPWE-2
338431			CH22_EM:AC005500.GENSCAN.351-4	2.9	BT474, MCF7, MB-MDA-453
339230			CH22_BA354I12.GENSCAN.1-6	2.89	NCI-H69, NCI-H345, PRSC_log
320586	NM_00365		EST cluster (not in UniGene)	2.89	OVCA-R, HT29, MB-MDA-231
304777	AA581692	Hs.2186	eukaryotic translation elongation factor	2.89	OVCA-R, EB, MCF7
337768			CH22_EM:AC000097.GENSCAN.119-6	2.88	NCI-H69, LnCap, DU145
319465	AA319115	Hs.191558	ESTs	2.88	NCI-H460, NCI-H520, NCI-358
319068	W93011	Hs.110155	ESTs	2.87	BT474, MB-MDA-453, MB-MDA-435s
330958	H08815	Hs.159824	EST	2.87	OVCA-R, PC3, A549
334215			CH22_FGENES.357_7	2.87	NCI-H69, PRSC_con, PRSC_log
333568			CH22_FGENES.185_1	2.87	PRSC_con, PRSC_log, NCI-H69
333142			CH22_FGENES.85_5	2.87	NCI-H69, HT29, HT29
330239			CH.05_p2 gi|6671857	2.87	MB-MDA-453, MB-MDA-453, EB
302120	R55140	Hs.31075	ESTs; Weakly similar to Weak similarity	2.87	CALU6, MB-MDA-435s, BT474
338679			CH22_EM:AC005500.GENSCAN.470-1	2.86	NCI-H345, PRSC_log, PRSC_con
329041			CH.X_hs gi|5868564	2.86	LnCap, PRSC_con, RPWE-2
333541			CH22_FGENES.178_3	2.86	NCI-H69, NCI-H345, PRSC_con
337011			CH22_FGENES.427-6	2.86	NCI-H69, PRSC_log, PRSC_con
324031	AA375646		EST cluster (not in UniGene)	2.86	NCI-H345, PRSC_log, LnCap
331842	AA416586	Hs.98232	ESTs	2.86	DU145, OVCA-R, HT29
336599			CH22_FGENES.350_3	2.85	LnCap, NCI-H69, NCI-H345
337586			CH22_C20H12.GENSCAN.5-4	2.85	NCI-H345, NCI-H69, PRSC_con
336177			CH22_FGENES.712_2	2.85	NCI-H69, PRSC_log, RPWE-2
337522			CH22_FGENES.819-1	2.85	CALU6, OVCA-R, HT29
338596			CH22_EM:AC005500.GENSCAN.437-2	2.85	NCI-H69, PRSC_con, NCI-H345
309522	AW150044	Hs.252259	ribosomal protein S3	2.85	MB-MDA-453, MB-MDA-435s, MB-MDA-435s
336981			CH22_FGENES.397-7	2.85	NCI-H69, PRSC_con, PRSC_log
330286			CH.05_p2 gi|6671913	2.84	NCI-H345, PRSC_log, NCI-H69
333713			CH22_FGENES.251_2	2.84	RPWE-2, PRSC_con, NCI-H69
335068			CH22_FGENES.483_5	2.83	MB-MDA-231, NCI-H345, RPWE-2
305075	AA641288	Hs.181165	eukaryotic translation elongation factor	2.83	EB, LnCap, DU145
326380			CH.19_hs gi|5867327	2.82	NCI-H69, PRSC_con, PRSC_log
334970			CH22_FGENES.466_3	2.82	PRSC_con, NCI-H69, RPWE-2
337097			CH22_FGENES.471-1	2.82	NCI-H345, NCI-H69, PRSC_log
323676	AI702835		EST cluster (not in UniGene)	2.82	LnCap, A549, CALU6
333785			CH22_FGENES.274_4	2.82	OVCA-R, Caco2, MB-MDA-453
334175			CH22_FGENES.349_10	2.81	RPWE-2, BT474, MCF7
337865			CH22_EM:AC005500.GENSCAN.46-5	2.81	Caco2, NCI-H23, BT474
302585	AA083564	Hs.249220	H sapiens mRNA for hTbr2; complete cds	2.81	EB, DU145, MB-MDA-453
336623			CH22_FGENES.4-5	2.81	NCI-H345, PRSC_con, NCI-H69
332854			CH22_FGENES.22_1	2.8	RPWE-2, PRSC_log, PRSC_con
336978			CH22_FGENES.384-10	2.8	PRSC_con, NCI-H345, RPWE-2
326874			CH.20_hs gi|6682507	2.8	RPWE-2, NCI-H345, PRSC_log
315121	AA565011	Hs.105902	ESTs	2.8	NCI-H345, PRSC_log, RPWE-2
311185	AI638294	Hs.224665	ESTs	2.8	NCI-H69, NCI-H345, PRSC_log
334682			CH22_FGENES.419_4	2.8	NCI-H69, PRSC_log, RPWE-2
316845	AW418715	Hs.250388	ESTs	2.79	RPWE-2, NCI-H345, PRSC_log
331599	N74626	Hs.50535	ESTs	2.79	A549, MB-MDA-453, MB-MDA-435s
315681	AW022054	Hs.136591	ESTs	2.78	NCI-H460, MB-MDA-453, MCF7
313012	AI207390	Hs.143929	ESTs	2.78	DU145, MB-MDA-453, MCF7
313476	AA010267		EST cluster (not in UniGene)	2.78	NCI-H520, NCI-H460, HT29
327277			CH.01_hs gi|5867473	2.78	DU145, CALU6, EB
310981	AI494514	Hs.171380	ESTs	2.78	LnCap, RPWE-2, NCI-H460
335090			CH22_FGENES.490_1	2.77	NCI-H69, PRSC_log, PRSC_con
328581			CH.07_hs gi|6006033	2.77	HT29, MB-MDA-453, MCF7
333219			CH22_FGENES.104_11	2.77	NCI-H69, PRSC_log, NCI-H345
308311	AI581855		EST singleton (not in UniGene) with exon	2.77	MB-MDA-231, HT29, CALU6
329760			CH.14_p2 gi|6048280	2.77	CALU6, DU145, EB
303925	AW469999	Hs.258523	ESTs	2.77	NCI-H69, LnCap, MB-MDA-231
337628			CH22_C20H12.GENSCAN.28-31	2.77	NCI-H69, LnCap, MB-MDA-453
333520			CH22_FGENES.174_3	2.77	NCI-H69, NCI-H345, PRSC_con
303168	AA872479	Hs.197770	ESTs; Weakly similar to estrogen-respons	2.76	DU145, OVCA-R, MB-MDA-453
313451	AW138189	Hs.122672	ESTs	2.76	OVCA-R, EB, DU145
328474			CH.07_hs gi|5868446	2.76	NCI-H69, NCI-H345, RPWE-2
331988	AA477414	Hs.9242	purine-rich element binding protein B	2.76	MB-MDA-435s, A549, OVCA-R
306180	AA922503		EST singleton (not in UniGene) with exon	2.76	NCI-H69, DU145, LnCap
321071	AA013011	Hs.241502	Cdc42 effector protein 4	2.76	PRSC_log, PRSC_con, NCI-H345
302972	W73400		EST	2.76	NCI-H345, RPWE-2, NCI-H69
305185	AA663985	Hs.248038	major histocompatibility complex; class	2.75	DU145, A549, BT474

335998			CH22_FGENES.656_16	2.75	NCI-H69, PRSC_con, RPWE-2
319138	R11699	Hs.73818	ubiquinol-cytochrome c reductase hinge p	2.75	NCI-H345, NCI-H69, PRSC_con
336387			CH22_FGENES.822_7	2.75	PRSC_con, RPWE-2, PRSC_log
338054			CH22_EM:AC005500.GENSCAN.158-2	2.75	OVCA-R, EB, DU145
316041	AA719183		EST cluster (not in UniGene)	2.74	DU145, MCF7, MB-MDA-453
336863			CH22_FGENES.297-4	2.74	MB-MDA-453, MCF7, OVCA-R
335975			CH22_FGENES.652_9	2.74	CALU6, EB, A549
302952	AF103179		EST	2.74	CALU6, MB-MDA-435s, BT474
326122			CH.17_hs gi|5867194	2.74	HT29, Caco2, PC3
337427			CH22_FGENES.761-4	2.74	RPWE-2, NCI-H69, PRSC_log
308063	AI469244	Hs.119252	tumor protein; translationally-controlle	2.74	NCI-358, NCI-H23, Caco2
325433			CH.12_hs gi|5866936	2.74	NCI-H345, PRSC_con, RPWE-2
316252	AI572633	Hs.190406	ESTs	2.74	OVCA-R, MCF7, A549
310837	AI418688	Hs.170301	ESTs	2.74	NCI-H345, PRSC_con, RPWE-2
313562	AW467335	Hs.257676	ESTs	2.74	HT29, MCF7, MB-MDA-231
335455			CH22_FGENES.562_15	2.74	NCI-H69, LnCap, PRSC_con
304792	AA583101	Hs.29797	ribosomal protein L10	2.73	EB, OVCA-R, MB-MDA-453
331979	AA469937	Hs.105322	EST	2.73	MCF7, BT474, NCI-H460
336198			CH22_FGENES.719_2	2.73	NCI-H69, PRSC_con, PRSC_log
314698	AI660452	Hs.187127	ESTs	2.73	MB-MDA-231, LnCap, BT474
307954	AI419692		EST singleton (not in UniGene) with exon	2.73	HT29, HT29, EB
318288	AI088590	Hs.134702	ESTs	2.73	PRSC_log, NCI-H345, PRSC_con
327833			CH.05_hs gi|5867968	2.73	BT474, PC3, MB-MDA-231
300221	AW449602	Hs.217953	ESTs; Highly similar to NK-TUMOR RECOGNI	2.73	NCI-H520, NCI-358, MB-MDA-453
326039			CH.17_hs gi|5867179	2.73	MB-MDA-453, EB, EB
318457	AI149678	Hs.143952	ESTs	2.72	PRSC_con, PRSC_log, NCI-H345
336753			CH22_FGENES.128-9	2.72	MB-MDA-435s, NCI-H520, MCF7
330086			CH.19_p2 gi|6015293	2.72	HT29, MB-MDA-453, MCF7
333566			CH22_FGENES.183_2	2.72	HT29, BT474, OVCA-R
339384			CH22_BA232E17.GENSCAN.3-22	2.71	NCI-H69, NCI-H345, PRSC_log
338668			CH22_EM:AC005500.GENSCAN.465-1	2.71	NCI-H69, RPWE-2, PRSC_con
300798	AI382618	Hs.194613	ESTs	2.71	PRSC_con, NCI-H345, PRSC_log
303745	AI142379		EST	2.71	PRSC_log, PRSC_con, RPWE-2
305197	AA666301		EST singleton (not in UniGene) with exon	2.71	EB, NCI-H520, OVCA-R
338725			CH22_EM:AC005500.GENSCAN.499-1	2.7	CALU6, MB-MDA-453, PC3
307799	AI351112		EST singleton (not in UniGene) with exon	2.7	HT29, BT474, MCF7
309598	AW173642	Hs.250106	EST	2.69	NCI-358, NCI-H69, NCI-H23
302727	L10141		EST	2.69	OVCA-R, BT474, PC3
308544	AI695133		EST singleton (not in UniGene) with exon	2.69	HT29, CALU6, MB-MDA-435s
322877	AA079727		EST cluster (not in UniGene)	2.69	NCI-H345, NCI-H69, PRSC_con
325695			CH.14_hs gi|6552446	2.69	NCI-H69, NCI-H460, NCI-H460
307728	AI335557		EST singleton (not in UniGene) with exon	2.68	NCI-H69, PRSC_log, NCI-358
302399	N79624		EST	2.68	NCI-H69, PRSC_con, NCI-H345
309343	AW028652		EST singleton (not in UniGene) with exon	2.68	HT29, MB-MDA-231, MB-MDA-231
339360			CH22_BA354I12.GENSCAN.32-2	2.68	NCI-H69, PRSC_log, PRSC_con
337821			CH22_EM:AC005500.GENSCAN.13-11	2.68	PRSC_con, PRSC_log, PRSC_log
337338			CH22_FGENES.717-7	2.68	NCI-H69, PRSC_con, PRSC_log
334510			CH22_FGENES.398_8	2.68	NCI-H460, NCI-H23, NCI-358
300918	AA491286	Hs.128792	ESTs	2.68	MB-MDA-435s, CALU6, DU145
335536			CH22_FGENES.574_2	2.67	NCI-H69, NCI-H345, PRSC_log
335311			CH22_FGENES.532_4	2.67	MB-MDA-435s, Caco2, A549
338959			CH22_DJ32I10.GENSCAN.23-31	2.67	NCI-H345, PRSC_con, NCI-H69
339081			CH22_DA59H18.GENSCAN.37-10	2.67	NCI-H345, RPWE-2, NCI-H69
334068			CH22_FGENES.327_23	2.67	PRSC_con, RPWE-2, PRSC_log
338976			CH22_DA59H18.GENSCAN.1-3	2.66	PRSC_con, PRSC_log, RPWE-2
325524			CH.12_hs gi|5866981	2.66	NCI-H345, RPWE-2, PRSC_con
333069			CH22_FGENES.76_5	2.66	NCI-H69, NCI-H345, PRSC_con
336203			CH22_FGENES.719_7	2.66	OVCA-R, PC3, A549
333133			CH22_FGENES.83_9	2.66	HT29, OVCA-R, A549
304074	T77842	Hs.142528	ESTs	2.65	DU145, CALU6, EB
330919	AA224594	Hs.86941	ESTs	2.65	PRSC_con, RPWE-2, LnCap
333248			CH22_FGENES.115_5	2.65	NCI-H345, PRSC_con, MB-MDA-231
336665			CH22_FGENES.42-2	2.65	NCI-H69, PRSC_log, PRSC_con
315322	AA770599		EST cluster (not in UniGene)	2.65	A549, MB-MDA-453, MB-MDA-435s
307474	AI264023		EST singleton (not in UniGene) with exon	2.65	NCI-H69, NCI-H345, RPWE-2
320221	AL050020	Hs.127384	DKFZP564C196 protein	2.65	MB-MDA-453, MCF7, HT29
301767	AW361892		EST	2.65	NCI-H345, PRSC_con, PRSC_log
327246			CH.01_hs gi|5867547	2.65	EB, OVCA-R, DU145
337403			CH22_FGENES.752-2	2.65	PRSC_con, PRSC_log, RPWE-2
328221			CH.06_hs gi|5868099	2.64	MCF7, MB-MDA-231, BT474
336759			CH22_FGENES.133-2	2.64	NCI-H69, PRSC_log, PRSC_con
327532			CH.02_hs gi|6469818	2.64	PC3, CALU6, A549
305621	AA789095		EST singleton (not in UniGene) with exon	2.64	HT29, MB-MDA-231, MB-MDA-453
322931	AA099329	Hs.151764	ESTs	2.64	PRSC_con, RPWE-2, NCI-H345
327278			CH.01_hs gi|5867473	2.64	EB, NCI-H460, NCI-H69
332235	N51413	Hs.109284	ESTs	2.64	DU145, EB, OVCA-R

332792			CH22_FGENES.3_2	2.63	HT29, Caco2, A549
312340	AI862668	Hs.176333	ESTs	2.63	NCI-358, NCI-358, HT29
337484			CH22_FGENES.795-8	2.63	NCI-H69, NCI-H345, PRSC_con
325783			CH.14_hs gi|6456780	2.63	EB, OVCA-R, PC3
303672	AW502380	Hs.210527	ESTs	2.63	PRSC_log, NCI-H345, NCI-H69
306009	AA894560		EST singleton (not in UniGene) with exon	2.63	HT29, MB-MDA-231, CALU6
308548	AI695484		EST singleton (not in UniGene) with exon	2.63	PC3, A549, NCI-358
337930			CH22_EM:AC005500.GENSCAN.81-3	2.62	PC3, OVCA-R, MCF7
327791			CH.05_hs gi|5867977	2.62	PRSC_log, PRSC_con, NCI-H345
330925	AA232678	Hs.87073	ESTs	2.62	OVCA-R, MCF7, LnCap
327259			CH.01_hs gi|5867454	2.62	NCI-H345, PRSC_con, RPWE-2
302150	AF061756	Hs.152531	heart and neural crest derivatives expre	2.61	OVCA-R, PC3, A549
304881	AA598501	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.61	MB-MDA-435s, NCI-H23, MCF7
335956			CH22_FGENES.647_3	2.61	DU145, PRSC_con, PC3
326506			CH.19_hs gi|5867435	2.61	RPWE-2, NCI-H460, NCI-358
335863			CH22_FGENES.629_8	2.61	PC3, HT29, NCI-358
334752			CH22_FGENES.428_1	2.61	PRSC_con, NCI-H69, PRSC_log
333288			CH22_FGENES.128_19	2.61	HT29, NCI-358, Caco2
306709	AI024215	Hs.131477	EST	2.61	MB-MDA-435s, MCF7, BT474
305816	AA854776		EST singleton (not in UniGene) with exon	2.6	MB-MDA-453, MCF7, MB-MDA-435s
327264			CH.01_hs gi|5867461	2.6	MB-MDA-435s, MB-MDA-435s, MB-MDA-453
310905	AW075527	Hs.252259	ribosomal protein S3	2.6	OVCA-R, EB, DU145
324492	AA479507	Hs.135179	ESTs	2.6	DU145, EB, OVCA-R
322649	AA526549		EST cluster (not in UniGene)	2.6	PRSC_con, RPWE-2, PRSC_log
329384			CH.X_hs gi|5868869	2.6	NCI-H69, NCI-H345, PRSC_con
321240	M62378		EST cluster (not in UniGene)	2.6	BT474, CALU6, MB-MDA-231
302751	AA299576	Hs.156110	Immunoglobulin kappa variable 1D-8	2.59	MCF7, MB-MDA-453, OVCA-R
305841	AA860348		EST singleton (not in UniGene) with exon	2.59	NCI-H345, PRSC_log, PRSC_con
324180	AA402242	Hs.122799	ESTs	2.58	EB, PC3, HT29
334196			CH22_FGENES.353_4	2.58	NCI-H345, NCI-H69, PRSC_con
338451			CH22_EM:AC005500.GENSCAN.359-39	2.58	MB-MDA-435s, NCI-H23, MCF7
300333	AW297396	Hs.227052	ESTs	2.58	PRSC_con, PRSC_log, NCI-H69
305046	AA632201		EST singleton (not in UniGene) with exon	2.58	NCI-H460, MB-MDA-453, MB-MDA-435s
305648	AA807652	Hs.156110	Immunoglobulin kappa variable 1D-8	2.57	PRSC_con, RPWE-2, NCI-H345
301744	W22230		EST	2.57	PRSC_con, PRSC_log, NCI-H345
329182			CH.X_hs gi|6056331	2.57	PRSC_con, RPWE-2, NCI-H345
318178	AW137425	Hs.158401	ESTs	2.57	MB-MDA-231, PRSC_con, BT474
330057			CH.17_p2 gi|6478962	2.57	NCI-H345, RPWE-2, PRSC_con
326552			CH.19_hs gi|5867308	2.57	NCI-H345, PRSC_con, RPWE-2
311956	T67085	Hs.188464	ESTs	2.57	HT29, MB-MDA-453, NCI-H460
327185			CH.01_hs gi|6117805	2.57	CALU6, HT29, EB
302183	NM_00224		EST	2.57	MCF7, PC3, OVCA-R
327263			CH.01_hs gi|6525274	2.56	PRSC_con, NCI-H69, PRSC_log
339164			CH22_DA59H18.GENSCAN.69-4	2.56	NCI-H69, PRSC_con, NCI-H345
332763	AA063554	Hs.90959	ESTs	2.56	RPWE-2, NCI-H345, PRSC_con
330579	U67733	Hs.154437	phosphodiesterase 2A; cGMP-stimulated	2.55	HT29, CALU6, PC3
329948			CH.16_p2 gi|5540101	2.55	NCI-H460, MCF7, MB-MDA-453
300282	AW044305	Hs.236131	ESTs; Highly similar to homeodomain-inte	2.55	NCI-H460, NCI-H23, NCI-H23
335448			CH22_FGENES.562_5	2.55	MB-MDA-453, BT474, MCF7
330959	H09174	Hs.26484	HIRA-interacting protein 3	2.55	MB-MDA-453, HT29, MCF7
307262	AI202100		EST singleton (not in UniGene) with exon	2.55	MCF7, DU145, MB-MDA-435s
335806			CH22_FGENES.616_8	2.55	NCI-H345, NCI-H69, PRSC_con
335782			CH22_FGENES.609_4	2.55	Caco2, MB-MDA-453, MB-MDA-435s
301703	AW301478		EST	2.55	PC3, MCF7, MB-MDA-453
329018			CH.X_hs gi|6249620	2.54	NCI-H69, PRSC_log, PRSC_con
329870			CH.14_p2 gi|6706435	2.54	NCI-H23, NCI-H460, NCI-358
334504			CH22_FGENES.398_2	2.54	HT29, BT474, MB-MDA-231
304707	AA564846		EST singleton (not in UniGene) with exon	2.53	NCI-H520, EB, NCI-H460
329326			CH.X_hs gi|5868806	2.53	MB-MDA-231, NCI-H345, NCI-H69
334418			CH22_FGENES.384_5	2.53	NCI-H23, NCI-358, NCI-H460
338124			CH22_EM:AC005500.GENSCAN.196-2	2.53	NCI-H69, PRSC_con, PRSC_log
318423	AI362671	Hs.214491	ESTs	2.53	OVCA-R, EB, DU145
333006			CH22_FGENES.60_3	2.53	NCI-H69, PRSC_con, PRSC_log
333668			CH22_FGENES.245_2	2.53	NCI-H69, PRSC_log, PRSC_con
333567			CH22_FGENES.184_2	2.53	NCI-H69, NCI-H345, PRSC_con
309592	AW172384		EST singleton (not in UniGene) with exon	2.52	LnCap, NCI-H69, DU145
328989			CH.09_hs gi|5868535	2.52	MB-MDA-435s, OVCA-R, EB
326725			CH.20_hs gi|6552456	2.52	PRSC_con, NCI-H345, NCI-H69
302996	AF054663		EST	2.52	HT29, BT474, CALU6
335733			CH22_FGENES.601_3	2.52	NCI-H69, PRSC_log, NCI-H345
336000			CH22_FGENES.658_1	2.52	LnCap, OVCA-R, DU145
327774			CH.05_hs gi|5867964	2.52	DU145, CALU6, HT29
328557			CH.07_hs gi|5868489	2.52	MB-MDA-453, MB-MDA-435s, MCF7
328228			CH.06_hs gi|5868105	2.52	NCI-H69, NCI-H345, PRSC_con
328305			CH.07_hs gi|6004478	2.52	NCI-H69, NCI-H460, PRSC_log
334010			CH22_FGENES.313_1	2.51	NCI-H69, PRSC_log, PRSC_con

339033			CH22_DA59H18.GENSCAN.26-1	2.51	NCI-H69, NCI-H345, PRSC_con
335340			CH22_FGENES.535_17	2.51	NCI-H69, PRSC_con, PRSC_log
300156	AI245582	Hs.233395	ESTs	2.51	PRSC_con, PRSC_log, NCI-H345
305880	AA866065	Hs.156110	Immunoglobulin kappa variable 1D-8	2.5	EB, OVCA-R, DU145
310841	AI968009	Hs.232024	ESTs	2.5	LnCap, NCI-358, CALU6
336908			CH22_FGENES.343-2	2.5	NCI-H345, RPWE-2, PRSC_log
304674	AA541735		EST singleton (not in UniGene) with exon	2.5	RPWE-2, NCI-H69, MCF7
314521	AW503939	Hs.107149	ESTs; Weakly similar to PTB-ASSOCIATED S	2.5	NCI-H460, EB, Caco2
307592	AI285739		EST singleton (not in UniGene) with exon	2.5	PRSC_con, NCI-H345, PRSC_log
331476	N26190	Hs.43768	ESTs	2.5	NCI-H345, NCI-H69, PRSC_con
325803			CH.14_hs gi|6552451	2.5	NCI-H345, RPWE-2, PRSC_con
306549	AA993796		EST singleton (not in UniGene) with exon	2.49	A549, OVCA-R, CALU6
304833	AA586504		EST singleton (not in UniGene) with exon	2.49	MCF7, DU145, LnCap
336333			CH22_FGENES.813_1	2.49	NCI-H345, PRSC_con, PRSC_log
332320	T71134	Hs.100551	EST	2.49	NCI-H345, LnCap, RPWE-2
328236			CH.06_hs gi|5868117	2.49	PRSC_con, NCI-H345, PRSC_log
317335	AI656979	Hs.130210	ESTs	2.49	MCF7, MB-MDA-453, PC3
339188			CH22_DA59H18.GENSCAN.72-16	2.48	NCI-H69, PRSC_con, PRSC_log
334235			CH22_FGENES.361_19	2.48	NCI-H520, MB-MDA-453, A549
301214	AW450950	Hs.157034	ESTs; Weakly similar to Unknown [H.sapie	2.48	HT29, A549, A549
332843			CH22_FGENES.19_1	2.48	DU145, CALU6, EB
337431			CH22_FGENES.763-7	2.48	PRSC_con, RPWE-2, NCI-H69
336757			CH22_FGENES.131-1	2.48	NCI-H69, PRSC_log, PRSC_con
305403	AA723748		EST singleton (not in UniGene) with exon	2.48	NCI-H23, DU145, OVCA-R
330065			CH.19_p2 gi|6165044	2.48	PRSC_con, PRSC_log, NCI-H69
309245	AI972447		EST singleton (not in UniGene) with exon	2.48	MB-MDA-231, NCI-H69, HT29
328876			CH.07_hs gi|6525286	2.47	MB-MDA-231, CALU6, PC3
333944			CH22_FGENES.302_2	2.47	NCI-H69, RPWE-2, PRSC_log
328504			CH.07_hs gi|5868471	2.47	LnCap, MB-MDA-453, MB-MDA-435s
338120			CH22_EM:AC005500.GENSCAN.195-1	2.47	MB-MDA-231, NCI-H69, PRSC_con
306710	AI024221		EST singleton (not in UniGene) with exon	2.47	OVCA-R, EB, LnCap
305064	AA636012		EST singleton (not in UniGene) with exon	2.47	NCI-H69, RPWE-2, PRSC_con
329995			CH.16_p2 gi|4567166	2.47	OVCA-R, DU145, MB-MDA-453
315694	AI821743	Hs.168418	ESTs; Moderately similar to !!!! ALU SUB	2.46	EB, A549, LnCap
331004	H64622	Hs.32748	ESTs	2.46	EB, MCF7, MB-MDA-435s
305259	AA679225		EST singleton (not in UniGene) with exon	2.46	PRSC_con, NCI-H345, RPWE-2
304576	AA496563		EST singleton (not in UniGene) with exon	2.46	PRSC_con, RPWE-2, PRSC_log
318887	R60487	Hs.21065	ESTs	2.46	NCI-H345, Caco2, Caco2
308954	AI868958		EST singleton (not in UniGene) with exon	2.46	PRSC_con, PRSC_log, RPWE-2
301140	AI807692	Hs.207128	ESTs	2.46	OVCA-R, MB-MDA-231, HT29
322085	AA088500	Hs.170298	ESTs	2.46	PRSC_log, PRSC_con, NCI-H345
339130			CH22_DA59H18.GENSCAN.56-3	2.46	NCI-H345, PRSC_con, RPWE-2
337612			CH22_C20H12.GENSCAN.22-5	2.46	EB, A549, Caco2
313765	AW206181	Hs.185981	ESTs; Weakly similar to gag [H.sapiens]	2.45	RPWE-2, PRSC_log, PRSC_con
311665	AW294254	Hs.223742	ESTs	2.45	PRSC_log, RPWE-2, PRSC_con
328620			CH.07_hs gi|5868241	2.45	MB-MDA-453, MCF7, MB-MDA-435s
305361	AA708902		EST singleton (not in UniGene) with exon	2.45	HT29, MB-MDA-435s, A549
336243			CH22_FGENES.746_1	2.44	OVCA-R, MB-MDA-453, MB-MDA-435s
320299	H08323	Hs.177181	ESTs	2.44	PRSC_con, RPWE-2, NCI-H345
302535	H48676		EST	2.44	MB-MDA-453, EB, DU145
333465			CH22_FGENES.160_2	2.44	NCI-H69, PRSC_con, PRSC_log
334109			CH22_FGENES.330_8	2.44	NCI-H69, NCI-H345, PRSC_log
301749	F12998	Hs.90790	ESTs	2.44	NCI-H345, RPWE-2, PRSC_log
324575	AW502257		EST cluster (not in UniGene)	2.44	NCI-H345, PRSC_con, RPWE-2
337114			CH22_FGENES.494-17	2.44	NCI-H69, PRSC_log, PRSC_con
336087			CH22_FGENES.688_16	2.44	PRSC_con, Caco2, PRSC_log
315678	AI657119	Hs.120036	ESTs	2.44	NCI-358, PC3, NCI-H23
333258			CH22_FGENES.118_6	2.44	MB-MDA-231, HT29, CALU6
303798	V00505	Hs.36977	hemoglobin; delta	2.44	MB-MDA-435s, MCF7, MB-MDA-453
309759	AW268822		EST singleton (not in UniGene) with exon	2.44	MB-MDA-453, EB, MCF7
318946	AI122843		EST cluster (not in UniGene)	2.44	PC3, OVCA-R, DU145
321986	AL133656		EST cluster (not in UniGene)	2.44	DU145, CALU6, CALU6
338151			CH22_EM:AC005500.GENSCAN.207-5	2.44	PRSC_con, PRSC_log, RPWE-2
327056			CH.21_hs gi|6531965	2.44	PRSC_con, NCI-H345, RPWE-2
309605	AW182800		EST singleton (not in UniGene) with exon	2.43	NCI-358, NCI-H23, NCI-H520
335783			CH22_FGENES.610_3	2.43	PRSC_con, PRSC_log, NCI-H345
325790			CH.14_hs gi|6381957	2.43	MB-MDA-435s, MB-MDA-453, MB-MDA-453
339342			CH22_BA354I12.GENSCAN.27-10	2.43	BT474, MB-MDA-231, MB-MDA-453
335777			CH22_FGENES.607_13	2.43	DU145, EB, BT474
309972	AW450350	Hs.257283	ESTs	2.43	MCF7, MB-MDA-453, OVCA-R
308718	AI798009		EST singleton (not in UniGene) with exon	2.43	NCI-H345, PRSC_con, PRSC_log
338087			CH22_EM:AC005500.GENSCAN.174-16	2.43	DU145, PC3, CALU6
306930	AI124518		EST singleton (not in UniGene) with exon	2.43	NCI-H69, MCF7, BT474
319032	AW409728	Hs.80449	ESTs; Weakly similar to cytoplasmic dyne	2.43	RPWE-2, A549, NCI-H69
304330	AA157834		EST singleton (not in UniGene) with exon	2.43	MB-MDA-453, PC3, OVCA-R
320638	R54766	Hs.101120	ESTs	2.43	MCF7, MB-MDA-435s, MB-MDA-453

335281			CH22_FGENES.524_4	2.43	PC3, LnCap, A549
317431	AI675790	Hs.132453	ESTs	2.43	NCI-H345, RPWE-2, PRSC_log
306511	AA988891		EST singleton (not in UniGene) with exon	2.43	OVCA-R, EB, DU145
333298			CH22_FGENES.133_4	2.43	EB, DU145, PC3
328436			CH.07_hs gi|5868417	2.43	EB, LnCap, A549
333420			CH22_FGENES.146_11	2.43	NCI-H345, NCI-H69, PRSC_log
338113			CH22_EM:AC005500.GENSCAN.188-13	2.42	DU145, EB, CALU6
335188			CH22_FGENES.507_3	2.42	EB, A549, BT474
329164			CH.X_hs gi|5868691	2.42	RPWE-2, PRSC_con, PRSC_log
336316			CH22_FGENES.799_11	2.42	MB-MDA-435s, MCF7, NCI-H69
310831	AI927594	Hs.161142	ESTs	2.42	NCI-H345, PRSC_con, PRSC_log
327334			CH.01_hs gi|5902477	2.42	MB-MDA-453, MB-MDA-435s, MCF7
334017			CH22_FGENES.315_2	2.42	PRSC_con, PRSC_log, RPWE-2
308138	AI494446		EST singleton (not in UniGene) with exon	2.42	DU145, LnCap, EB
333074			CH22_FGENES.76_10	2.42	NCI-H69, RPWE-2, PRSC_log
306546	AA993109		EST singleton (not in UniGene) with exon	2.42	HT29, CALU6, LnCap
336516			CH22_FGENES.836_1	2.42	NCI-H69, PRSC_con, PRSC_log
306791	AI042387		EST singleton (not in UniGene) with exon	2.42	CALU6, DU145, EB
329411			CH.X_hs gi|6682549	2.42	OVCA-R, EB, LnCap
308659	AI750091		EST singleton (not in UniGene) with exon	2.41	EB, DU145, CALU6
313504	AI190405	Hs.143127	ESTs	2.41	DU145, EB, CALU6
326073			CH.17_hs gi|6682495	2.41	DU145, A549, MB-MDA-435s
334047			CH22_FGENES.326_5	2.41	PRSC_con, PRSC_log, NCI-H345
325464			CH.12_hs gi|5866947	2.41	NCI-358, NCI-H23, NCI-H460
334764			CH22_FGENES.428_13	2.41	NCI-H69, NCI-H345, RPWE-2
312737	AI033500	Hs.132895	ESTs	2.41	OVCA-R, DU145, CALU6
306591	AI000248		EST singleton (not in UniGene) with exon	2.41	MB-MDA-231, MCF7, DU145
333582			CH22_FGENES.201_2	2.41	NCI-H69, PRSC_con, PRSC_log
337843			CH22_EM:AC005500.GENSCAN.30-8	2.4	EB, LnCap, A549
335284			CH22_FGENES.526_6	2.4	NCI-H69, NCI-H345, PRSC_log
305134	AA653159		EST singleton (not in UniGene) with exon	2.4	DU145, HT29, MB-MDA-453
335527			CH22_FGENES.572_7	2.4	DU145, OVCA-R, EB
336795			CH22_FGENES.176-5	2.4	NCI-H69, NCI-H345, PRSC_log
303144	AF202889		EST	2.4	PRSC_con, PRSC_log, NCI-H69
334948			CH22_FGENES.465_15	2.4	PRSC_con, PRSC_log, RPWE-2
328860			CH.07_hs gi|6381928	2.4	PRSC_con, PRSC_log, NCI-H345
322929	AI365585	Hs.146246	ESTs	2.4	NCI-H460, A549, HT29
333561			CH22_FGENES.180_18	2.4	OVCA-R, EB, DU145
338239			CH22_EM:AC005500.GENSCAN.264-5	2.4	NCI-H69, NCI-H345, PRSC_con
323670	AL040411	Hs.161763	ESTs; Weakly similar to KIAA0738 protein	2.4	DU145, MB-MDA-453, EB
305903	AA873085		EST singleton (not in UniGene) with exon	2.4	MCF7, A549, NCI-H520
312573	AW297673	Hs.190526	ESTs	2.4	LnCap, NCI-H460, NCI-H23
334470			CH22_FGENES.394_1	2.4	NCI-H520, HT29, NCI-H23
333272			CH22_FGENES.122_1	2.39	NCI-H345, PRSC_con, RPWE-2
304010	AW518383	Hs.177592	ribosomal protein; large; P1	2.39	DU145, CALU6, EB
337316			CH22_FGENES.692-1	2.39	MCF7, BT474, OVCA-R
316769	AI914939	Hs.212184	ESTs	2.39	PRSC_con, NCI-H345, RPWE-2
336280			CH22_FGENES.763_4	2.39	NCI-H345, PRSC_log, PRSC_con
331223	T98872	Hs.194181	ESTs	2.39	DU145, HT29, PC3
337172			CH22_FGENES.565-2	2.39	EB, OVCA-R, DU145
300625	AI671992	Hs.143631	ESTs; Weakly similar to WASP-family prot	2.39	EB, NCI-H520, LnCap
337092			CH22_FGENES.465-12	2.39	PRSC_con, PRSC_log, NCI-H69
334528			CH22_FGENES.402_8	2.39	NCI-H345, PRSC_con, NCI-H69
338411			CH22_EM:AC005500.GENSCAN.341-7	2.39	NCI-H345, NCI-H69, PRSC_con
331344	AA357927	Hs.70208	ESTs	2.39	PC3, EB, A549
334044			CH22_FGENES.323_2	2.38	MB-MDA-231, MCF7, LnCap
333918			CH22_FGENES.296_7	2.38	RPWE-2, NCI-H345, EB
317168	AI042614	Hs.125910	ESTs	2.38	NCI-H345, PRSC_con, RPWE-2
333424			CH22_FGENES.147_4	2.38	DU145, MCF7, OVCA-R
317779	AW450515	Hs.128381	ESTs	2.38	EB, DU145, OVCA-R
315142	AI380577	Hs.190219	ESTs	2.38	OVCA-R, EB, CALU6
310471	AW270515	Hs.149596	ESTs	2.38	NCI-H460, NCI-H23, NCI-H23
325049	AW410339	Hs.256310	ESTs; Weakly similar to centaurin beta2	2.38	PRSC_con, RPWE-2, NCI-H345
305234	AA670431		EST singleton (not in UniGene) with exon	2.38	MB-MDA-453, MB-MDA-231, A549
337760			CH22_EM:AC000097.GENSCAN.116-8	2.38	PRSC_con, PRSC_log, RPWE-2
311502	AW204380	Hs.208662	ESTs	2.38	NCI-H345, NCI-H69, LnCap
337548			CH22_FGENES.844-5	2.38	MB-MDA-453, MCF7, CALU6
326981			CH.21_hs gi|6588016	2.38	NCI-H345, NCI-H69, PRSC_con
309600	AW182066		EST singleton (not in UniGene) with exon	2.37	RPWE-2, NCI-358, NCI-H69
328936			CH.08_hs gi|5868500	2.37	OVCA-R, MB-MDA-453, CALU6
327937			CH.06_hs gi|5868192	2.37	BT474, EB, OVCA-R
328282			CH.07_hs gi|5868353	2.37	DU145, CALU6, CALU6
303607	AL046388	Hs.208206	ESTs; Weakly similar to Naf1 alpha prote	2.37	LnCap, PRSC_log, NCI-H345
304227	N94974	Hs.75344	ribosomal protein S4; X-linked	2.37	EB, PC3, OVCA-R
314101	AW452279	Hs.257542	ESTs	2.37	OVCA-R, CALU6, CALU6
325026	AI671168	Hs.12285	ESTs	2.37	NCI-H345, PRSC_con, PRSC_log

315015	AI659989	Hs.132625	ESTs	2.37	MB-MDA-453, MB-MDA-231, LnCap
328662			CH.07_hs gi|6004473	2.37	NCI-H345, RPWE-2, PRSC_con
305867	AA864572		EST singleton (not in UniGene) with exon	2.37	MCF7, MB-MDA-453, MB-MDA-231
333296			CH22_FGENES.132_3	2.37	EB, PC3, CALU6
331070	R01116	Hs.182059	ESTs	2.36	OVCA-R, MB-MDA-453, A549
333698			CH22_FGENES.250_12	2.36	HT29, OVCA-R, Caco2
316423	AA758756	Hs.121380	ESTs	2.36	HT29, MCF7, MB-MDA-435s
323189	AL121194	Hs.120589	ESTs	2.36	PC3, NCI-H460, DU145
318889	Z43296	Hs.18720	programmed cell death 8 (apoptosis-induc	2.36	OVCA-R, A549, MB-MDA-453
334237			CH22_FGENES.362_1	2.36	NCI-H345, NCI-H69, LnCap
315931	AI700148	Hs.117328	ESTs	2.36	MCF7, NCI-H345, DU145
326884			CH.20_hs gi|6682511	2.36	A549, EB, PC3
333132			CH22_FGENES.83_8	2.36	NCI-H69, HT29, EB
306574	AA995719	Hs.76067	heat shock 27kD protein 1	2.36	RPWE-2, PRSC_log, PRSC_con
324416	AI669524	Hs.194115	ESTs	2.36	NCI-H345, RPWE-2, PRSC_con
329496			CH.10_p2 gi|3983518	2.35	HT29, MCF7, MB-MDA-231
320994	H22381		EST cluster (not in UniGene)	2.35	NCI-H23, A549, CALU6
320481	AA461139	Hs.24372	ESTs; Weakly similar to dJ207H1.1 [H.sap	2.35	PRSC_con, RPWE-2, PRSC_log
309958	AW444488		EST singleton (not in UniGene) with exon	2.35	NCI-H345, PRSC_con, PRSC_log
327009			CH.21_hs gi|5867664	2.35	HT29, BT474, MCF7
309594	AW172821	Hs.181165	eukaryotic translation elongation factor	2.35	HT29, DU145, EB
335468			CH22_FGENES.567_4	2.35	NCI-H69, PRSC_con, NCI-H345
304269	AA069029		EST singleton (not in UniGene) with exon	2.35	PRSC_con, PRSC_log, RPWE-2
305877	AA865649		EST singleton (not in UniGene) with exon	2.35	A549, MCF7, OVCA-R
305700	AA815428		EST singleton (not in UniGene) with exon	2.35	PRSC_con, NCI-H345, PRSC_log
326423			CH.19_hs gi|5867369	2.34	PC3, MCF7, LnCap
334560			CH22_FGENES.404_3	2.34	HT29, NCI-H460, MB-MDA-435s
337100			CH22_FGENES.472-3	2.34	PRSC_log, PRSC_con, RPWE-2
301505	AW014374	Hs.144849	ESTs	2.34	CALU6, MB-MDA-231, DU145
312142	AW298359	Hs.221069	ESTs	2.34	PRSC_con, RPWE-2, PRSC_log
305787	AA845035		EST singleton (not in UniGene) with exon	2.34	NCI-H23, NCI-H520, NCI-H460
338686			CH22_EM:AC005500.GENSCAN.472-5	2.33	BT474, MB-MDA-231, MB-MDA-453
331977	AA465207	Hs.125887	ESTs	2.33	OVCA-R, A549, MB-MDA-435s
314687	M79114	Hs.135177	ESTs	2.33	NCI-H69, PRSC_con, NCI-H345
336089			CH22_FGENES.688_18	2.33	PRSC_con, Caco2, PRSC_log
338952			CH22_DJ32I10.GENSCAN.23-22	2.33	PC3, OVCA-R, HT29
334612			CH22_FGENES.411_11	2.33	OVCA-R, MB-MDA-453, EB
338223			CH22_EM:AC005500.GENSCAN.250-10	2.33	DU145, MB-MDA-453, MCF7
327845			CH.05_hs gi|6531962	2.32	OVCA-R, MB-MDA-453, PC3
308187	AI538108	Hs.156110	Immunoglobulin kappa variable 1D-8	2.32	NCI-H69, NCI-358, PRSC_con
317767	AW294164	Hs.128340	ESTs; Weakly similar to Cdc42 GTPase-act	2.32	BT474, CALU6, MB-MDA-231
330468	L10343	Hs.112341	protease inhibitor 3; skin-derived (SKAL	2.32	PC3, Caco2, HT29
319003	R17712		EST cluster (not in UniGene)	2.32	MCF7, PC3, MB-MDA-453
323022	AI066733	Hs.133865	ESTs	2.32	CALU6, MB-MDA-231, DU145
303148	R73167	Hs.127317	ESTs; Weakly similar to CYTOCHROME P450	2.32	NCI-H345, PRSC_con, RPWE-2
303215	AW250314		EST	2.32	NCI-H345, PRSC_con, PRSC_log
318891	H10477	Hs.196208	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.32	NCI-H69, LnCap, NCI-H345
336653			CH22_FGENES.33-4	2.32	DU145, EB, LnCap
333329			CH22_FGENES.138_22	2.32	DU145, BT474, MB-MDA-231
301980	U69962	Hs.121498	potassium voltage-gated channel; Shab-re	2.31	NCI-H345, MB-MDA-231, LnCap
336968			CH22_FGENES.375-28	2.31	HT29, BT474, EB
308539	AI694191		EST singleton (not in UniGene) with exon	2.31	NCI-H345, NCI-H69, PRSC_log
326417			CH.19_hs gi|5867362	2.31	HT29, MCF7, BT474
328851			CH.07_hs gi|6381923	2.31	NCI-H520, NCI-H460, NCI-H23
329254			CH.X_hs gi|5868733	2.31	RPWE-2, NCI-H345, PRSC_con
303075	W88779	Hs.59125	ESTs	2.3	DU145, OVCA-R, EB
335131			CH22_FGENES.497_15	2.3	NCI-H69, NCI-H345, PRSC_log
303129	AA308334	Hs.172210	MUF1 protein	2.3	LnCap, DU145, HT29
327067			CH.21_hs gi|6531965	2.3	NCI-H345, NCI-H69, MB-MDA-435s
324064	AW137650		EST cluster (not in UniGene)	2.3	DU145, HT29, EB
325965			CH.16_hs gi|5867147	2.3	NCI-H69, NCI-H345, RPWE-2
334525			CH22_FGENES.402_4	2.3	NCI-H345, PRSC_con, NCI-H69
336654			CH22_FGENES.34-2	2.3	BT474, PC3, MB-MDA-453
302348	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.3	LnCap, CALU6, DU145
309275	AI989570		EST singleton (not in UniGene) with exon	2.3	NCI-H460, NCI-H23, NCI-H520
329246			CH.X_hs gi|5868732	2.3	NCI-H69, NCI-H345, PRSC_log
305557	AA774834		EST singleton (not in UniGene) with exon	2.3	CALU6, CALU6, MCF7
322907	AA084941		EST cluster (not in UniGene)	2.3	MB-MDA-231, CALU6, EB
318683	AI703241	Hs.202653	ESTs; Weakly similar to Xin [M.musculus]	2.29	NCI-H345, PRSC_con, RPWE-2
309233	AI971416		EST singleton (not in UniGene) with exon	2.29	CALU6, OVCA-R, EB
308913	AI860692	Hs.119122	ribosomal protein L13a	2.29	MB-MDA-435s, MCF7, HT29
335827			CH22_FGENES.620_1	2.29	PRSC_con, PRSC_log, RPWE-2
334066			CH22_FGENES.327_21	2.29	PRSC_con, PRSC_log, NCI-H345
302656	AW293005	Hs.220905	ESTs	2.29	NCI-H23, Caco2, CALU6
308974	AI872290	Hs.140	immunoglobulin gamma 3 (Gm marker)	2.29	CALU6, A549, NCI-H69
333607			CH22_FGENES.216_2	2.29	OVCA-R, MCF7, A549

335174			CH22_FGENES.504_4	2.29	HT29, A549, MB-MDA-453
332028	AA489680	Hs.134406	ESTs; Weakly similar to Dim1p homolog [H	2.29	EB, A549, DU145
336417			CH22_FGENES.823_39	2.29	NCI-H69, NCI-H345, PRSC_log
323426	AA251401		EST cluster (not in UniGene)	2.29	HT29, MB-MDA-231, BT474
336618			CH22_FGENES.2-1	2.29	NCI-358, NCI-H460, NCI-H69
310017	AI188739	Hs.148488	ESTs	2.29	NCI-H345, PRSC_log, PRSC_con
334055			CH22_FGENES.327_6	2.28	DU145, OVCA-R, MB-MDA-453
337168			CH22_FGENES.562-28	2.28	NCI-H69, PRSC_log, NCI-H345
329824			CH.14_p2 gi|6630758	2.28	NCI-H23, CALU6, RPWE-2
333891			CH22_FGENES.292_13	2.28	NCI-H69, MB-MDA-231, RPWE-2
339127			CH22_DA59H18.GENSCAN.55-1	2.28	PRSC_con, NCI-H345, RPWE-2
305686	AA812726		EST singleton (not in UniGene) with exon	2.28	NCI-H520, NCI-H23, NCI-H460
329782			CH.14_p2 gi|5912597	2.28	NCI-H69, NCI-H345, PRSC_log
311059	AI810001	Hs.175346	ESTs	2.28	MCF7, BT474, MB-MDA-435s
336934			CH22_FGENES.351-1	2.28	BT474, HT29, MB-MDA-435s
314893	AA761093		EST cluster (not in UniGene)	2.28	OVCA-R, HT29, DU145
331596	N72574	Hs.50220	ESTs	2.28	A549, MCF7, NCI-358
330729	AA258559	Hs.3736	ESTs; Weakly similar to DELTA-LIKE PROTE	2.28	MB-MDA-231, CALU6, MCF7
338285			CH22_EM:AC005500.GENSCAN.293-3	2.27	NCI-H69, PRSC_log, PRSC_con
300154	AI245127	Hs.179331	ESTs	2.27	NCI-H23, NCI-H520, NCI-358
306383	AA969078	Hs.183698	ribosomal protein L29	2.27	RPWE-2, NCI-H345, PRSC_log
309005	AI884454		EST singleton (not in UniGene) with exon	2.27	A549, MCF7, BT474
332995			CH22_FGENES.58_2	2.27	RPWE-2, NCI-H345, PRSC_log
337426			CH22_FGENES.761-3	2.27	DU145, EB, CALU6
337778			CH22_EM:AC000097.GENSCAN.119-20	2.27	NCI-H69, PRSC_con, PRSC_log
329705			CH.14_p2 gi|6065790	2.27	PRSC_con, PRSC_log, RPWE-2
335971			CH22_FGENES.652_4	2.27	PRSC_log, MB-MDA-231, NCI-H23
315862	AI075846	Hs.133996	ESTs	2.27	HT29, MB-MDA-435s, OVCA-R
316466	AI911204	Hs.126365	ESTs	2.27	NCI-H460, NCI-358, BT474
334430			CH22_FGENES.385_3	2.27	NCI-H345, NCI-H69, PRSC_con
331941	AA452257	Hs.99272	ESTs	2.26	PRSC_con, LnCap, PRSC_log
301230	AW269804	Hs.153019	ESTs	2.26	NCI-H345, PRSC_log, NCI-H520
317394	AI935024	Hs.190518	ESTs	2.26	NCI-H345, PRSC_con, PRSC_log
306220	AA928363		EST singleton (not in UniGene) with exon	2.26	NCI-H345, PRSC_con, PRSC_log
304134	H54627		EST singleton (not in UniGene) with exon	2.26	DU145, CALU6, PC3
335421			CH22_FGENES.551_1	2.26	NCI-H69, PRSC_con, PRSC_log
305260	AA679280	Hs.156110	Immunoglobulin kappa variable 1D-8	2.26	NCI-H345, NCI-H69, PRSC_con
303592	AA421129		EST	2.26	CALU6, OVCA-R, DU145
317982	AI004985	Hs.130607	ESTs	2.26	PC3, MB-MDA-435s, A549
325304			CH.11_hs gi|5866910	2.26	MCF7, CALU6, A549
334118			CH22_FGENES.330_19	2.26	PRSC_con, NCI-H69, PRSC_log
335687			CH22_FGENES.596_2	2.26	A549, CALU6, LnCap
334035			CH22_FGENES.322_3	2.26	NCI-H345, PRSC_con, RPWE-2
305454	AA738413		EST singleton (not in UniGene) with exon	2.25	EB, HT29, CALU6
335902			CH22_FGENES.635_10	2.25	EB, DU145, HT29
339215			CH22_FF113D11.GENSCAN.6-10	2.25	PRSC_con, PRSC_log, RPWE-2
328810			CH.07_hs gi|5868327	2.25	PC3, OVCA-R, MB-MDA-453
337396			CH22_FGENES.749-1	2.25	EB, A549, DU145
336808			CH22_FGENES.205-3	2.25	NCI-H345, NCI-H69, PRSC_con
305808	AA853958		EST singleton (not in UniGene) with exon	2.24	MB-MDA-453, DU145, EB
333571			CH22_FGENES.188_2	2.24	MCF7, MB-MDA-453, PC3
323023	AA225188	Hs.258539	ESTs	2.24	EB, DU145, CALU6
334626			CH22_FGENES.416_2	2.24	NCI-H69, NCI-H345, PRSC_log
333593			CH22_FGENES.210_2	2.24	NCI-H69, NCI-H345, PRSC_con
326708			CH.20_hs gi|5867593	2.24	NCI-H460, NCI-H23, NCI-H520
314502	AI041717	Hs.132141	ESTs	2.23	NCI-H345, RPWE-2, PRSC_con
309181	AI951727		EST singleton (not in UniGene) with exon	2.23	PRSC_con, PC3, MB-MDA-231
324926	H56196	Hs.117798	ESTs	2.23	EB, EB, DU145
333632			CH22_FGENES.227_3	2.23	CALU6, CALU6, MB-MDA-453
328243			CH.06_hs gi|6056292	2.23	PC3, LnCap, LnCap
327037			CH.21_hs gi|6531965	2.23	LnCap, DU145, EB
307380	AI222985		EST singleton (not in UniGene) with exon	2.23	NCI-H345, PRSC_con, PRSC_log
334766			CH22_FGENES.428_15	2.23	PRSC_log, NCI-H345, RPWE-2
335236			CH22_FGENES.515_8	2.23	OVCA-R, MCF7, BT474
336615			CH22_FGENES.613_5	2.23	NCI-H69, PRSC_log, PRSC_con
307558	AI281998		EST singleton (not in UniGene) with exon	2.23	DU145, OVCA-R, CALU6
308029	AI457115	Hs.62954	ferritin; heavy polypeptide 1	2.23	EB, OVCA-R, MB-MDA-453
331508	N47559	Hs.46732	EST	2.23	MB-MDA-453, MCF7, BT474
320980	AJ237672	Hs.214142	5;10-methylenetetrahydrofolate reductase	2.23	OVCA-R, EB, EB
304241	AA010976		EST singleton (not in UniGene) with exon	2.23	BT474, MB-MDA-435s, MB-MDA-231
314682	AI190864	Hs.178226	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.23	MB-MDA-231, MCF7, OVCA-R
308382	AI624301		EST singleton (not in UniGene) with exon	2.22	OVCA-R, BT474, CALU6
314476	AW207857	Hs.169604	ESTs	2.22	DU145, EB, A549
327864			CH.06_hs gi|5868130	2.22	NCI-H69, PRSC_log, PRSC_con
337279			CH22_FGENES.665-2	2.22	NCI-H345, NCI-H69, PRSC_con
302263	AA325517		EST	2.22	BT474, NCI-H520, DU145

322840	AA083710		EST cluster (not in UniGene)	2.22	HT29, MB-MDA-453, CALU6
307574	AI283549		EST singleton (not in UniGene) with exon	2.22	OVCA-R, CALU6, BT474
319027	AA716612		EST cluster (not in UniGene)	2.22	LnCap, NCI-H69, NCI-H69
305925	AA877883		EST singleton (not in UniGene) with exon	2.22	NCI-H345, NCI-H69, NCI-H69
329725			CH.14_p2 gi|6065785	2.22	NCI-H69, PRSC_con, NCI-H345
316194	AW298529	Hs.255774	ESTs	2.22	CALU6, EB, NCI-H520
301119	AF142579		EST	2.22	A549, OVCA-R, EB
333815			CH22_FGENES.282_4	2.22	MB-MDA-435s, EB, MB-MDA-453
334358			CH22_FGENES.378_1	2.22	NCI-H345, RPWE-2, PRSC_con
303763	AF043250	Hs.30928	DNA segment on chromosome 19 (unique) 11	2.21	Caco2, NCI-H23, NCI-H520
335593			CH22_FGENES.581_32	2.21	NCI-H345, PRSC_log, RPWE-2
334026			CH22_FGENES.318_3	2.21	NCI-H69, PRSC_con, NCI-H345
322224	AF086064		EST cluster (not in UniGene)	2.21	PRSC_con, PRSC_log, RPWE-2
309836	AW295497	Hs.157397	ESTs	2.21	NCI-H345, PRSC_con, RPWE-2
332669	M33374	Hs.661	NADH dehydrogenase (ubiquinone) 1 beta s	2.21	NCI-H520, CALU6, OVCA-R
307629	AI300246		EST singleton (not in UniGene) with exon	2.21	MB-MDA-231, MB-MDA-453, HT29
300470	T87841		EST	2.21	PC3, EB, CALU6
330064			CH.19_p2 gi|6165044	2.21	NCI-H69, PRSC_con, BT474
338819			CH22_DJ246D7.GENSCAN.1-24	2.21	NCI-H69, RPWE-2, PRSC_log
337797			CH22_EM:AC005500.GENSCAN.3-4	2.21	LnCap, NCI-H69, NCI-H520
328025			CH.06_hs gi|5902482	2.2	RPWE-2, PRSC_con, PRSC_log
326240			CH.17_hs gi|5867260	2.2	EB, LnCap, MB-MDA-453
312865	AW005376	Hs.173280	ESTs	2.2	DU145, DU145, OVCA-R
338450			CH22_EM:AC005500.GENSCAN.359-36	2.2	MCF7, MB-MDA-453, MB-MDA-435s
302532	U60181	Hs.248115	growth hormone secretagogue receptor	2.2	PRSC_con, PRSC_log, PRSC_log
321132	AA081495		EST cluster (not in UniGene)	2.2	NCI-H23, NCI-H520, NCI-358
337787			CH22_EM:AC000097.GENSCAN.123-3	2.2	EB, PC3, LnCap
337032			CH22_FGENES.438-3	2.2	NCI-H69, NCI-H345, RPWE-2
300026	M11507		AFFX control: transferrin receptor	2.2	HT29, EB, MB-MDA-231
333139			CH22_FGENES.83_16	2.2	HT29, MB-MDA-453, Caco2
334298			CH22_FGENES.372_4	2.2	PRSC_con, PRSC_log, RPWE-2
335002			CH22_FGENES.470_7	2.2	PRSC_con, NCI-H345, NCI-H345
335000			CH22_FGENES.470_5	2.2	EB, PC3, A549
337298			CH22_FGENES.678-3	2.2	NCI-H69, A549, HT29
302461	AF104253	Hs.241381	cofactor required for Sp1 transcriptiona	2.2	EB, CALU6, LnCap
334819			CH22_FGENES.436_15	2.19	CALU6, BT474, Caco2
300426	AW452660	Hs.253296	ESTs	2.19	DU145, CALU6, HT29
302569	AC004472		multiple UniGene matches	2.19	RPWE-2, PRSC_log, PRSC_con
339401			CH22_BA232E17.GENSCAN.7-7	2.19	NCI-H345, NCI-H69, PRSC_log
328791			CH.07_hs gi|5868309	2.19	DU145, PC3, HT29
337333			CH22_FGENES.711-3	2.19	NCI-H69, NCI-H345, PRSC_log
339363			CH22_BA354I12.GENSCAN.33-6	2.19	NCI-H69, PRSC_log, PRSC_con
329429			CH.Y_hs gi|5868882	2.19	CALU6, HT29, OVCA-R
336927			CH22_FGENES.348-3	2.19	NCI-H69, PRSC_log, NCI-358
336351			CH22_FGENES.816_3	2.19	DU145, EB, MB-MDA-231
313466	AA004731	Hs.148876	ESTs	2.19	CALU6, DU145, OVCA-R
307433	AI244895		EST singleton (not in UniGene) with exon	2.19	NCI-H23, NCI-H23, NCI-358
336590			CH22_FGENES.51_2	2.19	PRSC_con, NCI-H69, PRSC_log
310758	AI770001	Hs.209445	ESTs	2.18	EB, MB-MDA-231, BT474
327823			CH.05_hs gi|5867968	2.18	PRSC_con, NCI-H69, NCI-H345
313257	N92638		EST cluster (not in UniGene)	2.18	PRSC_log, RPWE-2, PRSC_con
335377			CH22_FGENES.543_17	2.18	PC3, MB-MDA-435s, CALU6
303958	AL042931		EST singleton (not in UniGene) with exon	2.18	NCI-H345, RPWE-2, PRSC_con
320153	AF064594	Hs.120360	phospholipase A2; group VI	2.18	LnCap, PC3, MB-MDA-435s
335201			CH22_FGENES.508_10	2.18	OVCA-R, DU145, HT29
338591			CH22_EM:AC005500.GENSCAN.434-4	2.18	NCI-H69, NCI-H345, RPWE-2
331958	AA455960	Hs.99405	ESTs	2.18	MCF7, NCI-H23, NCI-H460
337218			CH22_FGENES.614-2	2.18	CALU6, A549, MCF7
309470	AW118833		EST singleton (not in UniGene) with exon	2.18	PC3, EB, MB-MDA-435s
331896	AA435495	Hs.97174	H sapiens mRNA; cDNA DKFZp566E164 (from	2.18	RPWE-2, NCI-H69, PRSC_log
330275			CH.05_p2 gi|6671904	2.18	NCI-H345, PRSC_log, PRSC_con
335817			CH22_FGENES.618_5	2.18	A549, Caco2, PC3
332896			CH22_FGENES.35_10	2.18	NCI-H345, RPWE-2, PRSC_log
303294	AA205300		EST	2.17	MB-MDA-435s, A549, MCF7
338703			CH22_EM:AC005500.GENSCAN.480-2	2.17	HT29, BT474, NCI-H69
300115	AI215044	Hs.208130	ESTs	2.17	PC3, OVCA-R, HT29
330979	H22466	Hs.31795	ESTs	2.17	MCF7, EB, MB-MDA-435s
317246	AW105092	Hs.155690	ESTs	2.17	MB-MDA-453, DU145, EB
329078			CH.X_hs gi|5868597	2.17	MB-MDA-453, MB-MDA-231, BT474
312554	AI222630	Hs.109390	ESTs	2.17	NCI-H520, OVCA-R, MCF7
323207	AI052795	Hs.192201	ESTs	2.17	NCI-H69, NCI-H345, PRSC_log
301894	AA484435	Hs.41997	alpha-1-B glycoprotein	2.17	PRSC_con, LnCap, PRSC_log
329097			CH.X_hs gi|5868624	2.16	MB-MDA-231, MCF7, NCI-358
328328			CH.07_hs gi|5868375	2.16	NCI-H345, PRSC_con, NCI-H69
302671	AA522440	Hs.135917	ESTs	2.16	BT474, DU145, A549
329201			CH.X_hs gi|5868718	2.16	OVCA-R, PC3, MB-MDA-435s

329902			CH.15_p2 gi|6634760	2.16	PRSC_con, NCI-H69, NCI-H345
334435			CH22_FGENES.385_10	2.16	PRSC_con, NCI-H345, RPWE-2
330742	AA400979	Hs.25691	calcitonin receptor-like receptor activi	2.16	MCF7, MB-MDA-453, PC3
328484			CH.07_hs gi|5868454	2.16	NCI-H69, PRSC_log, NCI-H345
334784			CH22_FGENES.432_9	2.16	PRSC_log, RPWE-2, PRSC_con
337771			CH22_EM:AC000097.GENSCAN.119-10	2.16	NCI-H69, PRSC_con, RPWE-2
300181	AI284955	Hs.157568	ESTs; Weakly similar to ataxin-2 [M.musc	2.16	DU145, EB, CALU6
300268	AI539446	Hs.245450	ESTs	2.16	PRSC_con, RPWE-2, PRSC_log
309575	AW168096	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.16	A549, NCI-H23, MB-MDA-453
336548			CH22_FGENES.841_5	2.16	NCI-H345, NCI-H69, MB-MDA-231
328506			CH.07_hs gi|5868471	2.16	EB, A549, CALU6
330189			CH.05_p2 gi|6165182	2.16	NCI-H460, MCF7, MB-MDA-453
305480	AA746500	Hs.25911	HLA-B associated transcript-2	2.16	EB, DU145, NCI-358
302270	R56151		EST	2.16	OVCA-R, MB-MDA-435s, PRSC_con
306669	AI004899		EST singleton (not in UniGene) with exon	2.16	PRSC_log, PRSC_con, NCI-H345
325887			CH.16_hs gi|5867087	2.16	EB, CALU6, NCI-358
327015			CH.21_hs gi|5867664	2.15	EB, PC3, HT29
338576			CH22_EM:AC005500.GENSCAN.429-1	2.15	NCI-H69, NCI-H345, PRSC_con
333592			CH22_FGENES.209_2	2.15	NCI-H69, OVCA-R, PRSC_con
317253	AW071241	Hs.199685	ESTs	2.15	MB-MDA-435s, NCI-H23, MB-MDA-453
302301	R67493	Hs.127150	ESTs; Weakly similar to ZINC FINGER PROT	2.15	PC3, MCF7, MB-MDA-435s
336858			CH22_FGENES.293-8	2.15	RPWE-2, PRSC_con, NCI-H69
308417	AI640693	Hs.2186	eukaryotic translation elongation factor	2.15	EB, OVCA-R, CALU6
338177			CH22_EM:AC005500.GENSCAN.219-5	2.15	NCI-H345, NCI-H23, NCI-H520
337592			CH22_C20H12.GENSCAN.6-7	2.15	PC3, A549, HT29
325945			CH.16_hs gi|5867138	2.15	MB-MDA-453, MB-MDA-435s, DU145
335262			CH22_FGENES.520_3	2.15	EB, PC3, A549
333665			CH22_FGENES.244_1	2.15	PRSC_con, RPWE-2, PRSC_log
333710			CH22_FGENES.250_25	2.14	PRSC_log, NCI-H69, PRSC_con
304927	AA604728	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.14	LnCap, PC3, MCF7
336999			CH22_FGENES.417-20	2.14	NCI-H69, NCI-H345, PRSC_con
313283	W32480	Hs.157099	ESTs	2.14	EB, MB-MDA-231, A549
306221	AA928686		EST singleton (not in UniGene) with exon	2.14	NCI-H460, PRSC_con, NCI-H23
333205			CH22_FGENES.102_5	2.14	NCI-H69, PRSC_con, PRSC_log
312932	AI804218	Hs.209614	ESTs	2.14	PRSC_con, NCI-H345, RPWE-2
328938			CH.08_hs gi|5868500	2.14	HT29, PC3, MB-MDA-453
326746			CH.20_hs gi|5867611	2.14	NCI-H345, NCI-H69, PRSC_con
337964			CH22_EM:AC005500.GENSCAN.100-9	2.14	RPWE-2, PRSC_con, PRSC_log
337984			CH22_EM:AC005500.GENSCAN.110-2	2.14	EB, DU145, NCI-H345
337704			CH22_EM:AC000097.GENSCAN.87-6	2.14	NCI-H69, NCI-H460, NCI-358
302162	AF119046		EST	2.14	MB-MDA-435s, PC3, EB
303192	AA081755	Hs.8059	ESTs; Highly similar to SYNAPTOTAGMIN IV	2.14	MB-MDA-435s, MB-MDA-435s, MB-MDA-453
306200	AA926816		EST singleton (not in UniGene) with exon	2.14	MB-MDA-453, CALU6, DU145
303996	AW515979	Hs.84298	CD74 antigen (invariant polypptd of majo	2.14	LnCap, MB-MDA-231, BT474
325409			CH.12_hs gi|5866921	2.14	PRSC_log, PRSC_con, RPWE-2
308558	AI700145	Hs.172182	poly(A)-binding protein; cytoplasmic 1	2.14	MCF7, EB, MB-MDA-435s
302185	AA243837	Hs.156915	ESTs	2.14	MB-MDA-453, MCF7, EB
303021	W39612		EST	2.14	PRSC_con, NCI-H69, RPWE-2
301005	AW451916	Hs.210848	ESTs	2.14	DU145, EB, HT29
336029			CH22_FGENES.672_4	2.14	NCI-H69, PRSC_con, RPWE-2
305443	AA736653		EST singleton (not in UniGene) with exon	2.14	NCI-358, NCI-H520, NCI-H23
335485			CH22_FGENES.570_17	2.13	NCI-H460, MB-MDA-435s, MCF7
304817	AA584712		EST singleton (not in UniGene) with exon	2.13	MCF7, MCF7, NCI-H520
309859	AW298760		EST singleton (not in UniGene) with exon	2.13	NCI-H69, PRSC_con, LnCap
326206			CH.17_hs gi|5867219	2.13	EB, MB-MDA-231, LnCap
303656	AA437189	Hs.122574	ESTs	2.13	LnCap, MB-MDA-435s, EB
334745			CH22_FGENES.426_3	2.13	OVCA-R, DU145, MB-MDA-453
318504	T26453		EST cluster (not in UniGene)	2.13	RPWE-2, LnCap, CALU6
306839	AI077385		EST singleton (not in UniGene) with exon	2.13	MCF7, MB-MDA-453, MB-MDA-435s
303843	W94322	Hs.58094	melanoma inhibitory activity	2.13	MB-MDA-435s, NCI-H345, RPWE-2
308444	AI659398	Hs.197097	EST	2.13	MB-MDA-453, MCF7, BT474
301322	AW448965	Hs.256305	ESTs	2.13	NCI-H345, LnCap, PC3
326997			CH.21_hs gi|5867660	2.13	HT29, A549, CALU6
326793			CH.20_hs gi|5867631	2.13	PRSC_log, PRSC_con, MB-MDA-453
320360	H12405		EST cluster (not in UniGene)	2.12	MB-MDA-231, BT474, HT29
316301	AW206279	Hs.192009	ESTs	2.12	DU145, DU145, EB
335371			CH22_FGENES.543_9	2.12	PC3, MB-MDA-435s, DU145
301178	AA828385		EST	2.12	EB, OVCA-R, LnCap
326136			CH.17_hs gi|5867202	2.12	RPWE-2, PRSC_log, PRSC_con
339213			CH22_FF113D11.GENSCAN.6-8	2.12	OVCA-R, PC3, MB-MDA-231
335980			CH22_FGENES.653_2	2.12	BT474, BT474, OVCA-R
314380	AA758797	Hs.192807	ESTs	2.11	PRSC_con, PRSC_log, RPWE-2
306779	AI041302		EST singleton (not in UniGene) with exon	2.11	NCI-H345, PRSC_con, PRSC_log
335774			CH22_FGENES.607_10	2.11	PC3, A549, MB-MDA-453
334914			CH22_FGENES.457_3	2.11	PRSC_con, NCI-H345, NCI-H69
304619	AA515554	Hs.119598	ribosomal protein L3	2.11	EB, MB-MDA-453, MB-MDA-435s

	303358	AI199714	Hs.158149	ESTs	2.11	CALU6, OVCA-R, DU145
	306558	AA994743		EST singleton (not in UniGene) with exon	2.11	HT29, MB-MDA-453, CALU6
	337781			CH22_EM:AC000097.GENSCAN.121-3	2.11	PRSC_log, PRSC_con, RPWE-2
	333140			CH22_FGENES.84_1	2.11	HT29, NCI-H69, OVCA-R
5	315081	AI247134	Hs.155281	ESTs	2.11	MB-MDA-453, MCF7, HT29
	302965	AA446441	Hs.138842	ESTs	2.11	NCI-358, NCI-H23, CALU6
	302138	N83965		EST	2.11	PRSC_log, PRSC_con, NCI-H345
	320802	D83824	Hs.185055	BENE protein	2.11	A549, PC3, HT29
	322152	AA565332		EST cluster (not in UniGene)	2.11	A549, CALU6, EB
10	326418			CH.19_hs gi|5867365	2.1	EB, OVCA-R, DU145
	308709	AI783498	Hs.181165	eukaryotic translation elongation factor	2.1	MB-MDA-435s, MB-MDA-453, DU145
	332737	C01852	Hs.84359	hypothetical protein	2.1	NCI-H23, A549, DU145
	333283			CH22_FGENES.128_13	2.1	NCI-H345, RPWE-2, PRSC_con
	328636			CH.07_hs gi|6004473	2.1	DU145, EB, MB-MDA-453
15	329187			CH.X_hs gi|5868713	2.1	NCI-358, NCI-H23, NCI-H460
	305999	AA889603		EST singleton (not in UniGene) with exon	2.1	HT29, OVCA-R, PC3
	333220			CH22_FGENES.104_12	2.1	PRSC_con, PRSC_log, RPWE-2
	335092			CH22_FGENES.492_2	2.1	NCI-H69, PRSC_con, NCI-H345
	304887	AA599355		EST singleton (not in UniGene) with exon	2.1	DU145, EB, MCF7
20	325359			CH.12_hs gi|5866920	2.1	MB-MDA-453, EB, MB-MDA-435s
	330956	H08730	Hs.6933	ESTs	2.1	NCI-H520, PRSC_con, NCI-H345
	323786	AW449315	Hs.165795	ESTs	2.1	OVCA-R, A549, LnCap
	333619			CH22_FGENES.219_3	2.1	BT474, OVCA-R, HT29
	324538	AW502979		EST cluster (not in UniGene)	2.09	CALU6, A549, DU145
25	303405	AA308601		EST	2.09	DU145, CALU6, NCI-H69
	328570			CH.07_hs gi|5868231	2.09	LnCap, MB-MDA-231, DU145
	308971	AI871218	Hs.224731	EST	2.09	NCI-H23, NCI-H460, NCI-358
	330467	K02268	Hs.22584	prodynorphin	2.09	PC3, BT474, MB-MDA-453
	334793			CH22_FGENES.433_5	2.09	EB, DU145, LnCap
30	300908	AA618335	Hs.146137	ESTs; Weakly similar to putative [C.eleg	2.09	NCI-H345, PRSC_log, PRSC_con
	309656	AW197060	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.09	A549, NCI-H23, NCI-H460
	320963	AB029041	Hs.209646	KIAA1118 protein	2.09	PRSC_con, PRSC_log, NCI-H345
	310833	AW295351	Hs.169136	ESTs	2.09	PC3, LnCap, MB-MDA-453
	335693			CH22_FGENES.596_8	2.09	NCI-H69, LnCap, PRSC_log
35	325966			CH.16_hs gi|5867147	2.09	MCF7, CALU6, MB-MDA-453
	329319			CH.X_hs gi|6381976	2.09	NCI-H460, EB, DU145
	338526			CH22_EM:AC005500.GENSCAN.396-14	2.09	NCI-H69, NCI-H345, PRSC_log
	336751			CH22_FGENES.128-5	2.09	NCI-H69, NCI-H345, PRSC_log
	325510			CH.12_hs gi|5866974	2.09	HT29, OVCA-R, CALU6
40	323553	AA292626	Hs.122854	ESTs	2.08	NCI-H345, RPWE-2, NCI-358
	326343			CH.17_hs gi|6525295	2.08	EB, LnCap, DU145
	335470			CH22_FGENES.568_3	2.08	NCI-H69, PRSC_con, PRSC_log
	320122	T93681	Hs.187515	ESTs	2.08	MCF7, MB-MDA-453, BT474
	335320			CH22_FGENES.534_7	2.08	BT474, MB-MDA-231, HT29
45	307120	AI184343		EST singleton (not in UniGene) with exon	2.08	HT29, MCF7, PC3
	338080			CH22_EM:AC005500.GENSCAN.172-11	2.08	LnCap, PC3, HT29
	313113	AI056258	Hs.122523	ESTs	2.08	MCF7, DU145, MB-MDA-453
	337685			CH22_EM:AC000097.GENSCAN.77-1	2.08	NCI-H69, NCI-H345, PRSC_log
	327461			CH.02_hs gi|6004455	2.08	NCI-H23, BT474, NCI-358
50	335895			CH22_FGENES.635_3	2.08	HT29, MB-MDA-231, NCI-H520
	303933	AW471472		EST singleton (not in UniGene) with exon	2.08	MB-MDA-231, BT474, NCI-H345
	314803	AI935159	Hs.166841	ESTs; Weakly similar to MYOSIN LIGHT CHA NON-MUSCLE ISOZYMES [H.sapiens]	2.08	PC3, A549, BT474
	302722	U53530		EST	2.08	DU145, MB-MDA-435s, OVCA-R
55	307703	AI318588		EST singleton (not in UniGene) with exon	2.08	HT29, MB-MDA-435s, CALU6
	310558	AI334965	Hs.176976	ESTs	2.08	A549, LnCap, PC3
	315276	AA860090		EST cluster (not in UniGene)	2.08	PC3, MCF7, OVCA-R
	306443	AA976950		EST singleton (not in UniGene) with exon	2.07	OVCA-R, PC3, EB
	307961	AI421059		EST singleton (not in UniGene) with exon	2.07	HT29, OVCA-R, CALU6
60	329735			CH.14_p2 gi|6065780	2.07	EB, HT29, OVCA-R
	335193			CH22_FGENES.507_8	2.07	EB, A549, A549
	320347	R34423	Hs.221535	ESTs	2.07	CALU6, A549, EB
	316153	AA724474	Hs.147208	ESTs	2.07	MB-MDA-453, PC3, HT29
	300921	AW293224	Hs.232165	ESTs	2.07	HT29, CALU6, CALU6
65	319264	T65096		EST cluster (not in UniGene)	2.07	MB-MDA-453, MCF7, CALU6
	330204			CH.05_p2 gi|6013606	2.07	OVCA-R, DU145, EB
	317070	AI142037	Hs.125379	ESTs	2.07	PRSC_con, NCI-H345, OVCA-R
	337645			CH22_EM:AC000097.GENSCAN.10-8	2.07	NCI-H345, PRSC_log, NCI-H69
	312501	AW450490	Hs.132886	ESTs	2.07	NCI-H520, CALU6, MCF7
70	335587			CH22_FGENES.581_26	2.07	NCI-H69, NCI-H345, PRSC_log
	311482	AI917706	Hs.129997	ESTs	2.07	NCI-H520, MCF7, MB-MDA-435s
	302488	AF161441		EST	2.07	EB, DU145, CALU6
	304692	AA554202	Hs.76067	heat shock 27kD protein 1	2.07	MCF7, MB-MDA-453, PC3
	325369			CH.12_hs gi|5866920	2.07	DU145, DU145, MB-MDA-453
75	306284	AA936835		EST singleton (not in UniGene) with exon	2.07	BT474, MB-MDA-231, HT29
	337402			CH22_FGENES.752-1	2.07	A549, BT474, DU145

327418			CH.02_hs gi|5867750	2.07	MCF7, MB-MDA-453, MB-MDA-435s
317977	AI004775	Hs.205091	ESTs; Weakly similar to WW domain bindin	2.07	BT474, MB-MDA-453, PC3
331870	AA428560	Hs.161845	EST	2.07	MB-MDA-231, MB-MDA-435s, BT474
300750	AA514805	Hs.105464	ESTs	2.07	HT29, BT474, BT474
336657			CH22_FGENES.35-14	2.07	MB-MDA-453, MCF7, NCI-H460
336035			CH22_FGENES.678_6	2.07	NCI-H69, PRSC_con, RPWE-2
325320			CH.11_hs gi|5866870	2.06	NCI-H69, PRSC_log, PRSC_con
306053	AA905312		EST singleton (not in UniGene) with exon	2.06	HT29, OVCA-R, MB-MDA-231
333175			CH22_FGENES.95_2	2.06	LnCap, HT29, DU145
304491	AA437096	Hs.115502	EST	2.06	MB-MDA-435s, CALU6, CALU6
310632	AI697536	Hs.176991	ESTs	2.06	NCI-H69, PRSC_log, NCI-H345
338521			CH22_EM:AC005500.GENSCAN.395-35	2.06	NCI-H345, PRSC_log, PRSC_log
334900			CH22_FGENES.452_14	2.06	A549, CALU6, NCI-H69
337451			CH22_FGENES.774-2	2.06	PRSC_con, PRSC_log, RPWE-2
308792	AI815153	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.06	DU145, BT474, MB-MDA-453
336854			CH22_FGENES.280-1	2.06	LnCap, EB, MB-MDA-435s
304485	AA434076		EST singleton (not in UniGene) with exon	2.06	MB-MDA-231, BT474, CALU6
326458			CH.19_hs gi|5867400	2.06	EB, DU145, LnCap
303506	AA340605	Hs.105887	ESTs	2.06	LnCap, MCF7, CALU6
333628			CH22_FGENES.226_2	2.06	NCI-H520, NCI-358, NCI-358
300763	AA190753		EST	2.06	NCI-H69, NCI-H345, PRSC_con
334836			CH22_FGENES.439_6	2.06	NCI-H345, PRSC_con, RPWE-2
335217			CH22_FGENES.512_3	2.06	PRSC_log, PRSC_con, NCI-H69
338970			CH22_DJ32I10.GENSCAN.26-3	2.06	A549, MB-MDA-453, LnCap
334842			CH22_FGENES.439_21	2.06	DU145, HT29, CALU6
309309	AW006428	Hs.232857	EST	2.06	EB, DU145, OVCA-R
332949			CH22_FGENES.47_12	2.06	EB, DU145, OVCA-R
310530	AW369663	Hs.150150	ESTs	2.06	PRSC_con, PRSC_log, RPWE-2
329401			CH.X_hs gi|6682544	2.06	NCI-H69, PRSC_con, RPWE-2
316893	AA837332		EST cluster (not in UniGene)	2.06	OVCA-R, MCF7, MB-MDA-453
325022	W95840	Hs.59745	NADH dehydrogenase (ubiquinone) flavopro	2.06	Caco2, NCI-358, OVCA-R
329839			CH.14_p2 gi|6672062	2.05	MB-MDA-231, RPWE-2, CALU6
306668	AI004890		EST singleton (not in UniGene) with exon	2.05	DU145, MB-MDA-453, MCF7
315604	AW137442	Hs.136965	ESTs	2.05	LnCap, EB, PC3
318551	AI909951	Hs.239307	tyrosyl-tRNA synthetase	2.05	NCI-H345, PRSC_con, RPWE-2
339344			CH22_BA354I12.GENSCAN.28-1	2.05	BT474, MB-MDA-231, A549
310621	AI632098	Hs.198099	ESTs	2.05	NCI-H69, RPWE-2, MCF7
327051			CH.21_hs gi|6531965	2.05	PRSC_con, NCI-H345, PRSC_log
336827			CH22_FGENES.236-2	2.05	NCI-H345, A549, MB-MDA-231
311846	AI078033	Hs.177170	ESTs; Moderately similar to !!!! ALU SUB	2.05	OVCA-R, DU145, CALU6
335036			CH22_FGENES.475_14	2.05	NCI-H69, PRSC_con, NCI-H345
313100	N52880	Hs.122817	ESTs	2.05	RPWE-2, NCI-H345, PRSC_log
301927	AF014459	Hs.113250	retinoschisis (X-linked; juvenile) 1	2.05	MB-MDA-231, NCI-H345, PRSC_con
326070			CH.17_hs gi|5867175	2.05	MB-MDA-435s, MB-MDA-231, BT474
338514			CH22_EM:AC005500.GENSCAN.392-4	2.05	PRSC_con, PRSC_log, RPWE-2
328098			CH.06_hs gi|5868020	2.05	DU145, CALU6, EB
301102	AA679361	Hs.249487	ESTs	2.05	NCI-H460, PRSC_con, NCI-H23
306193	AA923457		EST singleton (not in UniGene) with exon	2.05	NCI-H345, PRSC_con, RPWE-2
317027	AA883808	Hs.174148	ESTs	2.05	EB, DU145, CALU6
336102			CH22_FGENES.693_2	2.04	LnCap, NCI-H69, PRSC_log
301372	AI239895	Hs.130555	ESTs	2.04	PRSC_con, RPWE-2, PRSC_log
333252			CH22_FGENES.116_4	2.04	NCI-358, A549, HT29
322516	AW372340	Hs.159717	ESTs	2.04	HT29, MB-MDA-231, BT474
324148	AA393624		EST cluster (not in UniGene)	2.04	RPWE-2, PRSC_con, MB-MDA-231
338770			CH22_EM:AC005500.GENSCAN.520-1	2.04	PRSC_con, NCI-H69, NCI-H460
314795	AI798611	Hs.157277	ESTs	2.04	EB, PC3, LnCap
333004			CH22_FGENES.60_1	2.04	A549, NCI-358, DU145
302405	AW245825	Hs.211914	NADH dehydrogenase (ubiquinone) Fe-S pro	2.04	NCI-H520, CALU6, Caco2
323587	AI905527	Hs.141901	ESTs; Moderately similar to !!!! ALU SUB	2.04	EB, A549, HT29
300898	AI276278	Hs.157176	ESTs	2.04	PC3, MB-MDA-453, BT474
301506	AI149878	Hs.143519	ESTs; Weakly similar to testicular tekti	2.04	NCI-H69, RPWE-2, NCI-H345
325851			CH.16_hs gi|5867067	2.04	MB-MDA-231, HT29, EB
323945	AI125604	Hs.155117	ESTs	2.04	MCF7, DU145, DU145
303265	AW160951		EST	2.04	LnCap, OVCA-R, DU145
334135			CH22_FGENES.336_2	2.04	PC3, A549, MB-MDA-435s
329793			CH.14_p2 gi|6522661	2.04	DU145, CALU6, HT29
332595	AA256431	Hs.3244	G protein pathway suppressor 2	2.04	A549, CALU6, NCI-H23
316059	AW166388	Hs.250181	ESTs	2.04	MCF7, HT29, A549
324104	AW246071	Hs.133122	ESTs	2.04	Caco2, A549, MCF7
306801	AI052653		EST singleton (not in UniGene) with exon	2.03	EB, LnCap, PC3
338096			CH22_EM:AC005500.GENSCAN.181-14	2.03	DU145, HT29, CALU6
327544			CH.03_hs gi|5867797	2.03	PRSC_con, NCI-H69, NCI-H345
318813	F13195		EST cluster (not in UniGene)	2.03	PRSC_con, RPWE-2, PRSC_log
325289			CH.11_hs gi|5866903	2.03	EB, OVCA-R, A549
311099	T56361	Hs.182167	hemoglobin; gamma A	2.03	HT29, BT474, EB
316079	AA922213	Hs.121735	ESTs	2.03	LnCap, OVCA-R, EB

	309533	AW151131		EST singleton (not in UniGene) with exon	2.03	MB-MDA-231, BT474, LnCap
	338579			CH22_EM:AC005500.GENSCAN.431-3	2.03	NCI-H69, NCI-H345, RPWE-2
	326549			CH.19_hs gi|5867307	2.03	NCI-H69, Caco2, NCI-H345
	320012	AI628384	Hs.193745	ESTs	2.03	BT474, MB-MDA-453, MCF7
5	334111			CH22_FGENES.330_10	2.03	NCI-H69, MB-MDA-231, BT474
	327123			CH.21_hs gi|6531971	2.03	NCI-H345, NCI-H69, RPWE-2
	324568	AW502311		EST cluster (not in UniGene)	2.03	NCI-H345, NCI-H520, NCI-H460
	306012	AA896989		EST singleton (not in UniGene) with exon	2.03	NCI-H69, PRSC_log, PRSC_con
	303106	AA012877		EST	2.03	RPWE-2, OVCA-R, EB
10	302194	U52219	Hs.158329	G protein-coupled receptor 50	2.03	NCI-H520, NCI-H23, PC3
	326646			CH.20_hs gi|5867562	2.03	NCI-H460, OVCA-R, HT29
	304060	T61464		EST singleton (not in UniGene) with exon	2.03	NCI-H345, PRSC_con, PRSC_log
	304667	AA535602		EST singleton (not in UniGene) with exon	2.03	A549, DU145, EB
	330514	M83652	Hs.53155	properdin P factor; complement	2.02	NCI-H23, NCI-H460, NCI-358
15	310324	AI473273	Hs.159674	ESTs; Weakly similar to GLUTAMATE [H.sap	2.02	NCI-H345, MB-MDA-231, BT474
	330327			CH.08_p2 gi|5919194	2.02	NCI-H345, NCI-H69, PRSC_log
	308447	AI659985		EST singleton (not in UniGene) with exon	2.02	NCI-H345, RPWE-2, PRSC_log
	307778	AI344972	Hs.231496	EST	2.02	NCI-H69, CALU6, OVCA-R
	319459	T87351	Hs.194121	ESTs	2.02	NCI-H460, NCI-358, NCI-H520
20	300935	AA513644	Hs.222815	ESTs; Weakly similar to Wiskott-Aldrich	2.02	DU145, EB, OVCA-R
	314318	AL037405	Hs.176141	ESTs	2.02	PRSC_con, LnCap, PRSC_log
	334779			CH22_FGENES.432_1	2.02	EB, HT29, DU145
	336994			CH22_FGENES.410-2	2.02	NCI-H345, PRSC_con, NCI-H69
	334076			CH22_FGENES.327_31	2.02	OVCA-R, CALU6, EB
25	318116	AW452865	Hs.132339	ESTs	2.02	MB-MDA-231, NCI-H69, NCI-H345
	326783			CH.20_hs gi|6525298	2.02	NCI-H69, PRSC_con, RPWE-2
	336142			CH22_FGENES.705_4	2.02	NCI-H69, PRSC_log, PRSC_con
	320913	AA663733		EST cluster (not in UniGene)	2.02	DU145, EB, CALU6
	301644	AW239364		EST	2.02	PRSC_con, RPWE-2, PRSC_log
30	300944	AW081072	Hs.164624	ESTs; Weakly similar to Slit-3 protein [	2.01	RPWE-2, NCI-H69, NCI-H23
	310080	AW137088	Hs.144857	ESTs	2.01	PRSC_con, NCI-H345, PRSC_log
	311248	AI863918	Hs.195078	ESTs	2.01	NCI-H345, NCI-H69, RPWE-2
	319207	R87679		EST cluster (not in UniGene)	2.01	HT29, A549, NCI-H460
	334760			CH22_FGENES.428_9	2.01	NCI-358, NCI-H69, PRSC_log
35	338368			CH22_EM:AC005500.GENSCAN.325-2	2.01	NCI-H23, NCI-H520, NCI-H460
	317300	AI417007	Hs.166338	ESTs	2.01	NCI-H460, DU145, NCI-H23
	323699	AW178750		EST cluster (not in UniGene)	2.01	MCF7, MB-MDA-453, OVCA-R
	301366	AA907713	Hs.221667	ESTs	2.01	PRSC_con, NCI-H345, RPWE-2
	333306			CH22_FGENES.137_3	2.01	NCI-H69, NCI-H345, PRSC_con
40	328031			CH.06_hs gi|5902482	2.01	MB-MDA-231, NCI-H345, PRSC_con
	301806	AA326007	Hs.12056	asialoglycoprotein receptor 1	2.01	MB-MDA-453, DU145, EB
	300993	AA584930	Hs.191777	ESTs; Weakly similar to XAP-5-like prote	2.01	HT29, NCI-H23, NCI-358
	320042	T84520		EST cluster (not in UniGene)	2.01	PRSC_con, NCI-H345, NCI-H69
	331082	R17059	Hs.22100	ESTs	2.01	EB, DU145, MB-MDA-435s
45	308851	AI829820		EST singleton (not in UniGene) with exon	2.01	DU145, EB, PC3
	301163	AA732066		EST	2.01	OVCA-R, PC3, MB-MDA-435s
	304734	AA576428		EST singleton (not in UniGene) with exon	2.01	LnCap, MB-MDA-453, DU145
	334855			CH22_FGENES.442_6	2.01	NCI-H345, RPWE-2, PRSC_log
	337121			CH22_FGENES.519-1	2.01	NCI-H69, NCI-H345, PRSC_con
50	331838	AA412498	Hs.104778	ESTs	2.01	BT474, BT474, MCF7
	339181			CH22_DA59H18.GENSCAN.72-6	2.01	NCI-H345, PRSC_con, NCI-H69
	327564			CH.03_hs gi|5867811	2.01	BT474, HT29, DU145
	304108	R63932	Hs.28467	EST	2	BT474, OVCA-R, MCF7
	315036	AA534953	Hs.163297	ESTs	2	MB-MDA-435s, MB-MDA-453, LnCap
55	312777	W92809	Hs.138557	ESTs	2	PRSC_con, NCI-H345, MB-MDA-231
	305888	AA868536	Hs.126145	EST	2	HT29, HT29, BT474
	323185	R52177		EST cluster (not in UniGene)	2	EB, A549, BT474
	308681	AI761307		EST singleton (not in UniGene) with exon	2	RPWE-2, PRSC_con, NCI-H345
	325755			CH.14_hs gi|6682474	2	NCI-H345, PRSC_con, PRSC_log
60	324376	AW499705		EST cluster (not in UniGene)	2	DU145, BT474, PC3
	331890	AA432166	Hs.3577	succinate dehydrogenase complex; subunit	2	CALU6, MB-MDA-453, A549

Table 4

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Exr_Accn	UniG_ID	Complete_Title	Ratio Met/BS	Top 3 expressing cell lines
313166	AI801098	Hs.151500	ESTs	12.23	Caco2, EB, OVCA-R
334593			CH22_FGENES.408_3	8.06	NCI-H69, OVCA-R, OVCA-R
331084	R20655	Hs.81281	Human clone 23732 mRNA; partial cds	7.89	LnCap, OVCA-R, EB
324598	AA502659	Hs.163986	ESTs	7.77	OVCA-R, EB, CALU6
314071	AA192455	Hs.188690	ESTs	7.76	CALU6, EB, DU145
315178	AW362945	Hs.162459	ESTs	6.81	OVCA-R, EB, CALU6
325519			CH.12_hs gi|6017036	6.34	NCI-H69, NCI-H345, PRSC_con
331433	H68097	Hs.161023	EST	6.16	OVCA-R, A549, EB
315021	AA533447		EST cluster (not in UniGene)	6.15	PC3, EB, CALU6
337695			CH22_EM:AC000097.GENSCAN.84-1	5.84	NCI-H69, NCI-H345, DU145
324048	AA378739		EST cluster (not in UniGene)	5.77	OVCA-R, DU145, EB
300781	AA731209		EST cluster (not in UniGene) with exon h	5.72	MB-MDA-453, MCF7, MB-MDA-435s
320701	AI093177	Hs.134923	ESTs	5.68	A549, NCI-H345, NCI-H69
332471	AA416967	Hs.120980	nuclear receptor co-repressor 2	5.68	LnCap, A549, OVCA-R
331858	AA421163	Hs.163848	ESTs	5.66	OVCA-R, DU145, Caco2
330987	H40988	Hs.131965	ESTs5.35	NCI-H345, OVCA-R, LnCap	
322309	AF086372		EST cluster (not in UniGene)	5.31	OVCA-R, DU145, PC3
324733	AA582082	Hs.199410	ESTs	5.17	PRSC_con, PRSC_log, NCI-H345
313577	AA565051	Hs.155029	ESTs	5.16	OVCA-R, PC3, EB
310966	AW271974	Hs.210295	ESTs	5.15	NCI-H69, PRSC_log, PRSC_con
311332	AW292247	Hs.255052	ESTs	5.05	Caco2, OVCA-R, EB
314522	AI732331	Hs.187750	ESTs; Moderately similar to !!!! ALU CLA	5.04	EB, DU145, HT29
330886	AA135606	Hs.189384	ESTs; Weakly similar to !!!! ALU SUBFAMI	4.93	OVCA-R, DU145, Caco2
313597	AW162263	Hs.249990	ESTs	4.84	NCI-H460, NCI-H345, NCI-H23
314439	AI539443	Hs.137447	ESTs	4.84	DU145, Caco2, MB-MDA-231
320807	AA086110	Hs.188536	H sapiens clone 24838 mRNA seq	4.83	PC3, OVCA-R, DU145
311804	AA135159	Hs.203349	ESTs	4.82	OVCA-R, PC3, Caco2
321354	AA078493		EST cluster (not in UniGene)	4.81	DU145, EB, OVCA-R
325169	H01560	Hs.163818	ESTs; Weakly similar to !!!! ALU SUBFAMI	4.8	NCI-H345, DU145, LnCap
312828	AI865455	Hs.211818	ESTs; Moderately similar to !!!! ALU SUB	4.78	DU145, DU145, DU145
321226	AA311443	Hs.251416	H sapiens mRNA; cDNA DKFZp586E2317 (from	4.75	DU145, OVCA-R, MB-MDA-453
327772			CH.05_hs gi|5867964	4.74	HT29, MB-MDA-231, NCI-H345
315642	AA742222	Hs.120634	ESTs	4.7	DU145, EB, MB-MDA-453
311905	AA555215	Hs.151913	ESTs	4.7	DU145, Caco2, PRSC_con
312754	R99834	Hs.250383	ESTs	4.59	OVCA-R, PC3, EB
336637			CH22_FGENES.13-7	4.58	NCI-H69, PRSC_log, NCI-H345
331644	T99544	Hs.173734	ESTs; Weakly similar to !!!! ALU CLASS B	4.55	OVCA-R, NCI-H345, Caco2
336984			CH22_FGENES.401-2	4.55	Caco2, Caco2, EB
316261	AW134485	Hs.144967	ESTs	4.53	NCI-H460, NCI-H345, Caco2
300417	AW139492	Hs.245887	ESTs	4.52	DU145, CALU6, EB
300610	N72596	Hs.99120	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	4.52	OVCA-R, PC3, EB
324718	AI557019	Hs.116467	ESTs	4.5	LnCap, PC3, PRSC_con
332170	F04112	Hs.177178	ESTs	4.47	Caco2, DU145, DU145
324042	AA377589		EST cluster (not in UniGene)	4.45	NCI-H345, PRSC_con, PRSC_log
331148	R73816	Hs.17385	ESTs	4.44	CALU6, OVCA-R, EB
328981			CH.09_hs gi|5868527	4.43	HT29, BT474, NCI-H69
321920	N63915		EST cluster (not in UniGene)	4.34	Caco2, A549, A549
320832	AA214584		EST cluster (not in UniGene)	4.34	NCI-H23, CALU6, OVCA-R
321971	AI680459	Hs.201441	ESTs	4.33	DU145, HT29, CALU6
308572	AI707882		EST singleton (not in UniGene) with exon	4.33	MCF7, NCI-H345, OVCA-R
302459	AF169255		EST cluster (not in UniGene) with exon h	4.28	MB-MDA-231, OVCA-R, LnCap
321847	T08401		EST cluster (not in UniGene)	4.25	MB-MDA-453, MB-MDA-435s, MB-MDA-231
337884			CH22_EM:AC005500.GENSCAN.54-2	4.23	HT29, NCI-H23, MB-MDA-435s
307494	AI269188	Hs.175656	EST	4.23	NCI-H23, NCI-H520, NCI-358
314915	AA573072	Hs.187748	ESTs; Weakly similar to !!!! ALU SUBFAMI	4.21	PC3, OVCA-R, Caco2
336638			CH22_FGENES.14-2	4.21	NCI-H69, NCI-H345, PRSC_log
319379	T91443	Hs.193963	ESTs	4.2	PC3, OVCA-R, LnCap
312332	R33041	Hs.106200	ESTs	4.19	NCI-H69, OVCA-R, NCI-H460
331445	H89093	Hs.41215	ESTs	4.19	EB, HT29, DU145
315841	AW136397	Hs.247572	ESTs	4.19	Caco2, MB-MDA-453, LnCap
315712	AI950133	Hs.120882	ESTs; Moderately similar to !!!! ALU SUB	4.18	LnCap, NCI-H345, OVCA-R
319559	AA773876	Hs.251597	ESTs	4.15	NCI-H345, Caco2, DU145
300791	AL138455	Hs.256135	ESTs; Moderately similar to !!!! ALU SUB	4.13	NCI-358, RPWE-2, NCI-H460

312129	AW300867		EST cluster (not in UniGene)	4.12	OVCA-R, MCF7, A549
321166	AA411263	Hs.128783	ESTs	4.11	OVCA-R, Caco2, PRSC_con
313220	AI971981	Hs.118241	ESTs	4.1	OVCA-R, DU145, Caco2
314022	AW452420	Hs.248678	ESTs	4.1	OVCA-R, EB, PC3
321359	AW474412		EST cluster (not in UniGene)	4.1	DU145, OVCA-R, PC3
328841			CH.07_hs gi|6381920	4.09	NCI-H69, PRSC_log, NCI-H345
337898			CH22_EM:AC005500.GENSCAN.56-5	4.09	NCI-H345, NCI-H69, OVCA-R
333245			CH22_FGENES.115_2	4.09	PRSC_log, PRSC_con, NCI-H345
311958	AI247472	Hs.132965	ESTs	4.06	EB, DU145, CALU6
314775	AI149880	Hs.188809	ESTs	4.06	OVCA-R, PC3, EB
317901	AW150944	Hs.250541	ESTs	4.06	BT474, MB-MDA-453, MB-MDA-435s
309985	AW452919		EST singleton (not in UniGene) with exon	4.05	MB-MDA-453, NCI-H23, NCI-H520
311004	AA632846		EST cluster (not in UniGene)	4.05	MB-MDA-453, OVCA-R, EB
323497	AI523613	Hs.221544	ESTs	4.04	LnCap, OVCA-R, EB
332347	W60326	Hs.221716	ESTs	4.04	EB, CALU6, PC3
331388	AA456852	Hs.43543	suppressor of white apricot homolog 2	4.01	A549, EB, Caco2
313197	AI738851	Hs.222487	ESTs	3.96	OVCA-R, EB, PC3
315710	AA931550	Hs.192785	ESTs	3.95	EB, MB-MDA-231, OVCA-R
316897	AA838114		EST cluster (not in UniGene)	3.94	OVCA-R, A549, MB-MDA-453
322564	W86440	Hs.118344	ESTs	3.94	NCI-H460, Caco2, EB
304605	AA513225		EST singleton (not in UniGene) with exon	3.9	NCI-H345, RPWE-2, BT474
325726			CH.14_hs gi|6552447	3.9	OVCA-R, LnCap, LnCap
320190	R32047	Hs.141012	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.89	DU145, NCI-H23, PRSC_log
331566	N63062	Hs.48703	EST	3.87	NCI-H23, NCI-H460, NCI-358
319403	T98413		EST cluster (not in UniGene)	3.86	NCI-H345, PRSC_log, LnCap
324643	AI436356	Hs.130729	ESTs	3.84	OVCA-R, DU145, NCI-H345
315298	AI969314	Hs.211377	ESTs	3.82	NCI-H345, PRSC_con, PRSC_log
321632	AA419617		EST cluster (not in UniGene)	3.81	EB, OVCA-R, A549
313219	N74924	Hs.182099	ESTs	3.8	EB, Caco2, OVCA-R
330833	AA046804		ESTs; Weakly similar to !!!! ALU SUBFAMI	3.8	LnCap, DU145, PC3
327289			CH.01_hs gi|5867481	3.79	EB, HT29, DU145
314429	AW300749		EST cluster (not in UniGene)	3.79	OVCA-R, PC3, PRSC_con
314475	AI911160	Hs.127505	ESTs	3.79	DU145, CALU6, NCI-H69
317130	AW293995	Hs.192277	ESTs	3.78	EB, PC3, Caco2
336635			CH22_FGENES.13-5	3.77	NCI-H69, NCI-H345, PRSC_log
333323			CH22_FGENES.138_16	3.76	NCI-H460, NCI-H23, PRSC_con
332135	AA620331	Hs.245351	EST	3.75	NCI-H345, A549, Caco2
316979	AA861087		EST cluster (not in UniGene)	3.75	NCI-H345, NCI-H69, RPWE-2
316435	AI671871	Hs.192618	ESTs; Weakly similar to !!!! ALU CLASS C	3.74	MB-MDA-435s, MCF7, MB-MDA-453
315422	AW135357	Hs.192374	ESTs	3.73	OVCA-R, A549, EB
336616			CH22_FGENES.613_5	3.72	NCI-H69, NCI-H345, RPWE-2
320258	W93241		EST cluster (not in UniGene)	3.71	MB-MDA-231, NCI-H69, EB
300463	N52510	Hs.186470	ESTs	3.69	OVCA-R, A549, DU145
306881	AI088695		EST singleton (not in UniGene) with exon	3.68	CALU6, HT29, EB
337304			CH22_FGENES.681-6	3.67	MCF7, MB-MDA-453, LnCap
323693	AW297758	Hs.249721	ESTs	3.67	OVCA-R, MB-MDA-453, DU145
331073	R07998	Hs.18628	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.67	RPWE-2, NCI-H345, OVCA-R
318162	AW296277	Hs.132171	ESTs	3.67	MB-MDA-231, DU145, CALU6
318042	AW294522	Hs.149991	ESTs	3.66	EB, HT29, CALU6
308069	AI470895		EST singleton (not in UniGene) with exon	3.64	Caco2, Caco2, NCI-H23
327614			CH.04_hs gi|6525283	3.62	NCI-H460, NCI-H345, NCI-H69
337514			CH22_FGENES.809-7	3.62	NCI-358, NCI-H23, NCI-H460
332093	AA608794	Hs.112592	ESTs	3.6	EB, OVCA-R, DU145
327793			CH.05_hs gi|5867979	3.59	LnCap, OVCA-R, EB
331053	N70242	Hs.183146	ESTs	3.59	OVCA-R, EB, Caco2
303769	AA134888	Hs.173415	ESTs	3.58	HT29, CALU6, CALU6
319872	R97130	Hs.189699	ESTs	3.58	PRSC_con, LnCap, RPWE-2
317902	AI828602	Hs.211265	ESTs	3.57	CALU6, NCI-H345, OVCA-R
324090	AI656531	Hs.116070	ESTs	3.57	PRSC_con, NCI-H345, PRSC_log
300120	AW204314	Hs.170784	ESTs	3.57	NCI-H69, NCI-H345, PRSC_con
307752	AI339447		EST singleton (not in UniGene) with exon	3.56	NCI-358, HT29, MB-MDA-231
322438	W44531	Hs.167851	ESTs	3.55	NCI-H345, NCI-H69, Caco2
311275	AI659166	Hs.207144	ESTs	3.55	MB-MDA-231, PRSC_con, LnCap
338830			CH22_DJ246D7.GENSCAN.6-7	3.54	LnCap, PC3, OVCA-R
315647	AA648983	Hs.212911	ESTs	3.53	OVCA-R, MB-MDA-453, CALU6
331469	N22273	Hs.39140	ESTs	3.52	EB, A549, CALU6
313445	AI123657	Hs.127264	ESTs	3.51	EB, OVCA-R, A549
330139			CH.21_p2 gi|4210430	3.5	EB, CALU6, DU145
304450	AA404521	Hs.10326	coatomer protein complex; subunit epsilo	3.49	NCI-H345, NCI-H69, NCI-H460
325763			CH.14_hs gi|6682475	3.49	PC3, BT474, OVCA-R
312803	AA677934	Hs.117864	ESTs	3.47	OVCA-R, Caco2, MB-MDA-453
303654	AA436942	Hs.168308	ESTs	3.46	DU145, NCI-H460, NCI-H69
317924	AI222324	Hs.166306	ESTs; Weakly similar to zinc finger prot	3.46	PRSC_con, PRSC_log, NCI-H69
312354	AA036955	Hs.167040	ESTs	3.44	Caco2, MB-MDA-435s, NCI-H460
337517			CH22_FGENES.814-6	3.43	NCI-H69, HT29, PC3
324865	AA702138	Hs.114103	ESTs	3.42	NCI-H23, NCI-H460, NCI-H520

323755	AW300094		EST cluster (not in UniGene)	3.42	PRSC_con, RPWE-2, NCI-H345
314452	AL042699	Hs.209222	ESTs	3.42	NCI-H345, PRSC_con, PRSC_log
337911			CH22_EM:AC005500.GENSCAN.59-6	3.42	OVCA-R, PC3, HT29
318086	AI025499	Hs.132238	ESTs	3.41	CALU6, LnCap, OVCA-R
311859	AA704705	Hs.181044	ESTs; Weakly similar to Chain A; Human O Complexed With L-Canaline [H.sapiens]	3.41	LnCap, MB-MDA-435s, A549
314409	H15560	Hs.131833	ESTs	3.41	NCI-H69, LnCap, LnCap
323333	AA228883		EST cluster (not in UniGene)	3.41	Caco2, OVCA-R, NCI-H69
325690			CH.14_hs gi|5867021	3.4	HT29, CALU6, DU145
314539	AA398216	Hs.190092	ESTs	3.4	MB-MDA-231, BT474, EB
310567	AI691065	Hs.155780	ESTs	3.4	PRSC_con, NCI-H345, NCI-H69
330527	S77356		transcript ch21=oligomycin sensitivity c 8 stomach cancer cell lines, mRNA, 262 n	3.39	NCI-H23, Caco2, A549
314660	AA436007	Hs.188780	ESTs	3.39	OVCA-R, BT474, Caco2
321321	AB033072		EST cluster (not in UniGene)	3.39	NCI-358, EB, Caco2
323356	AA234009	Hs.188715	ESTs	3.38	DU145, CALU6, CALU6
328592			CH.07_hs gi|5868227	3.38	MCF7, NCI-358, MB-MDA-231
311116	AI631195	Hs.232193	ESTs	3.36	NCI-H520, NCI-H23, PRSC_log
323853	AA393460		EST cluster (not in UniGene)	3.36	DU145, EB, Caco2
327740			CH.05_hs gi|5867943	3.35	EB, LnCap, OVCA-R
326857			CH.20_hs gi|6552460	3.33	NCI-H69, MCF7, NCI-H345
317787	AW339612	Hs.249364	ESTs	3.31	NCI-H345, PRSC_con, PRSC_log
325760			CH.14_hs gi|6552449	3.3	EB, CALU6, HT29
337513			CH22_FGENES.809-4	3.29	LnCap, NCI-H23, NCI-H460
336606			CH22_FGENES.429_3	3.29	NCI-H69, A549, NCI-H23
322895	AW470295	Hs.192152	ESTs	3.29	DU145, Caco2, EB
314312	AA814971	Hs.257634	ESTs	3.29	RPWE-2, NCI-H69, NCI-H345
328224			CH.06_hs gi|5868101	3.28	DU145, NCI-H345, LnCap
336128			CH22_FGENES.701_16	3.27	BT474, NCI-H520, MB-MDA-231
332442	AA281323	Hs.4947	ESTs	3.27	Caco2, PC3, NCI-H345
302514	M14269		EST cluster (not in UniGene) with exon h	3.27	DU145, CALU6, NCI-H520
313749	AW450376	Hs.130803	ESTs	3.26	OVCA-R, NCI-H69, DU145
302891	AI681578	Hs.114164	ESTs	3.26	LnCap, NCI-H345, PRSC_log
334690			CH22_FGENES.420_3	3.25	NCI-H69, RPWE-2, PRSC_con
308676	AI761036		EST singleton (not in UniGene) with exon	3.25	DU145, MB-MDA-231, HT29
304254	AA046273	Hs.111334	ferritin; light polypeptide	3.24	OVCA-R, DU145, A549
311994	AA648314	Hs.13849	ESTs	3.24	NCI-H460, NCI-H23, MB-MDA-453
321020	AB023170	Hs.227850	KIAA0953 protein	3.24	EB, MCF7, MB-MDA-435s
316724	AA810788	Hs.123337	ESTs	3.23	DU145, OVCA-R, BT474
326942			CH.21_hs gi|6004446	3.22	HT29, BT474, NCI-H23
324824	AI826999	Hs.224624	ESTs	3.21	OVCA-R, MB-MDA-453, EB
320789	R78712		EST cluster (not in UniGene)	3.21	DU145, LnCap, EB
315070	AW131368	Hs.186736	ESTs	3.21	Caco2, NCI-358, NCI-H460
303794	AW241987	Hs.197025	ESTs	3.19	OVCA-R, PC3, LnCap
310237	AI884313	Hs.158906	ESTs	3.19	NCI-358, NCI-H345, MCF7
313960	AA130859		EST cluster (not in UniGene)	3.18	MB-MDA-231, HT29, BT474
336634			CH22_FGENES.13-4	3.18	NCI-H69, NCI-H345, BT474
301085	AA779058	Hs.190428	ESTs; Weakly similar to NG26 [H.sapiens]	3.17	NCI-H345, NCI-H345, NCI-358
313774	AW136836	Hs.144583	ESTs	3.17	Caco2, EB, OVCA-R
307177	AI188864		EST singleton (not in UniGene) with exon	3.17	EB, CALU6, CALU6
324025	AI174861	Hs.190623	ESTs	3.17	OVCA-R, DU145, PC3
313099	AI307359	Hs.128064	ESTs	3.17	MB-MDA-231, BT474, EB
305536	AA770682		EST singleton (not in UniGene) with exon	3.17	NCI-358, Caco2, HT29
331916	AA446131	Hs.124918	ESTs	3.17	EB, OVCA-R, Caco2
314912	AI431345	Hs.161784	ESTs	3.17	EB, BT474, MCF7
303388	AL039604		EST cluster (not in UniGene) with exon h	3.17	HT29, NCI-358, Caco2
332273	R05818	Hs.173830	ESTs	3.16	MCF7, DU145, EB
314697	AW088739	Hs.243770	ESTs	3.16	MB-MDA-453, DU145, MCF7
335344			CH22_FGENES.536_3	3.15	PRSC_log, NCI-H345, PRSC_con
326162			CH.17_hs gi|5867168	3.15	BT474, HT29, HT29
304467	AA424703		EST singleton (not in UniGene) with exon	3.15	NCI-H23, RPWE-2, NCI-H460
339340			CH22_BA354I12.GENSCAN.27-8	3.15	LnCap, OVCA-R, MB-MDA-453
325393			CH.12_hs gi|5866921	3.13	Caco2, NCI-H23, NCI-358
315367	AA732484	Hs.169399	ESTs	3.13	OVCA-R, EB, MB-MDA-453
307085	AI160868		EST singleton (not in UniGene) with exon	3.12	RPWE-2, PRSC_con, PRSC_log
313001	N29264	Hs.249591	ESTs; Moderately similar to !!!! ALU SUB	3.12	NCI-H345, OVCA-R, Caco2
307606	AI290006		EST singleton (not in UniGene) with exon	3.12	MB-MDA-231, HT29, NCI-H23
325710			CH.14_hs gi|6682473	3.09	NCI-H69, MB-MDA-453, BT474
313810	AA400079	Hs.257854	ESTs	3.09	EB, DU145, CALU6
335482			CH22_FGENES.570_11	3.09	NCI-H460, NCI-358, NCI-H23
326310			CH.17_hs gi|5867277	3.08	MCF7, MB-MDA-453, PC3
325742			CH.14_hs gi|6552448	3.08	NCI-H23, NCI-H460, HT29
312467	AI241809	Hs.75458	ribosomal protein L18	3.08	NCI-358, NCI-H23, NCI-H460
327309			CH.01_hs gi|6456757	3.07	NCI-H69, MB-MDA-435s, MB-MDA-435s
310583	AW205632	Hs.211198	ESTs	3.07	OVCA-R, A549, Caco2
322373	W25673	Hs.130829	ESTs	3.07	NCI-H69, PRSC_con, NCI-H345

	324497	AW152624	Hs.136340	ESTs	3.06	NCI-H345, RPWE-2, PRSC_con
	315095	AA831815	Hs.243788	ESTs	3.06	Caco2, DU145, EB
	302445	N79647		EST cluster (not in UniGene) with exon h	3.05	OVCA-R, A549, NCI-H460
	302842	AW383226	Hs.163834	ESTs; Highly similar to Chp [R.norvegicu	3.05	A549, DU145, NCI-H23
5	317346	AA952875	Hs.221274	ESTs	3.04	BT474, HT29, HT29
	334650			CH22_FGENES.417_17	3.04	MCF7, BT474, OVCA-R
	306644	AI002913		EST singleton (not in UniGene) with exon	3.04	CALU6, MCF7, BT474
	322682	AI110679		EST cluster (not in UniGene)	3.03	NCI-H345, RPWE-2, OVCA-R
	311065	AW204582	Hs.224906	ESTs	3.03	PRSC_log, PRSC_con, NCI-H460
10	318623	AA355439	Hs.151547	ESTs	3.03	DU145, MB-MDA-435s, HT29
	304978	AA617735		EST singleton (not in UniGene) with exon	3.03	CALU6, BT474, MB-MDA-435s
	305554	AA774567	Hs.121774	EST	3.03	EB, NCI-H460, Caco2
	302574	U66199	Hs.249165	fibroblast growth factor 11	3.03	HT29, DU145, PC3
	336202			CH22_FGENES.719_6	3.02	NCI-H69, NCI-H23, NCI-H23
15	302893	AL117539	Hs.173515	H sapiens mRNA; cDNA DKFZp586H021 (from	3.02	EB, DU145, CALU6
	315166	AI343966	Hs.158528	ESTs	3.01	Caco2, EB, NCI-H69
	335606			CH22_FGENES.582_3	3.01	NCI-H23, NCI-H520, NCI-H345
	330058			CH.17_p2 gi|6634847	3.01	OVCA-R, HT29, LnCap
	303179	AA071215		EST cluster (not in UniGene) with exon h	3.01	MCF7, RPWE-2, MB-MDA-453
20	307625	AI299617		EST singleton (not in UniGene) with exon	3	MB-MDA-231, LnCap, BT474
	323074	AL119445	Hs.203213	ESTs	3	NCI-H23, NCI-H520, NCI-H460
	336232			CH22_FGENES.736_7	3	HT29, BT474, MB-MDA-231
	334915			CH22_FGENES.457_4	3	NCI-H345, PRSC_con, NCI-H69
	329116			CH.X_hs gi|5868650	3	NCI-H69, PRSC_con, RPWE-2
25	333495			CH22_FGENES.168_5	3	OVCA-R, NCI-H69, NCI-H345
	303756	AI738488	Hs.115838	ESTs	2.99	HT29, PRSC_con, DU145
	332134	AA610123	Hs.139240	DKFZP564F1422 protein	2.99	EB, A549, MCF7
	322916	AW367294	Hs.154091	ESTs	2.99	DU145, DU145, OVCA-R
	318050	AI052093	Hs.133132	ESTs	2.99	NCI-H345, DU145, NCI-H520
30	301019	AI147356	Hs.98722	ESTs	2.99	NCI-358, NCI-H69, MB-MDA-435s
	315213	AA587773	Hs.136494	ESTs	2.98	MB-MDA-231, BT474, LnCap
	339251			CH22_BA354I12.GENSCAN.7-5	2.98	NCI-H69, PRSC_log, HT29
	303835	T05645		EST cluster (not in UniGene) with exon h	2.97	BT474, NCI-H345, LnCap
	300070	AI174603	Hs.256832	ESTs	2.97	DU145, A549, OVCA-R
35	320954	AB028953	Hs.204121	KIAA1030 protein	2.97	LnCap, DU145, PC3
	327624			CH.04_hs gi|5867871	2.97	EB, DU145, LnCap
	329029			CH.X_hs gi|6525302	2.96	NCI-H69, PRSC_log, LnCap
	317040	AA868584	Hs.126154	ESTs	2.96	DU145, EB, LnCap
	328016			CH.06_hs gi|5902482	2.96	NCI-H345, PRSC_con, DU145
40	312674	AI762475	Hs.151327	ESTs; Moderately similar to !!!! ALU SUB	2.96	OVCA-R, NCI-H69, NCI-H69
	332301	R70253	Hs.127826	ESTs	2.96	OVCA-R, DU145, MB-MDA-231
	300951	AI732374	Hs.105834	ESTs; Weakly similar to 25 kDa trypsin i	2.95	NCI-358, NCI-H460, Caco2
	318226	AI078446	Hs.134125	ESTs	2.95	NCI-H460, NCI-H23, NCI-358
	311349	AW292933	Hs.254110	ESTs	2.94	EB, DU145, OVCA-R
45	312757	AI285970	Hs.183817	ESTs	2.94	DU145, LnCap, LnCap
	316507	AI381515	Hs.158381	ESTs	2.94	PRSC_con, PRSC_log, RPWE-2
	302278	AF018080	Hs.173730	Mediterranean fever	2.93	EB, NCI-H69, DU145
	311016	AW173166	Hs.243468	ESTs	2.93	NCI-H345, LnCap, LnCap
	323864	AA340724	Hs.214028	ESTs	2.92	EB, Caco2, HT29
50	336632			CH22_FGENES.13-2	2.92	NCI-H69, NCI-H345, MB-MDA-231
	328886			CH.07_hs gi|6588003	2.92	HT29, PC3, LnCap
	301859	T61587		EST cluster (not in UniGene) with exon h	2.92	LnCap, EB, EB
	323775	AA329856	Hs.143022	ESTs	2.92	PRSC_con, PRSC_log, RPWE-2
	315426	AI391486	Hs.128171	ESTs	2.92	CALU6, EB, A549
55	322264	AF086242		EST cluster (not in UniGene)	2.92	Caco2, OVCA-R, DU145
	315135	AA627561	Hs.192446	ESTs	2.91	EB, HT29, DU145
	327982			CH.06_hs gi|5868216	2.91	LnCap, MB-MDA-453, NCI-H69
	314530	AI052358	Hs.131741	ESTs	2.91	NCI-H460, NCI-H520, RPWE-2
	315003	AA527650	Hs.156037	ESTs	2.9	PRSC_con, RPWE-2, MB-MDA-231
60	339032			CH22_DA59H18.GENSCAN.25-1	2.9	NCI-H69, PRSC_con, RPWE-2
	308379	AI623950	Hs.2186	eukaryotic translation elongation factor	2.89	BT474, MB-MDA-231, HT29
	312133	T87714	Hs.221665	ESTs	2.88	Caco2, MB-MDA-453, MCF7
	307992	AI434166		EST singleton (not in UniGene) with exon	2.88	NCI-H520, MCF7, NCI-H23
	308010	AI439190	Hs.181165	eukaryotic translation elongation factor	2.88	Caco2, NCI-H69, NCI-H345
65	320154	AA336019	Hs.119559	ESTs	2.88	MB-MDA-453, DU145, EB
	331496	N34929	Hs.171984	ESTs	2.86	MB-MDA-453, PC3, MCF7
	320016	H57622	Hs.194574	ESTs	2.86	PRSC_con, RPWE-2, PRSC_log
	317923	AW450544	Hs.220751	ESTs	2.86	NCI-H345, PRSC_con, PRSC_log
	301822	X17033	Hs.1142	integrin; alpha 2 (CD49B; alpha 2 subuni	2.86	PC3, BT474, CALU6
70	311759	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	2.85	DU145, HT29, MB-MDA-231
	315083	AI221325	Hs.210655	ESTs	2.84	PRSC_con, RPWE-2, NCI-H345
	317759	AI908455	Hs.202460	ESTs; Weakly similar to hypothetical L1	2.83	HT29, MB-MDA-231, BT474
	313980	AI633205	Hs.159914	ESTs	2.83	Caco2, MB-MDA-453, A549
	310941	AI453402	Hs.173705	ESTs; Weakly similar to !!!! ALU CLASS C	2.83	NCI-H345, MCF7, Caco2
75	313593	AI911488	Hs.213724	ESTs	2.83	LnCap, Caco2, NCI-H460
	314973	AW273128	Hs.254669	EST	2.82	BT474, LnCap, RPWE-2

310950	AI582758	Hs.170561	ESTs	2.82	EB, MB-MDA-453, LnCap
323626	AL039822	Hs.207604	ESTs	2.82	PC3, HT29, CALU6
325410			CH.12_hs gi|5866921	2.81	MB-MDA-453, PRSC_con, NCI-358
313911	AI565458	Hs.116385	ESTs	2.81	PRSC_con, EB, RPWE-2
334244			CH22_FGENES.365_5	2.81	OVCA-R, PC3, MB-MDA-453
309333	AW025709		EST singleton (not in UniGene) with exon	2.81	NCI-H460, NCI-H23, NCI-358
328467			CH.07_hs gi|5868434	2.81	EB, OVCA-R, HT29
318563	AW250501		EST cluster (not in UniGene)	2.81	BT474, NCI-H23, MB-MDA-231
326412			CH.19_hs gi|5867362	2.81	BT474, PRSC_log, RPWE-2
303407	AA309616		EST cluster (not in UniGene) with exon h	2.8	CALU6, NCI-H345, DU145
328462			CH.07_hs gi|5868433	2.8	BT474, CALU6, MCF7
335157			CH22_FGENES.501_7	2.8	NCI-H69, NCI-H345, PRSC_log
313458	AA007259	Hs.255853	ESTs	2.79	OVCA-R, DU145, LnCap
310416	AI695047	Hs.202395	ESTs	2.79	DU145, MB-MDA-435s, PC3
317709	AI435973	Hs.128056	ESTs	2.79	NCI-H460, NCI-358, DU145
321415	AI377596	Hs.3337	transmembrane 4 superfamily member 1	2.79	A549, PC3, OVCA-R
313693	AW469180	Hs.170651	ESTs	2.79	OVCA-R, MCF7, EB
309438	AW102802	Hs.225787	ESTs; Moderately similar to hypothetical	2.79	PC3, OVCA-R, DU145
308961	AI870248		EST singleton (not in UniGene) with exon	2.78	BT474, MB-MDA-231, EB
329107			CH.X_hs gi|5868626	2.78	DU145, MCF7, MB-MDA-435s
313975	AW025024	Hs.65114	keratin 18	2.78	Caco2, EB, DU145
330901	AA157818	Hs.238380	Human endogenous retroviral protease mRN	2.78	PC3, NCI-H520, BT474
311749	R06249	Hs.13911	ESTs	2.78	OVCA-R, MB-MDA-453, MCF7
329853			CH.14_p2 gi|6682295	2.78	BT474, BT474, HT29
322340	AF088076		EST cluster (not in UniGene)	2.77	NCI-H345, Caco2, LnCap
326806			CH.20_hs gi|6469835	2.77	NCI-H69, NCI-H345, MB-MDA-231
314661	AA436432		EST cluster (not in UniGene)	2.77	NCI-H460, MB-MDA-435s, CALU6
322135	AF075082		EST cluster (not in UniGene)	2.77	NCI-358, NCI-H460, Caco2
331849	AA417078	Hs.193767	ESTs	2.77	DU145, EB, CALU6
301056	AI797955	Hs.208076	ESTs; Weakly similar to D(4) DOPAMINE RE	2.76	NCI-H69, RPWE-2, PRSC_con
327739			CH.05_hs gi|5867942	2.76	EB, PC3, LnCap
308016	AI445116		EST singleton (not in UniGene) with exon	2.76	LnCap, HT29, MB-MDA-231
331549	N56866	Hs.237507	EST	2.76	MB-MDA-453, MCF7, OVCA-R
331851	AA418599	Hs.98303	caveolin 3	2.75	MB-MDA-231, NCI-H345, BT474
315023	AA533505	Hs.185844	ESTs	2.75	PRSC_con, OVCA-R, EB
335565			CH22_FGENES.579_1	2.75	OVCA-R, EB, A549
306137	AA916176		EST singleton (not in UniGene) with exon	2.74	EB, LnCap, DU145
332240	N54803		yv31d2.s1 Soares fetal liver spleen 1NFL 3' similar to contains L1.t3 L1 repetit	2.74	DU145, EB, CALU6
313246	N90762	Hs.159454	ESTs	2.74	NCI-H69, NCI-H345, PRSC_log
303642	AW299459		EST cluster (not in UniGene) with exon h	2.74	EB, A549, Caco2
325513			CH.12_hs gi|6017035	2.74	MB-MDA-231, NCI-H345, BT474
337236			CH22_FGENES.639-2	2.74	MCF7, MB-MDA-453, NCI-H69
311555	AW407892	Hs.244807	ESTs	2.74	BT474, NCI-H345, NCI-H69
339266			CH22_BA354I12.GENSCAN.10-4	2.73	CALU6, DU145, OVCA-R
300127	AW028615	Hs.235224	ESTs; Weakly similar to KIAA0422 [H.sapi	2.73	NCI-H345, RPWE-2, PRSC_log
311741	R00099	Hs.193642	ESTs	2.72	LnCap, PC3, OVCA-R
310915	AW449673	Hs.201893	ESTs	2.72	DU145, EB, MB-MDA-435s
324982	T31689	Hs.98518	ESTs	2.71	PRSC_con, PRSC_log, RPWE-2
305030	AA629988		EST singleton (not in UniGene) with exon	2.71	DU145, DU145, NCI-358
315396	AW296107	Hs.152686	ESTs	2.69	OVCA-R, Caco2, EB
319098	AI908374		EST cluster (not in UniGene)	2.69	RPWE-2, LnCap, PC3
309119	AI927384	Hs.228499	EST; Moderately similar to PK-120 precur	2.69	LnCap, NCI-H23, NCI-358
312095	AW444937	Hs.233482	ESTs	2.68	Caco2, OVCA-R, HT29
324316	AI291330		EST cluster (not in UniGene)	2.68	NCI-H460, Caco2, PRSC_log
331367	AA425688	Hs.41641	ESTs; Weakly similar to CAGH4 [H.sapiens	2.68	MB-MDA-435s, NCI-H520, NCI-H460
339116			CH22_DA59H18.GENSCAN.49-4	2.68	DU145, EB, CALU6
324297	AI565566	Hs.168587	ESTs	2.68	PRSC_con, OVCA-R, PRSC_log
318728	Z30201		EST cluster (not in UniGene)	2.68	LnCap, Caco2, PC3
304813	AA584540		EST singleton (not in UniGene) with exon	2.68	BT474, OVCA-R, RPWE-2
312393	N34376	Hs.191659	ESTs; Weakly similar to !!!! ALU CLASS E	2.68	NCI-H345, PRSC_con, EB
330671	AB002302	Hs.92236	KIAA0304 gene product	2.67	NCI-358, OVCA-R, Caco2
305406	AA723860		EST singleton (not in UniGene) with exon	2.66	OVCA-R, EB, MCF7
330957	H08778	Hs.133521	ESTs	2.66	EB, PC3, OVCA-R
300350	AI871129	Hs.172597	ESTs; Weakly similar to zinc finger prot	2.66	NCI-H23, NCI-H520, NCI-H460
322302	W76021		EST cluster (not in UniGene)	2.66	DU145, OVCA-R, PC3
321891	AW157424	Hs.165954	ESTs	2.66	EB, OVCA-R, Caco2
300124	AI217394	Hs.242447	ESTs	2.65	PRSC_con, A549, HT29
302747	AF062275		EST cluster (not in UniGene) with exon h	2.65	NCI-H23, BT474, MCF7
308741	AI802780	Hs.209002	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.65	PC3, EB, OVCA-R
310802	AI631546	Hs.159732	ESTs	2.65	PRSC_con, PRSC_log, NCI-H69
300694	AA063406		EST cluster (not in UniGene) with exon h	2.65	BT474, EB, MCF7
311395	R23313		EST cluster (not in UniGene)	2.64	EB, OVCA-R, DU145
336538			CH22_FGENES.840_2	2.64	DU145, NCI-H460, NCI-358
316473	AA829961		EST cluster (not in UniGene)	2.64	LnCap, OVCA-R, EB
328134			CH.06_hs gi|5868039	2.64	LnCap, EB, CALU6

329330			CH.X_hs gi|5868806	2.64	EB, CALU6, DU145
316664	AI042101		EST cluster (not in UniGene)	2.64	NCI-H345, MB-MDA-231, PRSC_log
328015			CH.06_hs gi|5902482	2.63	BT474, HT29, MB-MDA-231
308991	AI879831		EST singleton (not in UniGene) with exon	2.63	BT474, EB, NCI-H23
323899	AL042966		EST cluster (not in UniGene)	2.62	DU145, A549, CALU6
321708	AA476817		EST cluster (not in UniGene)	2.62	EB, A549, CALU6
301752	T75247		EST cluster (not in UniGene) with exon h	2.62	HT29, BT474, NCI-H345
309351	AW057547		EST singleton (not in UniGene) with exon	2.62	NCI-H23, PRSC_con, LnCap
314412	AI864270	Hs.155654	ESTs	2.62	CALU6, MB-MDA-231, BT474
309441	AW103055	Hs.244230	EST	2.62	BT474, MB-MDA-231, MB-MDA-453
335993			CH22_FGENES.656_6	2.61	NCI-H460, NCI-358, NCI-H520
318196	AI056776	Hs.133397	ESTs	2.6	EB, CALU6, HT29
322880	AA310521	Hs.50848	ESTs; Weakly similar to KIAA0862 protein	2.6	DU145, A549, PC3
300558	AI540051	Hs.122638	ESTs	2.6	OVCA-R, NCI-H69, MCF7
318594	AA918320	Hs.224581	ESTs	2.6	PC3, MB-MDA-453, DU145
308554	AI698132	Hs.201923	EST	2.6	LnCap, EB, NCI-H345
335108			CH22_FGENES.494_14	2.6	NCI-H69, NCI-H345, MB-MDA-231
312483	AI417526	Hs.184636	ESTs	2.59	PC3, DU145, OVCA-R
311981	AW452773	Hs.257612	EST	2.59	NCI-H460, MB-MDA-453, NCI-H23
319359	F13458		EST cluster (not in UniGene)	2.59	LnCap, NCI-H460, MB-MDA-231
300230	AI377746	Hs.158846	ESTs	2.59	HT29, NCI-358, NCI-H345
316504	AW135854	Hs.132458	ESTs	2.59	DU145, EB, CALU6
322337	AA249804		EST cluster (not in UniGene)	2.59	NCI-H69, NCI-H345, NCI-H345
301775	AW247670		EST cluster (not in UniGene) with exon h	2.59	NCI-H345, RPWE-2, PRSC_log
301089	AA666396	Hs.220727	ESTs	2.58	PRSC_log, PRSC_con, RPWE-2
331213	T88698	Hs.163862	ESTs	2.58	DU145, EB, OVCA-R
321121	W23285		EST cluster (not in UniGene)	2.58	NCI-H69, MB-MDA-435s, PC3
316634	AW241910	Hs.122254	ESTs	2.58	MCF7, HT29, BT474
322141	AF075092		EST cluster (not in UniGene)	2.58	PC3, OVCA-R, HT29
312108	T82331	Hs.127453	ESTs	2.58	A549, CALU6, Caco2
339071			CH22_DA59H18.GENSCAN.34-1	2.58	CALU6, DU145, EB
311666	AW389509	Hs.223747	ESTs	2.57	OVCA-R, MB-MDA-231, BT474
318662	AI285898	Hs.115367	ESTs	2.57	OVCA-R, DU145, EB
317010	AA863395		EST cluster (not in UniGene)	2.57	NCI-H520, PRSC_con, NCI-358
324710	AI742028	Hs.120884	ESTs; Weakly similar to RAS-RELATED PROT	2.57	LnCap, DU145, MB-MDA-453
327888			CH.06_hs gi|5868149	2.56	NCI-H345, MB-MDA-435s, RPWE-2
336149			CH22_FGENES.706_5	2.56	NCI-H69, PC3, A549
312816	H74319	Hs.188620	ESTs	2.56	EB, Caco2, NCI-H460
327999			CH.06_hs gi|5867994	2.56	NCI-358, NCI-H520, NCI-H23
316761	AI911173	Hs.213722	ESTs	2.55	NCI-H345, NCI-H460, MB-MDA-231
336958			CH22_FGENES.367-1	2.55	HT29, CALU6, CALU6
325043	W27919	Hs.32944	inositol polyphosphate-4-phosphatase; ty	2.55	NCI-H460, NCI-H23, HT29
315417	AW452360	Hs.186770	ESTs	2.55	NCI-H345, NCI-H69, PRSC_con
331603	N78656	Hs.161535	EST	2.55	NCI-H345, PRSC_con, PRSC_log
309403	AW082954		EST singleton (not in UniGene) with exon	2.55	BT474, MB-MDA-231, MCF7
337289			CH22_FGENES.672-8	2.54	BT474, HT29, MB-MDA-231
314242	AI570943	Hs.246280	ESTs	2.54	Caco2, MB-MDA-435s, MB-MDA-453
328053			CH.06_hs gi|5902482	2.54	MB-MDA-231, DU145, MB-MDA-453
307215	AI193189		EST singleton (not in UniGene) with exon	2.53	HT29, CALU6, MB-MDA-231
327566			CH.03_hs gi|5867811	2.53	NCI-H69, NCI-H520, NCI-H345
326338			CH.17_hs gi|6056311	2.53	PC3, A549, DU145
318115	AI384027	Hs.159130	ESTs; Moderately similar to !!!! ALU SUB	2.53	DU145, EB, PC3
307437	AI245683		EST singleton (not in UniGene) with exon	2.52	NCI-H23, NCI-H520, NCI-358
322059	AA412371	Hs.121344	ESTs	2.52	EB, DU145, OVCA-R
322505	AF147315		EST cluster (not in UniGene)	2.52	PRSC_con, RPWE-2, NCI-H69
314032	AW081897	Hs.193211	ESTs	2.52	NCI-H345, LnCap, DU145
336125			CH22_FGENES.701_12	2.51	NCI-H69, LnCap, DU145
312765	AI692908	Hs.181873	ESTs	2.51	NCI-H23, NCI-358, NCI-H520
335523			CH22_FGENES.572_3	2.51	HT29, BT474, OVCA-R
327585			CH.03_hs gi|5867825	2.51	HT29, NCI-H460, MB-MDA-453
323183	AW393850		EST cluster (not in UniGene)	2.51	MB-MDA-231, LnCap, RPWE-2
314418	AI478722	Hs.232275	ESTs; Moderately similar to !!!! ALU SUB	2.51	EB, DU145, DU145
313361	AI359782	Hs.137312	ESTs	2.5	CALU6, HT29, DU145
305632	AA805276		EST singleton (not in UniGene) with exon	2.5	MB-MDA-453, NCI-H460, NCI-H23
331689	W90131	Hs.184675	ESTs	2.5	NCI-H69, EB, A549
323438	AI540243	Hs.113817	ESTs	2.5	NCI-H345, PRSC_con, MB-MDA-231
315742	AI821724	Hs.143198	H sapiens PAC clone DJ0872F07 from 7q31	2.5	MCF7, MB-MDA-453, MB-MDA-435s
305971	AA886874		EST singleton (not in UniGene) with exon	2.5	NCI-358, NCI-H23, NCI-H520
336633			CH22_FGENES.13-3	2.5	NCI-H69, NCI-H345, PRSC_log
304746	AA577793		EST singleton (not in UniGene) with exon	2.49	NCI-H69, BT474, MB-MDA-231
327925			CH.06_hs gi|5868172	2.49	NCI-358, NCI-358, NCI-H460
336055			CH22_FGENES.683_4	2.49	EB, HT29, MB-MDA-231
328888			CH.07_hs gi|6588003	2.48	MB-MDA-435s, MB-MDA-453, PRSC_log
311244	AW016694	Hs.197689	ESTs	2.48	NCI-H345, MCF7, PC3
327155			CH.01_hs gi|5867549	2.48	NCI-H69, MB-MDA-231, NCI-H345
334907			CH22_FGENES.453_2	2.48	DU145, NCI-H345, MB-MDA-231

	314887	AA910236	Hs.139469	ESTs	2.48	DU145, A549, A549
	339435			CH22_DJ579N16.GENSCAN.18-10	2.48	NCI-H69, MCF7, BT474
	334172			CH22_FGENES.349_5	2.48	NCI-H69, NCI-H345, PRSC_log
	320767	AA299525		EST cluster (not in UniGene)	2.48	NCI-358, NCI-H23, NCI-H460
5	336772			CH22_FGENES.156-1	2.47	NCI-358, NCI-358, NCI-H23
	326957			CH.21_hs gi|6469836	2.47	BT474, RPWE-2, PRSC_con
	308505	AI686615	Hs.200778	EST; Weakly similar to SALIVARY PROLINE-	2.47	MCF7, MB-MDA-453, MB-MDA-435s
	321325	AB033100		EST cluster (not in UniGene)	2.47	EB, CALU6, A549
	313149	AW291092	Hs.201058	ESTs	2.47	NCI-H345, PRSC_con, RPWE-2
10	338325			CH22_EM:AC005500.GENSCAN.307-7	2.46	BT474, LnCap, EB
	307877	AI368880		EST singleton (not in UniGene) with exon	2.46	NCI-H23, PRSC_log, NCI-H520
	311525	AI799444	Hs.247095	ESTs; Moderately similar to !!!! ALU SUB	2.46	PRSC_con, PRSC_log, NCI-H345
	337023			CH22_FGENES.433-12	2.46	OVCA-R, CALU6, PRSC_con
	300916	AI361798	Hs.164675	ESTs	2.45	LnCap, DU145, CALU6
15	302919	AL137382		EST cluster (not in UniGene) with exon h	2.45	LnCap, MB-MDA-231, CALU6
	320303	AL079289	Hs.137154	H sapiens mRNA full length insert cDNA c	2.45	BT474, MB-MDA-231, MB-MDA-453
	318359	AI097439	Hs.135548	ESTs	2.45	NCI-H460, MB-MDA-453, NCI-H345
	314384	AA535840	Hs.162203	ESTs; Weakly similar to alternatively sp	2.45	OVCA-R, PC3, EB
	326763			CH.20_hs gi|6598307	2.45	NCI-H69, NCI-H345, RPWE-2
20	319900	AW408392		EST cluster (not in UniGene)	2.45	Caco2, NCI-H460, NCI-H23
	314451	AA586368	Hs.190232	ESTs	2.45	PRSC_con, NCI-H345, MB-MDA-231
	300641	AW237699	Hs.118346	ESTs	2.44	NCI-H345, PRSC_log, PRSC_con
	324368	AW299374		EST cluster (not in UniGene)	2.44	PC3, DU145, OVCA-R
	336510			CH22_FGENES.834_5	2.44	NCI-H69, RPWE-2, PRSC_con
25	326876			CH.20_hs gi|6682507	2.44	NCI-H23, NCI-H460, NCI-H520
	307753	AI340509	Hs.182426	ribosomal protein S2	2.44	NCI-H23, NCI-H460, Caco2
	317071	M78728	Hs.132694	ESTs	2.44	NCI-H345, NCI-H69, RPWE-2
	313877	AA767869	Hs.250113	ESTs; Moderately similar to thyroid horm component TRAP150 [H.sapiens]	2.44	DU145, LnCap, CALU6
30	315974	AW029203	Hs.191952	ESTs	2.43	EB, DU145, OVCA-R
	322970	AI885052	Hs.142287	ESTs; Weakly similar to !!!! ALU CLASS F	2.43	NCI-H345, RPWE-2, EB
	317733	AI028257	Hs.132317	ESTs	2.43	CALU6, RPWE-2, OVCA-R
	313599	AA748749	Hs.136742	ESTs	2.42	NCI-H460, NCI-358, NCI-H520
	323014	AA305198		EST cluster (not in UniGene)	2.42	PRSC_con, NCI-H460, RPWE-2
35	324980	AA969121	Hs.254296	ESTs	2.41	MCF7, OVCA-R, PC3
	301326	AA883831	Hs.252924	ESTs	2.41	PRSC_con, PRSC_log, RPWE-2
	308695	AI763350		EST singleton (not in UniGene) with exon	2.41	RPWE-2, NCI-H69, NCI-H345
	330166			CH.02_p2 gi|6648220	2.41	CALU6, DU145, A549
	317552	AW451400	Hs.127019	ESTs	2.41	NCI-358, NCI-358, NCI-H23
40	320572	AI929508	Hs.159590	lymphocyte antigen 6 complex; locus H	2.41	CALU6, HT29, A549
	315618	AI287341	Hs.154029	ESTs; Weakly similar to TRANSCRIPTION FA	2.41	OVCA-R, Caco2, MB-MDA-231
	331610	N91109	Hs.54681	ESTs	2.41	NCI-H23, NCI-H520, NCI-358
	311731	AW393528	Hs.246875	ESTs	2.41	NCI-H69, NCI-H345, PRSC_con
	318571	Z43383	Hs.8053	ESTs	2.4	NCI-358, NCI-H23, NCI-H520
45	334958			CH22_FGENES.465_27	2.4	DU145, PRSC_con, RPWE-2
	323570	AL038623	Hs.208752	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.4	OVCA-R, EB, BT474
	301685	W67730		EST cluster (not in UniGene) with exon h	2.4	MB-MDA-231, NCI-H345, EB
	303849	AW163324		EST cluster (not in UniGene) with exon h	2.4	RPWE-2, PRSC_log, NCI-H345
	325702			CH.14_hs gi|5867028	2.4	NCI-H23, NCI-H460, NCI-H520
50	313074	N48261	Hs.127171	ESTs	2.4	MB-MDA-231, RPWE-2, PRSC_log
	308994	AI880051		EST singleton (not in UniGene) with exon	2.4	RPWE-2, EB, PRSC_con
	330338			CH.08_p2 gi|5457162	2.4	DU145, EB, LnCap
	327274			CH.01_hs gi|5867470	2.4	OVCA-R, DU145, MB-MDA-231
	325953			CH.16_hs gi|5867140	2.4	MB-MDA-453, MB-MDA-435s, MCF7
55	333281			CH22_FGENES.128_7	2.4	NCI-H23, HT29, DU145
	314778	AW079559	Hs.152258	ESTs	2.39	EB, CALU6, Caco2
	317005	AI800251	Hs.197773	ESTs	2.38	MB-MDA-231, BT474, HT29
	334257			CH22_FGENES.367_5	2.38	HT29, NCI-358, MB-MDA-231
	324783	AA640770		EST cluster (not in UniGene)	2.38	EB, OVCA-R, MB-MDA-453
60	300949	AA534325	Hs.162183	ESTs	2.38	NCI-H69, NCI-H345, PRSC_log
	314957	AW029274	Hs.208368	ESTs; Moderately similar to !!!! ALU SUB	2.38	LnCap, DU145, DU145
	324350	AW292501	Hs.157174	ESTs; Weakly similar to similar to SH3-b	2.38	HT29, NCI-H23, NCI-H23
	338235			CH22_EM:AC005500.GENSCAN.260-16	2.38	NCI-H69, NCI-H460, NCI-H23
	300937	AW297302	Hs.255631	ESTs	2.38	PRSC_log, PRSC_con, PRSC_con
65	317439	AW451327	Hs.170623	ESTs	2.38	A549, DU145, EB
	324745	AI742120	Hs.116506	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.38	NCI-358, NCI-H460, BT474
	338306			CH22_EM:AC005500.GENSCAN.302-2	2.38	NCI-H69, PRSC_con, PRSC_log
	318765	Z42071	Hs.23961	ESTs	2.38	LnCap, NCI-H23, NCI-H520
	310254	AI239811	Hs.157491	ESTs	2.37	OVCA-R, DU145, EB
70	305116	AA649244		EST singleton (not in UniGene) with exon	2.37	CALU6, MB-MDA-435s, MB-MDA-453
	324016	AL045285	Hs.246849	ESTs; Moderately similar to !!!! ALU SUB	2.37	EB, DU145, OVCA-R
	322774	AA131111		EST cluster (not in UniGene)	2.37	OVCA-R, EB, A549
	335745			CH22_FGENES.601_16	2.37	PRSC_log, PRSC_con, NCI-H69
	300972	AI979100	Hs.211518	ESTs	2.37	NCI-H69, NCI-H345, PRSC_log
75	338809			CH22_EM:AC005500.GENSCAN.531-10	2.37	NCI-H23, NCI-H69, NCI-H520
	316983	AI480204	Hs.177131	ESTs	2.37	NCI-H345, PRSC_con, PRSC_log

321308	AI247480	Hs.117029	ESTs	2.37	BT474, NCI-H69, HT29
323578	AA299492	Hs.168166	ESTs	2.37	LnCap, EB, MB-MDA-453
335747			CH22_FGENES.601_20	2.36	NCI-H69, LnCap, PRSC_con
322362	AF039697		EST cluster (not in UniGene)	2.36	DU145, PRSC_con, NCI-H345
314430	N76302	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elega	2.36	DU145, MB-MDA-453, CALU6
304831	AA586422		EST singleton (not in UniGene) with exon	2.36	NCI-H23, NCI-H460, CALU6
337432			CH22_FGENES.765-1	2.36	MB-MDA-231, BT474, HT29
305984	AA887654		EST singleton (not in UniGene) with exon	2.36	DU145, HT29, CALU6
313486	AW134523	Hs.247186	ESTs	2.36	DU145, A549, CALU6
309028	AI889109	Hs.212032	EST	2.36	NCI-358, NCI-H520, NCI-H23
318292	AI679966	Hs.150603	ESTs	2.35	NCI-H460, Caco2, NCI-H23
334198			CH22_FGENES.354_4	2.35	NCI-H69, PRSC_log, PRSC_con
314458	AI217440	Hs.143873	ESTs	2.35	Caco2, A549, PC3
333346			CH22_FGENES.139_15	2.35	CALU6, DU145, LnCap
325408			CH.12_hs gi|5866921	2.35	NCI-H460, NCI-H520, NCI-H23
313758	AA076743	Hs.129770	ESTs	2.35	NCI-H23, MB-MDA-435s, NCI-H345
309825	AW293701		EST singleton (not in UniGene) with exon	2.35	NCI-H460, NCI-H23, NCI-H520
303536	R55497	Hs.183941	ESTs; Moderately similar to H beta 58 ho	2.35	DU145, CALU6, NCI-H520
331534	N51583	Hs.133756	EST	2.35	NCI-H23, NCI-H520, NCI-358
325164	T16981	Hs.21963	ESTs	2.34	NCI-H345, PRSC_log, NCI-H460
327710			CH.04_hs gi|5867860	2.34	BT474, MB-MDA-231, NCI-H345
306351	AA961356		EST singleton (not in UniGene) with exon	2.34	BT474, MB-MDA-231, MB-MDA-435s
304968	AA614308		EST singleton (not in UniGene) with exon	2.34	CALU6, HT29, MB-MDA-453
334015			CH22_FGENES.313_7	2.34	HT29, MB-MDA-231, BT474
318315	AI091370	Hs.134852	ESTs	2.33	CALU6, NCI-H520, DU145
306809	AI057134		EST singleton (not in UniGene) with exon	2.33	PC3, DU145, EB
337697			CH22_EM:AC000097.GENSCAN.86-1	2.33	RPWE-2, PRSC_log, NCI-H345
329630			CH.11_p2 gi|6729060	2.33	NCI-H520, NCI-H23, NCI-H460
326577			CH.19_hs gi|5867317	2.33	NCI-H460, NCI-358, NCI-H23
333428			CH22_FGENES.149_1	2.33	NCI-H345, PRSC_con, RPWE-2
301080	AI479391	Hs.155405	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.33	OVCA-R, MCF7, MCF7
324829	AA714311		EST cluster (not in UniGene)	2.33	NCI-H460, NCI-358, NCI-H23
302776	AJ133798		EST cluster (not in UniGene) with exon h	2.32	NCI-H23, NCI-H460, NCI-H520
325801			CH.14_hs gi|6552451	2.32	PRSC_log, MCF7, NCI-H23
332122	AA609698	Hs.112389	ESTs	2.32	DU145, HT29, PC3
314167	AA243633	Hs.208983	ESTs	2.32	DU145, MCF7, PC3
324023	AA669615	Hs.214226	ESTs	2.31	DU145, NCI-H345, EB
320503	NM_00589		EST cluster (not in UniGene)	2.31	A549, OVCA-R, PC3
312217	T98289		EST cluster (not in UniGene)	2.31	NCI-H23, Caco2, NCI-H69
321304	AA078293		EST cluster (not in UniGene)	2.31	DU145, OVCA-R, EB
323517	AA527359	Hs.154366	ESTs	2.31	NCI-H345, DU145, EB
336455			CH22_FGENES.829_13	2.31	NCI-H345, PRSC_con, RPWE-2
313352	AW292127	Hs.144758	ESTs	2.31	MCF7, DU145, OVCA-R
331457	H93135	Hs.41840	ESTs	2.31	Caco2, NCI-H460, NCI-H23
333054			CH22_FGENES.73_8	2.31	NCI-H69, NCI-358, NCI-H23
308598	AI719237		EST singleton (not in UniGene) with exon	2.31	OVCA-R, CALU6, Caco2
327059			CH.21_hs gi|6531965	2.3	NCI-H460, LnCap, LnCap
334120			CH22_FGENES.333_1	2.3	NCI-H69, RPWE-2, MB-MDA-435s
324154	AI457449	Hs.192817	ESTs	2.3	NCI-H460, MB-MDA-453, NCI-358
326509			CH.19_hs gi|6682496	2.3	NCI-H345, CALU6, OVCA-R
316855	AW291384	Hs.254974	ESTs	2.3	NCI-H345, NCI-H460, BT474
337918			CH22_EM:AC005500.GENSCAN.66-4	2.3	RPWE-2, NCI-H345, PRSC_log
317471	AI825351	Hs.144084	ESTs	2.29	HT29, OVCA-R, DU145
331023	N32599	Hs.5856	ESTs	2.29	OVCA-R, LnCap, A549
332231	N48008	Hs.102629	EST	2.29	CALU6, DU145, EB
309912	AW339671		EST singleton (not in UniGene) with exon	2.29	MB-MDA-435s, PRSC_con, NCI-358
316427	AI241019	Hs.145644	ESTs	2.29	Caco2, HT29, EB
313329	AW293704	Hs.122658	ESTs	2.29	OVCA-R, DU145, Caco2
335019			CH22_FGENES.474_7	2.29	HT29, CALU6, MB-MDA-231
324394	F20654	Hs.152128	ESTs; Moderately similar to !!!! ALU SUB	2.29	NCI-H345, MB-MDA-231, RPWE-2
339357			CH22_BA354I12.GENSCAN.31-2	2.29	NCI-H69, OVCA-R, BT474
322128	AI346033		EST cluster (not in UniGene)	2.28	NCI-H23, NCI-H520, NCI-H460
301310	AI239457	Hs.130794	ESTs	2.28	OVCA-R, DU145, MB-MDA-231
300623	AI929130	Hs.118261	ESTs; Moderately similar to finger prote	2.28	BT474, RPWE-2, PRSC_con
323409	AL135534		EST cluster (not in UniGene)	2.27	NCI-H345, NCI-358, Caco2
308406	AI634885		EST singleton (not in UniGene) with exon	2.27	OVCA-R, EB, HT29
322518	AI133446		EST cluster (not in UniGene)	2.27	DU145, MB-MDA-435s, OVCA-R
338381			CH22_EM:AC005500.GENSCAN.330-10	2.27	NCI-H69, PRSC_con, PRSC_log
316003	AA704584	Hs.119993	ESTs	2.27	NCI-358, NCI-H520, NCI-H23
307090	AI161024		EST singleton (not in UniGene) with exon	2.27	NCI-H345, DU145, RPWE-2
300356	AA758411	Hs.121335	ESTs	2.27	LnCap, NCI-H460, Caco2
331887	AA431328	Hs.98660	ESTs	2.27	NCI-358, NCI-H520, CALU6
330951	H02566	Hs.191268	H sapiens mRNA; cDNA DKFZp434N174 (from	2.27	OVCA-R, BT474, BT474
305547	AA773111		EST singleton (not in UniGene) with exon	2.27	LnCap, DU145, BT474
312457	AA776743	Hs.191589	ESTs	2.26	NCI-H345, RPWE-2, PRSC_con
333929			CH22_FGENES.300_2	2.26	HT29, CALU6, EB

319845	AA649011	Hs.187902	ESTs	2.26	LnCap, DU145, MCF7
306739	AI028393		EST singleton (not in UniGene) with exon	2.26	MB-MDA-435s, NCI-358, CALU6
306919	AI096832		EST singleton (not in UniGene) with exon	2.26	HT29, BT474, PC3
333312			CH22_FGENES.138_4	2.26	OVCA-R, DU145, PC3
334955			CH22_FGENES.465_24	2.25	RPWE-2, PRSC_con, NCI-H345
312295	AA578233	Hs.173863	ESTs	2.25	OVCA-R, DU145, NCI-H345
307643	AI302124		EST singleton (not in UniGene) with exon	2.25	CALU6, CALU6, OVCA-R
324252	AA421989		EST cluster (not in UniGene)	2.25	OVCA-R, EB, A549
309767	AW271805		EST singleton (not in UniGene) with exon	2.25	DU145, NCI-H460, CALU6
311492	AW410240	Hs.4437	ribosomal protein L28	2.25	NCI-H69, NCI-H460, NCI-H520
312260	H05392	Hs.230597	EST	2.25	Caco2, EB, DU145
327125			CH.21_hs gi|6531971	2.25	HT29, NCI-358, BT474
316919	AA845382	Hs.204520	ESTs	2.24	NCI-H23, NCI-H345, NCI-H520
316361	AI433833	Hs.164159	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.24	DU145, EB, PC3
315772	AW515373	Hs.158893	ESTs	2.24	OVCA-R, EB, LnCap
320236	H03688		EST cluster (not in UniGene)	2.24	NCI-358, DU145, NCI-H23
315444	AW138821	Hs.221737	ESTs	2.24	NCI-358, CALU6, PRSC_con
333903			CH22_FGENES.294_1	2.24	MB-MDA-231, BT474, A549
335234			CH22_FGENES.515_3	2.24	NCI-H69, PRSC_con, PRSC_log
333727			CH22_FGENES.256_1	2.23	MB-MDA-231, NCI-H69, BT474
332002	AA482009	Hs.105104	ESTs	2.23	EB, NCI-H520, HT29
329611			CH.10_p2 gi|3962478	2.23	BT474, HT29, MB-MDA-231
310559	AI783594	Hs.155718	ESTs	2.22	BT474, MCF7, MB-MDA-231
327315			CH.01_hs gi|5867508	2.22	NCI-H69, EB, EB
323170	U83527		EST cluster (not in UniGene)	2.22	EB, DU145, LnCap
331522	N49309	Hs.117012	ESTs	2.22	A549, LnCap, DU145
313261	AA730472	Hs.142805	ESTs	2.22	OVCA-R, PC3, LnCap
312740	R97191	Hs.134106	ESTs	2.22	BT474, MCF7, OVCA-R
325055	Z44631	Hs.21658	ESTs	2.22	MB-MDA-453, DU145, CALU6
337895			CH22_EM:AC005500.GENSCAN.56-2	2.22	NCI-H345, PRSC_log, PRSC_con
307140	AI185762		EST singleton (not in UniGene) with exon	2.22	NCI-H520, NCI-H460, EB
321643	W76005	Hs.32094	ESTs	2.21	EB, NCI-H345, PRSC_con
302683	X85153		EST cluster (not in UniGene) with exon h	2.21	BT474, MB-MDA-231, MCF7
322644	AA340904		EST cluster (not in UniGene)	2.21	NCI-H460, NCI-H23, NCI-H520
330415	D83777	Hs.75137	KIAA0193 gene product	2.21	CALU6, A549, Caco2
302334	AF120491		EST cluster (not in UniGene) with exon h	2.21	NCI-H69, NCI-H345, PC3
326710			CH.20_hs gi|5867593	2.21	NCI-H520, NCI-358, NCI-H23
323561	AA825426	Hs.238832	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.21	NCI-H345, DU145, NCI-H69
337706			CH22_EM:AC000097.GENSCAN.87-11	2.21	MB-MDA-435s, NCI-358, NCI-H520
339309			CH22_BA354I12.GENSCAN.22-7	2.21	BT474, HT29, PC3
330436	HG2724-H		Oncogene Tls/Chop, Fusion Activated	2.21	PRSC_con, NCI-H69, Caco2
312360	AI922972	Hs.196073	ESTs	2.21	OVCA-R, MB-MDA-435s, DU145
301855	AF053356		multiple UniGene matches	2.2	NCI-H69, HT29, NCI-H23
331192	T55182	Hs.152571	ESTs; Highly similar to IGF-II mRNA-bind	2.2	OVCA-R, PC3, CALU6
315872	AW051819	Hs.204516	ESTs	2.2	LnCap, OVCA-R, EB
337904			CH22_EM:AC005500.GENSCAN.56-17	2.2	OVCA-R, LnCap, EB
308258	AI565612		EST singleton (not in UniGene) with exon	2.2	DU145, MB-MDA-231, CALU6
320965	H18166		EST cluster (not in UniGene)	2.2	DU145, EB, LnCap
333910			CH22_FGENES.295_3	2.2	DU145, MB-MDA-231, EB
300707	AA080921		EST cluster (not in UniGene) with exon h	2.2	BT474, MCF7, HT29
336011			CH22_FGENES.668_9	2.19	NCI-H460, BT474, NCI-H345
325712			CH.14_hs gi|6682473	2.19	NCI-H460, NCI-H23, NCI-358
322738	AF201832		EST cluster (not in UniGene)	2.19	PC3, RPWE-2, PRSC_con
335339			CH22_FGENES.535_16	2.19	HT29, PRSC_log, MCF7
320733	AA738436	Hs.134407	ESTs	2.19	DU145, EB, Caco2
319412	AA679426	Hs.187505	ESTs	2.19	NCI-H345, PRSC_log, PRSC_con
337132			CH22_FGENES.526-3	2.19	NCI-H69, NCI-H345, PRSC_con
301544	AI951651	Hs.224290	ESTs	2.19	PRSC_con, MB-MDA-231, NCI-H23
325285			CH.11_hs gi|5866903	2.18	PRSC_con, PRSC_log, MB-MDA-231
338280			CH22_EM:AC005500.GENSCAN.290-11	2.18	PC3, NCI-358, HT29
311421	AI701635	Hs.207077	ESTs	2.18	RPWE-2, NCI-H345, NCI-358
330638	X89576	Hs.159581	matrix metalloproteinase 17 (membrane-in	2.18	HT29, MB-MDA-435s, MB-MDA-453
326603			CH.20_hs gi|6056312	2.18	CALU6, DU145, HT29
319055	AA412305		EST cluster (not in UniGene)	2.18	A549, OVCA-R, MB-MDA-435s
335451			CH22_FGENES.562_9	2.18	DU145, LnCap, CALU6
317989	AI203009	Hs.130664	ESTs	2.18	NCI-H345, NCI-H69, NCI-H520
322024	AA334384		EST cluster (not in UniGene)	2.18	Caco2, PC3, NCI-H520
300734	AW205197	Hs.240951	ESTs	2.18	NCI-358, A549, EB
304022	T02990		EST singleton (not in UniGene) with exon	2.18	NCI-H23, NCI-358, NCI-H460
330082			CH.19_p2 gi|6015314	2.18	NCI-H23, Caco2, Caco2
312516	AA363245	Hs.189831	ESTs	2.18	BT474, HT29, MB-MDA-231
333932			CH22_FGENES.300_5	2.17	PC3, Caco2, EB
308115	AI479071		EST singleton (not in UniGene) with exon	2.17	BT474, OVCA-R, OVCA-R
320184	U91510	Hs.123036	CD39-like 1	2.17	NCI-H520, NCI-358, NCI-H23
324432	AA464510		EST cluster (not in UniGene)	2.17	CALU6, RPWE-2, HT29
320882	AI832098		EST cluster (not in UniGene)	2.17	OVCA-R, PC3, BT474

312251	H03952		EST cluster (not in UniGene)	2.17	NCI-H460, NCI-H23, NCI-358
315049	AW340486	Hs.121210	ESTs	2.17	NCI-H520, NCI-358, NCI-H23
305018	AA627127		EST singleton (not in UniGene) with exon	2.17	MB-MDA-231, MB-MDA-453, EB
303807	AI792785	Hs.130434	ESTs	2.16	NCI-H345, PRSC_con, PRSC_log
317792	AI653389	Hs.196121	ESTs	2.16	NCI-H345, PRSC_con, LnCap
321668	AA872730	Hs.125229	ESTs	2.16	OVCA-R, PC3, MCF7
328863			CH.07_hs gi|6381929	2.16	PRSC_con, NCI-H345, NCI-H460
319373	R00371		EST cluster (not in UniGene)	2.16	PRSC_con, RPWE-2, NCI-H345
320069	T86541	Hs.189732	ESTs	2.16	NCI-H23, NCI-358, NCI-H345
320235	AF064090	Hs.129708	tumor necrosis factor (ligand) superfami	2.16	NCI-H23, NCI-H460, NCI-H520
338880			CH22_DJ32I10.GENSCAN.6-2	2.16	BT474, MCF7, OVCA-R
318314	AI091349	Hs.161133	ESTs	2.16	NCI-H23, NCI-H520, NCI-H460
332696	D86973	Hs.75354	GCN1 (general control of amino-acid synt	2.16	A549, PC3, DU145
331352	AA406133	Hs.7482	KIAA0682 gene product	2.16	PC3, EB, MB-MDA-231
339019			CH22_DA59H18.GENSCAN.21-15	2.15	LnCap, EB, OVCA-R
306975	AI127042		EST singleton (not in UniGene) with exon	2.15	MB-MDA-435s, NCI-H520, NCI-358
318069	AI024557	Hs.131540	ESTs	2.15	Caco2, Caco2, BT474
312997	AW205686	Hs.135130	ESTs	2.15	NCI-H460, NCI-H23, NCI-358
331372	AA433935	Hs.55044	DKFZP586H2123 protein	2.15	PRSC_con, HT29, CALU6
335049			CH22_FGENES.481_5	2.15	NCI-H69, NCI-H345, PRSC_log
324280	AA429772	Hs.191610	ESTs	2.15	MB-MDA-453, MB-MDA-435s, MCF7
330363			CH.X_p2 gi|3126882	2.15	NCI-H23, NCI-H460, NCI-358
322896	AW470296	Hs.144830	ESTs	2.15	HT29, CALU6, EB
321981	AA948204	Hs.127361	ESTs	2.15	MB-MDA-231, DU145, HT29
333294			CH22_FGENES.130_6	2.14	EB, DU145, MB-MDA-453
330170			CH.02_p2 gi|6648220	2.14	HT29, MB-MDA-453, PC3
312973	AI123346	Hs.135241	ESTs	2.14	LnCap, DU145, EB
311104	AI627352	Hs.201449	ESTs	2.14	NCI-H520, NCI-H23, LnCap
325086	T10019	Hs.4194	ESTs	2.14	NCI-H460, NCI-H23, NCI-358
317182	AW183524	Hs.192298	ESTs	2.14	HT29, BT474, MB-MDA-435s
323644	AA310711	Hs.124340	ESTs	2.14	RPWE-2, PRSC_con, PRSC_log
308092	AI474896		EST singleton (not in UniGene) with exon	2.14	BT474, MCF7, MB-MDA-231
322265	AF086244		EST cluster (not in UniGene)	2.14	NCI-H345, RPWE-2, PRSC_con
303521	AA746272		EST cluster (not in UniGene) with exon h	2.14	DU145, MB-MDA-453, EB
312102	AW439340	Hs.189720	ESTs	2.14	NCI-H23, NCI-H460, MB-MDA-435s
316559	AI249468	Hs.228251	EST	2.14	NCI-H460, NCI-358, NCI-H23
338486			CH22_EM:AC005500.GENSCAN.382-8	2.14	NCI-H520, NCI-H23, NCI-H69
301302	AI825444	Hs.210956	ESTs	2.14	BT474, HT29, MB-MDA-231
310591	AI650372	Hs.195979	ESTs	2.14	CALU6, CALU6, Caco2
316231	AA732301		EST cluster (not in UniGene)	2.14	NCI-H23, NCI-H520, NCI-358
326559			CH.19_hs gi|5867310	2.14	DU145, NCI-H460, NCI-H23
324062	AA525291	Hs.204099	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.13	OVCA-R, DU145, EB
323844	AI811303	Hs.143490	ESTs	2.13	MB-MDA-453, MCF7, MB-MDA-435s
333895			CH22_FGENES.293_2	2.13	CALU6, LnCap, DU145
308264	AI567114	Hs.171454	EST	2.13	DU145, CALU6, MB-MDA-453
306081	AA908472		EST singleton (not in UniGene) with exon	2.13	HT29, BT474, MB-MDA-231
333101			CH22_FGENES.79_6	2.13	NCI-H345, NCI-H69, PRSC_log
328544			CH.07_hs gi|5868486	2.13	NCI-H23, NCI-H69, PRSC_log
333355			CH22_FGENES.141_6	2.13	DU145, EB, CALU6
323397	AI524519	Hs.239699	ESTs	2.13	EB, NCI-H460, NCI-H345
305697	AA814956		EST singleton (not in UniGene) with exon	2.13	NCI-H520, NCI-H460, NCI-358
327809			CH.05_hs gi|5867968	2.13	HT29, PC3, OVCA-R
325092	T10115	Hs.92423	ESTs	2.13	HT29, NCI-358, MB-MDA-231
322299	AI971935	Hs.252784	ESTs	2.13	PRSC_con, DU145, DU145
312145	AA029526	Hs.126706	ESTs	2.12	OVCA-R, A549, MB-MDA-435s
323704	AA319421	Hs.193577	ESTs	2.12	Caco2, LnCap, OVCA-R
328971			CH.08_hs gi|6478806	2.12	NCI-358, NCI-H23, NCI-H520
325338			CH.11_hs gi|5866883	2.12	LnCap, NCI-H69, NCI-H345
331332	AA282554	Hs.89034	ESTs	2.12	NCI-H520, NCI-H23, Caco2
327159			CH.01_hs gi|5867550	2.12	EB, DU145, PC3
335180			CH22_FGENES.505_2	2.12	LnCap, NCI-H69, A549
338062			CH22_EM:AC005500.GENSCAN.162-3	2.12	PRSC_con, PRSC_log, NCI-H69
318350	AI636018	Hs.135538	ESTs	2.12	EB, HT29, DU145
312070	AW293140	Hs.108790	ESTs	2.11	Caco2, NCI-H23, A549
328314			CH.07_hs gi|5868371	2.11	HT29, NCI-H23, NCI-H460
315869	AI033547	Hs.132826	ESTs	2.11	BT474, CALU6, MCF7
339246			CH22_BA354I12.GENSCAN.5-9	2.11	CALU6, CALU6, BT474
329921			CH.16_p2 gi|6165205	2.11	BT474, MB-MDA-231, HT29
324981	Z25333	Hs.4947	ESTs	2.11	A549, NCI-H460, NCI-H520
331291	AA159323	Hs.109929	ESTs	2.11	NCI-H345, A549, PRSC_con
332729	AA058907	Hs.83190	fatty acid synthase	2.11	NCI-358, LnCap, MB-MDA-453
325448			CH.12_hs gi|5866941	2.11	DU145, MCF7, CALU6
314929	AW188286	Hs.143612	ESTs	2.1	EB, BT474, MB-MDA-231
301063	AI057634	Hs.124596	ESTs	2.1	NCI-H23, NCI-H460, BT474
301952	AB029016	Hs.117333	KIAA1093 protein	2.1	OVCA-R, A549, CALU6
326309			CH.17_hs gi|5867277	2.1	MB-MDA-435s, NCI-H69, MB-MDA-453

315406	AI823453	Hs.146625	ESTs	2.1	OVCA-R, DU145, EB
302376	AB007867	Hs.200480	KIAA0407 protein	2.1	OVCA-R, Caco2, HT29
312181	AA417281	Hs.191595	ESTs	2.1	OVCA-R, A549, DU145
334254			CH22_FGENES.366_4	2.1	LnCap, OVCA-R, DU145
318073	AW167087	Hs.131562	ESTs	2.1	A549, CALU6, EB
304724	AA569881	Hs.65114	keratin 18	2.1	NCI-H23, NCI-H520, NCI-H460
332359	W87704	Hs.211558	ESTs	2.1	MB-MDA-435s, PRSC_con, NCI-H460
331884	AA431302	Hs.98721	EST; Weakly similar to N-copine [H.sapie	2.1	NCI-H345, MB-MDA-231, PRSC_con
308226	AI559106	Hs.181165	eukaryotic translation elongation factor	2.1	EB, CALU6, OVCA-R
324279	AA501412	Hs.191688	ESTs; Weakly similar to Pro-Pol-dUTPase	2.09	OVCA-R, LnCap, PC3
337203			CH22_FGENES.591-3	2.09	NCI-H69, NCI-H345, MB-MDA-231
322346	AA227618	Hs.10882	HMG-box containing protein 1	2.09	HT29, BT474, MB-MDA-231
304470	AA426654	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.09	NCI-H23, CALU6, NCI-H520
325977			CH.16_hs gi|6249602	2.09	NCI-H23, NCI-H520, HT29
304696	AA554758		EST singleton (not in UniGene) with exon	2.09	MB-MDA-435s, NCI-H23, BT474
317412	AI301528	Hs.132604	ESTs	2.09	Caco2, EB, NCI-358
315570	AI860360	Hs.160316	ESTs	2.08	PRSC_con, PRSC_log, NCI-H345
327341			CH.01_hs gi|6017016	2.08	MB-MDA-231, PRSC_con, NCI-H69
327431			CH.02_hs gi|5867754	2.08	NCI-H23, NCI-358, NCI-H520
314685	AI870811	Hs.158709	ESTs; Weakly similar to KIAA0938 protein	2.08	MB-MDA-453, MCF7, OVCA-R
328624			CH.07_hs gi|5868246	2.08	MCF7, NCI-358, RPWE-2
303596	AW303377		EST cluster (not in UniGene) with exon h	2.08	RPWE-2, PRSC_con, PRSC_log
336717			CH22_FGENES.81-1	2.08	BT474, HT29, MCF7
317370	AW204139	Hs.174424	ESTs; Weakly similar to p140mDia [M.musc	2.08	NCI-H23, NCI-H460, NCI-H69
331287	AA149061	Hs.172971	ESTs	2.08	OVCA-R, EB, NCI-H345
304211	N62228		EST singleton (not in UniGene) with exon	2.08	BT474, MCF7, MB-MDA-231
315613	AW137420	Hs.192311	ESTs	2.08	PRSC_con, PRSC_log, PRSC_log
325636			CH.14_hs gi|5867002	2.08	NCI-358, NCI-H460, MB-MDA-453
336406			CH22_FGENES.823_21	2.08	HT29, EB, DU145
301714	F06529		EST cluster (not in UniGene) with exon h	2.08	LnCap, PRSC_log, PRSC_con
300496	R45159	Hs.221804	ESTs	2.08	PRSC_con, LnCap, RPWE-2
318970	R21114	Hs.21383	ESTs	2.08	NCI-H23, NCI-H520, NCI-H460
334115			CH22_FGENES.330_15	2.08	BT474, NCI-H69, HT29
308082	AI473682		EST singleton (not in UniGene) with exon	2.08	MB-MDA-435s, NCI-H345, MB-MDA-231
308282	AI569456		EST singleton (not in UniGene) with exon	2.08	LnCap, EB, PRSC_con
313038	AW451618	Hs.124195	ESTs	2.07	NCI-H345, PRSC_con, LnCap
317974	AW444468	Hs.144900	ESTs	2.07	NCI-358, NCI-H23, NCI-H520
324063	AW292740	Hs.254815	ESTs	2.07	Caco2, NCI-358, NCI-H520
334759			CH22_FGENES.428_8	2.07	CALU6, HT29, NCI-H520
307864	AI367417		EST singleton (not in UniGene) with exon	2.07	NCI-H460, NCI-358, NCI-H23
304356	AA196027	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.07	HT29, MCF7, MB-MDA-435s
303929	AW470753		EST singleton (not in UniGene) with exon	2.07	NCI-H345, PRSC_con, RPWE-2
331857	AA421160	Hs.9456	SWI/SNF related; matrix assocd; actin de	2.07	EB, A549, PC3
322814	AI824495	Hs.211038	ESTs	2.06	PRSC_con, RPWE-2, Caco2
303650	AA430709		EST cluster (not in UniGene) with exon h	2.06	RPWE-2, NCI-H345, PRSC_con
333403			CH22_FGENES.144_21	2.06	OVCA-R, CALU6, PC3
313663	AI953261	Hs.169813	ESTs	2.06	NCI-H345, OVCA-R, NCI-H23
338594			CH22_EM:AC005500.GENSCAN.435-4	2.06	DU145, LnCap, EB
334676			CH22_FGENES.418_29	2.06	NCI-H69, PRSC_log, PRSC_con
310046	AI198032	Hs.210356	ESTs	2.06	MB-MDA-435s, NCI-H23, Caco2
309169	AI949216		EST singleton (not in UniGene) with exon	2.06	CALU6, EB, NCI-358
329752			CH.14_p2 gi|6065777	2.06	CALU6, HT29, DU145
325085	T10001	Hs.4188	ESTs	2.06	EB, OVCA-R, MB-MDA-435s
332062	AA521016	Hs.185375	ESTs	2.06	OVCA-R, MB-MDA-453, MCF7
302074	AA382871	Hs.132794	phosphate cytidylyltransferase 1; cholin	2.06	LnCap, EB, NCI-H69
326344			CH.17_hs gi|6525295	2.06	HT29, BT474, MB-MDA-453
330855	AA079318		zm98c2.s1 Stratagene colon HT29 (#937221 IMAGE:545954 3', mRNA seq	2.06	RPWE-2, LnCap, PRSC_con
302525	AF024690	Hs.248056	G protein-coupled receptor 43	2.05	NCI-358, NCI-H23, DU145
331903	AA436673	Hs.29417	H sapiens mRNA; cDNA DKFZp586B0323 (from	2.05	Caco2, DU145, A549
316322	AW296618	Hs.120637	ESTs	2.05	BT474, MB-MDA-453, OVCA-R
321525	H78875		EST cluster (not in UniGene)	2.05	NCI-H23, PRSC_con, NCI-H520
305071	AA640579		EST singleton (not in UniGene) with exon	2.05	MB-MDA-231, BT474, HT29
326033			CH.17_hs gi|5867178	2.05	HT29, DU145, BT474
334730			CH22_FGENES.424_5	2.05	BT474, EB, OVCA-R
305335	AA704235		EST singleton (not in UniGene) with exon	2.05	MCF7, OVCA-R, MB-MDA-453
320521	N31464	Hs.24743	ESTs	2.05	MB-MDA-453, MB-MDA-231, PC3
333515			CH22_FGENES.172_5	2.04	NCI-H345, RPWE-2, PRSC_con
311020	AI918672	Hs.213783	ESTs	2.04	NCI-H460, NCI-H23, NCI-H520
324323	AA393739		EST cluster (not in UniGene)	2.04	OVCA-R, PC3, LnCap
305486	AA748889		EST singleton (not in UniGene) with exon	2.04	NCI-H345, PRSC_log, CALU6
312162	T91823		EST cluster (not in UniGene)	2.04	NCI-H520, NCI-H23, NCI-358
330980	H28794	Hs.6659	ESTs	2.04	MCF7, MB-MDA-453, MB-MDA-435s
317463	AA927290	Hs.130462	ESTs	2.04	NCI-H23, Caco2, NCI-H69
303460	AA700155	Hs.117900	ESTs	2.04	DU145, EB, CALU6
337435			CH22_FGENES.766-2	2.03	NCI-H345, OVCA-R, LnCap

305464	AA742425		EST singleton (not in UniGene) with exon	2.03	CALU6, NCI-H520, NCI-358
307918	AI383496		EST singleton (not in UniGene) with exon	2.03	NCI-H23, BT474, MB-MDA-231
322209	H89360		EST cluster (not in UniGene)	2.03	DU145, OVCA-R, MB-MDA-453
310295	AW205198	Hs.149146	ESTs	2.03	NCI-H23, NCI-H460, NCI-358
325886			CH.16_hs gi|5867087	2.03	NCI-H345, NCI-H345, RPWE-2
329719			CH.14_p2 gi|6065785	2.03	NCI-H69, RPWE-2, PRSC_con
309247	AI972768		EST singleton (not in UniGene) with exon	2.03	LnCap, PRSC_con, RPWE-2
328277			CH.07_hs gi|6004471	2.03	LnCap, RPWE-2, A549
307296	AI205705	Hs.147222	EST	2.03	NCI-H460, NCI-358, NCI-H23
327203			CH.01_hs gi|5867447	2.03	HT29, BT474, MB-MDA-231
306866	AI086683		EST singleton (not in UniGene) with exon	2.03	BT474, NCI-H345, HT29
333339			CH22_FGENES.139_8	2.03	HT29, DU145, CALU6
323115	AI921875		EST cluster (not in UniGene)	2.03	BT474, BT474, MB-MDA-231
304811	AA584361		EST singleton (not in UniGene) with exon	2.03	NCI-H23, NCI-358, NCI-H460
323372	AL135125	Hs.13913	ESTs	2.02	DU145, EB, A549
312854	AA828713		EST cluster (not in UniGene)	2.02	NCI-H345, PRSC_con, PRSC_log
307904	AI381019		EST singleton (not in UniGene) with exon	2.02	HT29, MCF7, MB-MDA-453
332099	AA608983		af5d4.s1 Soares_testis_NHT H sapiens cDN	2.02	PRSC_con, NCI-H345, RPWE-2
324634	AI684571	Hs.175831	ESTs	2.02	NCI-H460, Caco2, NCI-358
335721			CH22_FGENES.599_24	2.02	NCI-H69, PRSC_log, NCI-H345
312452	AI692643	Hs.172749	ESTs	2.02	HT29, Caco2, MB-MDA-231
325396			CH.12_hs gi|5866921	2.01	HT29, NCI-H520, NCI-H460
328770			CH.07_hs gi|6017031	2.01	NCI-H23, NCI-H460, NCI-358
335585			CH22_FGENES.581_24	2.01	MB-MDA-453, DU145, MCF7
335634			CH22_FGENES.584_14	2.01	NCI-H23, NCI-H460, NCI-H69
338271			CH22_EM:AC005500.GENSCAN.287-1	2.01	MCF7, DU145, PC3
328607			CH.07_hs gi|5868233	2.01	NCI-H460, NCI-H23, NCI-358
307050	AI147341	Hs.146734	EST	2.01	NCI-H520, NCI-H23, NCI-358
334946			CH22_FGENES.465_13	2.01	CALU6, BT474, DU145
319793	R56360		EST cluster (not in UniGene)	2.01	NCI-H460, HT29, NCI-358
307223	AI193698	Hs.184776	ribosomal protein L23a	2.01	NCI-358, NCI-H520, NCI-H23
312627	AA344698	Hs.133169	ESTs	2.01	PC3, LnCap, MB-MDA-231
329221			CH.X_hs gi|5868727	2.01	NCI-H345, NCI-H69, NCI-358
305145	AA653589		EST singleton (not in UniGene) with exon	2.01	LnCap, EB, OVCA-R
328428			CH.07_hs gi|5868417	2.01	NCI-H69, MB-MDA-453, BT474
305990	AA888866	Hs.125919	EST	2.01	NCI-H520, NCI-358, NCI-H23
319368	R00003	Hs.133171	ESTs	2	OVCA-R, LnCap, PC3
324805	AA927002	Hs.131350	ESTs	2	NCI-H460, NCI-H23, NCI-358
301138	AA719179	Hs.189419	ESTs	2	NCI-H69, NCI-H23, PRSC_con
304675	AA541740		EST singleton (not in UniGene) with exon	2	NCI-H460, NCI-H520, MB-MDA-231
326194			CH.17_hs gi|5867213	2	HT29, NCI-358, BT474

Table 5: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Met/B surv.
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	5.56
128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.62
129093	AA262710	Hs.108614	KIAA0627 protein	4.23
124690	R05818	Hs.173830	ESTs	3.96
115558	AA393806	Hs.1010	regulator of mitotic spindle assembly 1	3.39
134261	AA227678	Hs.8084	Humn DNA sequence from clone 465N24 on c	3.22
104792	AA029288	Hs.29147	ESTs; Highly similar to ZINC FINGER PROT	3.17
133770	M69197	Hs.242279	haptoglobin-related protein	3.07

Table 6: H chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Met/B surv.
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.07
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	0.2
129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.2
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.2

Table 7: I chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/B surv
319379	T91443	Hs.193963	ESTs	19.65
321920	N63915			11.9
324302	AA543008	Hs.136806	ESTs; Weakly similar to !!!! ALU SUBFAMI	9.31
314522	AI732331	Hs.187750	ESTs; Moderately similar to !!!! ALU CLA	5.79
331433	H68097	Hs.161023	EST	4.79
324643	AI436356	Hs.130729	ESTs	4.59
332471	AA416967	Hs.120980	nuclear receptor co-repressor 2	4.58
314915	AA573072	Hs.187748	ESTs; Weakly similar to !!!! ALU SUBFAMI	4.3
321354	AA078493		EST cluster (not in UniGene)	4.26
322309	AF086372		EST cluster (not in UniGene)	3.89
325100	T10265	Hs.116122	ESTs; Weakly similar to coded for by C.	3.81
314071	AA192455	Hs.188690	ESTs	3.74
315178	AW362945	Hs.162459	ESTs	3.66
330987	H40988	Hs.131965	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.51
337898			CH22_EM:AC005500.GENSCAN.56-5	3.21
319403	T98413		EST cluster (not in UniGene)	3.2
331469	N22273	Hs.39140	ESTs	3.15
331549	N56866	Hs.237507	EST	3.14
331644	T99544	Hs.173734	ESTs; Weakly similar to !!!! ALU CLASS B	3.14
313220	AI971981	Hs.118241	ESTs	3.04

Table 8: I chip – B survivor vs Met query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/B surv
333658			CH22_FGENES.241_4	0.06
333657			CH22_FGENES.241_2	0.07
333654			CH22_FGENES.240_2	0.07
332859			CH22_FGENES.27_2	0.07
333656			CH22_FGENES.240_4	0.07
304480	AA430373		EST singleton (not in UniGene) with exon	0.08
333737			CH22_FGENES.261_1	0.09
308601	AI719930		EST singleton (not in UniGene) with exon	0.1
334030			CH22_FGENES.320_2	0.1
333637			CH22_FGENES.229_2	0.13
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	0.16
333653			CH22_FGENES.239_2	0.16
333635			CH22_FGENES.228_2	0.19
333647			CH22_FGENES.235_2	0.19
307588	AI285535		EST singleton (not in UniGene) with exon	0.2
337954			CH22_EM:AC005500.GENSCAN.96-3	0.2
333588			CH22_FGENES.206_2	0.21
320244	AA296922	Hs.129778	gastrointestinal peptide	0.22
333642			CH22_FGENES.231_2	0.23
337951			CH22_EM:AC005500.GENSCAN.94-1	0.23
333730			CH22_FGENES.258_1	0.23
333646			CH22_FGENES.234_2	0.24

Table 9: H chip – B survivor vs Met query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniGID	Complete_Title	Median Mets AI vs Median B-Sur AI
100655	HG2841-HT2970		Albumin, Alt. Splice 5	11.98
124875	R70506	Hs.207693	ESTs; Weakly similar to !!!! ALU SUBFAMI	9.21
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	6.73
100654	HG2841-HT2969		Albumin, Alt. Splice 3, Missplicing In Alloalbumin Venezia	6.18
118828	N79496	Hs.50824	EST	5.93
128046	AA873285	Hs.137947	ESTs	5.9
128896	D14446	Hs.107	fibrinogen-like 1	5.17
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	5.11
125090	T91518		ye20f05.s1 Stratagene lung (#937210) Hom	4.47
118579	N68905		small inducible cytokine A5 (RANTES)	4.23
123526	AA608657		ESTs; Moderately similar to !!!! ALU SUB	4.21
128062	AA379500	Hs.193155	ESTs	4.14
119174	R71234		yi54c08.s1 Soares placenta Nb2HP Homo sa	4.11
128530	AA504343	Hs.183475	Homo sapiens clone 25061 mRNA sequence	4.09
119404	T92950		ye27c10.s1 Stratagene lung (#937210) Hom	3.98
118475	N66845	Hs.165411	ESTs; Weakly similar to !!!! ALU CLASS B	3.96
129974	K00629	Hs.199300	Human kpni repeat mrna (cdna clone pcd-k	3.87
108888	AA135606	Hs.189384	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.85
123963	C13961	Hs.210115	EST	3.8
123523	AA608588	Hs.193634	ESTs	3.76
128230	AA984074	Hs.176757	ESTs	3.75
124090	H09570	Hs.143032	ESTs; Weakly similar to neuronal thread	3.67
124690	R05818	Hs.173830	ESTs	3.58
134261	AA227678	Hs.8084	Human DNA sequence from clone 465N24 on	3.57
126917	AA176225	Hs.193929	ESTs	3.52
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k	3.45
126649	AA856990	Hs.125058	ESTs	3.42
115096	AA255991	Hs.175319	ESTs	3.4
129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	3.38
123022	AA480909		aa28f10.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.38
106145	AA424791	Hs.5734	KIAA0679 protein	3.38
125191	W67257	Hs.138871	ESTs; Weakly similar to !!!! ALU CLASS B	3.36
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	3.3
128710	J04813	Hs.104117	cytochrome P450; subfamily IIIA (niphedi	3.27
123460	AA598981	Hs.251122	EST	3.25
133735	AC002045	Hs.251928	nuclear pore complex interacting protein	3.24
124696	R06273	Hs.186467	ESTs; Moderately similar to !!!! ALU SUB	3.24
120748	AA303153	Hs.237994	EST; Weakly similar to !!!! ALU SUBFAMIL	3.21
133770	M69197	Hs.242279	haptoglobin-related protein	3.17
128336	AI242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.14
135357	AA235803	Hs.79572	cathepsin D (lysosomal aspartyl protease	3.12
128088	R02443	Hs.186467	ESTs; Moderately similar to !!!! ALU SUB	3.08
124055	F10904	Hs.100516	Homo sapiens clone 23605 mRNA sequence	3.06
124896	R82063	Hs.101594	EST	3.06
127598	AA610677	Hs.168851	ESTs	3.04
116802	H44061	Hs.194026	ESTs	3.01

Table 10: H chip – B survivor vs Met query – Down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Met/B surv.
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.09
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.11
129982	M87789	Hs.140	immunoglobulin gamma 3 (Gm marker)	0.12
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.13
133806	M12759	Hs.76325	Human Ig J chain gene	0.17
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.18
131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.18
131791	S71043	Hs.32225	immunoglobulin alpha 1	0.2
133725	V00563	Hs.179543	immunoglobulin mu	0.22
101923	S75256		HNL=neutrophil lipocalin [human, ovarian	0.23
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	0.24
103448	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	0.24

Table 11: H chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Median Mets AI vs Median Normal AI
100655	HG2841-HT2970		Albumin, Alt. Splice 5	15.91
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	6.83
124875	R70506	Hs.207693	ESTs; Weakly similar to !!!! ALU SUBFAMI	6.68
100654	HG2841-HT2969		Albumin, Alt. Splice 3, Missplicing In Alloalbumin Venezia	5.28
124059	F13673	Hs.99769	ESTs	5.11
128896	D14446	Hs.107	fibrinogen-like 1	5.05
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	4.82
131564	AA491465	Hs.28792	ESTs	4.78
127917	AA211895	Hs.118831	EST; Highly similar to dJ1163J1.2.1 [H.s	4.76
115096	AA255991	Hs.175319	ESTs	4.67
104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	4.63
123526	AA608657		ESTs; Moderately similar to !!!! ALU SUB	4.61
125090	T91518		ye20f05.s1 Stratagene lung (#937210) Hom	4.59
129666	M77349	Hs.118787	transforming growth factor; beta-induced	4.58
118828	N79496	Hs.50824	EST	4.56
128046	AA873285	Hs.137947	ESTs	4.45
133421	AA436560	Hs.7327	claudin 1	4.09
129158	J05257	Hs.109	dipeptidase 1 (renal)	4.04
128062	AA379500	Hs.193155	ESTs	4.03
124696	R06273	Hs.186467	ESTs; Moderately similar to !!!! ALU SUB	4.01
118475	N66845	Hs.165411	ESTs; Weakly similar to !!!! ALU CLASS B	3.96
104755	AA024482	Hs.9029	DKFZP434G032 protein	3.83
104978	AA088458	Hs.19322	ESTs	3.74
118579	N68905		small inducible cytokine A5 (RANTES)	3.7
123796	AA620390	Hs.247444	ESTs	3.62
127240	AA888387	Hs.243845	ESTs; Moderately similar to !!!! ALU SUB	3.61
104105	AA422123	Hs.42457	ESTs	3.55
129349	D86974	Hs.110613	KIAA0220 protein	3.54
119329	T51832		ESTs; Moderately similar to !!!! ALU SUB	3.53
114617	AA084148	Hs.110659	ESTs	3.52
123143	AA487595		aa95e2.s1 Stratagene fetal retina 93722	3.48
103119	X63629	Hs.2877	cadherin 3; P-cadherin (placental)	3.48
119404	T92950		ye27c10.s1 Stratagene lung (#937210) Hom	3.47
123963	C13961	Hs.210115	EST	3.47
116480	C14088	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	3.4
108836	AA132061	Hs.222727	ESTs; Weakly similar to ubiquitous TPR m	3.39
120748	AA303153	Hs.237994	EST; Weakly similar to !!!! ALU SUBFAMIL	3.38
133770	M69197	Hs.242279	haptoglobin-related protein	3.38
132358	X60486	Hs.46423	H4 histone family; member G	3.37
127759	AI369384		arylsulfatase D	3.37
129095	L12350	Hs.108623	thrombospondin 2	3.37
128261	AI061213	Hs.13179	ESTs; Moderately similar to !!!! ALU SUB	3.36
126908	AA169866		ESTs; Weakly similar to !!!! ALU SUBFAMI	3.36
128954	N32118	Hs.209100	DKFZP434C171 protein	3.34
119174	R71234		yi54c08.s1 Soares placenta Nb2HP Homo sa	3.33
106687	AA463234	Hs.119387	KIAA0792 gene product	3.32
128230	AA984074	Hs.176757	ESTs	3.3
126649	AA856990	Hs.125058	ESTs	3.25
124620	N74051	Hs.194092	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.24
135427			AFFX control: human alu repeats	3.23
129967	H99653	Hs.138618	ESTs	3.22
125191	W67257	Hs.138871	ESTs; Weakly similar to !!!! ALU CLASS B	3.2
124684	R02401	Hs.221078	ESTs	3.2
128010	AA856953	Hs.23348	S-phase kinase-associated protein 2 (p45	3.17
119423	T99544	Hs.173734	ESTs; Weakly similar to !!!! ALU CLASS B	3.16
123022	AA480909		aa28f10.s1 NCI_CGAP_GCB1 Homo sapiens cD	3.15
103654	Z70759		H.sapiens mitochondrial 16S rRNA gene (p	3.13
128336	AI242720	Hs.146043	ESTs; Weakly similar to alternatively sp	3.12
124690	R05818	Hs.173830	ESTs	3.1
129791	F02778	Hs.173887	KIAA0876 protein	3.07
114472	AA028924	Hs.177407	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.07
115429	AA284139	Hs.89295	EST	3.06
130020	AA433930	Hs.240443	ESTs; Weakly similar to HNK-1 sulfotrans	3.06
126050	H27267	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-k	3.05

129906	H39216	Hs.239970	ESTs; Weakly similar to ZNF91L [H.sapien	3.04
123422	AA598484	Hs.238476	EST	3.03
103059	X57351	Hs.174195	interferon induced transmembrane protein	3.02
124253	H69742	Hs.102201	ESTs	3.02
123523	AA608588	Hs.193634	ESTs	3.02
132669	AA188378	Hs.54602	ESTs; Weakly similar to 60S RIBOSOMAL PR	3.02
123196	AA489250	Hs.59403	serine palmitoyltransferase; subunit II	3.01
122948	AA477483		zu44h2.s1 Soares ovary tumor NbHOT Homo	3.01
119053	R11501		yf28f1.s1 Soares fetal liver spleen 1NFL	3.01
125953	H40829		yo05d11.r1 Soares adult brain N2b5HB55Y	3
119155	R61715	Hs.138237	ESTs	3

Table 12: H chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Median Mets AI vs Median Normal AI
103466	Y00339	Hs.155097	carbonic anhydrase II	0.01
104258	AF007216	Hs.5462	solute carrier family 4; sodium bicarbon	0.02
108999	AA156064	Hs.72115	ESTs	0.04
101046	K01160		Accession not listed in Genbank	0.04
133565	H57056	Hs.204831	ESTs	0.05
101346	L76465	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.05
123137	AA487468	Hs.100686	ESTs; Weakly similar to secreted cement	0.05
134534	X73501	Hs.84905	H. Sapiens mRNA for cytokeratin 20	0.05
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	0.06
102095	U11313	Hs.75760	sterol carrier protein 2	0.06
111855	R37362	Hs.21351	ESTs	0.06
129105	AA224351	Hs.108681	ESTs	0.07
130320	U19495	Hs.237356	stromal cell-derived factor 1	0.07
113778	W15263	Hs.5422	ESTs	0.07
116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfami	0.07
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.07
104636	AA004415	Hs.106106	ESTs	0.07
107032	AA599472	Hs.247309	succinate-CoA ligase; GDP-forming; beta	0.08
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.08
128906	AA487557	Hs.10706	ESTs	0.08
130016	AA055811	Hs.143131	transmembrane glycoprotein	0.08
113523	T90037	Hs.16686	ESTs	0.08
102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine pr	0.09
124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (fr	0.09
129519	AA298786	Hs.112242	ESTs	0.09
134749	L10955	Hs.89485	carbonic anhydrase IV	0.09
130366	L11708	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.09
109272	AA195718	Hs.86030	ESTs	0.09
102124	U14528	Hs.29981	solute carrier family 26 (sulfate transp	0.1
132711	N73702	Hs.238927	ESTs	0.1
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	0.1
133806	M12759	Hs.76325	Human Ig J chain gene	0.1
102571	U60115		Homo sapiens skeletal muscle LIM-protein	0.1
114846	AA234929	Hs.44343	ESTs	0.11
131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.11
106569	AA455983	Hs.117816	sorcin	0.11
103542	Z11793	Hs.3314	selenoprotein P; plasma; 1	0.11
128915	C02386	Hs.107139	ESTs	0.11
120914	AA377254	Hs.97107	EST	0.11
130867	J04093	Hs.2056	UDP glycosyltransferase 1	0.11
110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	0.12
101877	M97496	Hs.778	guanylate cyclase activator 1B (retina)	0.12
132617	AA171913	Hs.5338	carbonic anhydrase XII	0.12
129113	AA147646	Hs.108740	DKFZP586A0522 protein	0.12
133435	T23983	Hs.7365	ESTs	0.13
132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.13
125832	AA628600	Hs.117587	ESTs	0.13
104613	AA001049	Hs.24713	Homo sapiens mRNA; cDNA DKFZp586G0123 (f	0.13
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	0.13
119479	W32094	Hs.55501	ESTs	0.14
131273	AA421139	Hs.173542	ESTs	0.14
106674	AA461303	Hs.7946	DKFZP586D1519 protein	0.14
108980	AA151676	Hs.33455	peptidyl arginine deiminase; type II	0.14
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	0.14
131219	C00476	Hs.24395	small inducible cytokine subfamily B (Cy	0.15
116459	AA621399	Hs.64193	ESTs	0.15
130219	R77539	Hs.15285	ESTs	0.15
113863	W68388	Hs.21288	ESTs; Weakly similar to KIAA0704 protein	0.15
101564	M32886	Hs.117816	sorcin	0.15
109502	AA233837	Hs.44755	ESTs; Weakly similar to membrane glycopr	0.15
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	0.15
135237	AA454930	Hs.9691	ESTs	0.15

112483	R66534	Hs.28403	ESTs	0.15
132387	R70914	Hs.8997	heat shock 70kD protein 1	0.15
130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROT	0.16
105496	AA256323	Hs.25264	DKFZP434N126 protein	0.16
104037	AA372630	Hs.100347	differentially expressed in hematopoieti	0.16
101461	M22430	Hs.76422	phospholipase A2; group IIA (platelets;	0.16
116551	D20458	Hs.229071	EST	0.16
133889	AA099391	Hs.211582	myosin; light polypeptide kinase	0.16
103653	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.16
101070	L02785	Hs.1650	down-regulated in adenoma	0.17
131501	AA121127	Hs.181307	H3 histone; family 3A	0.17
133515	X98311	Hs.74466	carcinoembryonic antigen-related cell ad	0.17
108604	AA099820	Hs.49696	ESTs	0.17
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.17
131676	C20785	Hs.30514	ESTs	0.17
134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	0.17
133441	M82962	Hs.179704	meprin A; alpha (PABA peptide hydrolase)	0.18
130455	X17059	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	0.18
131734	D62965	Hs.31297	ESTs	0.18
100749	HG3521-HT3715		Ras-Related Protein Rap1b	0.18
116724	F13665	Hs.65641	ESTs	0.18
129265	X68277	Hs.171695	dual specificity phosphatase 1	0.18
102347	U37518	Hs.83429	tumor necrosis factor (ligand) superfami	0.18
114542	AA055768	Hs.122576	ESTs	0.18
123900	AA621223	Hs.112953	EST	0.19
121780	AA422086	Hs.124660	ESTs	0.19
115662	AA405715	Hs.64179	hypothetical protein	0.19
113803	W42789	Hs.31446	ESTs	0.19
105493	AA256268	Hs.10283	ESTs	0.19
113195	T57112		yc20g11.s1 Stratagene lung (#937210) Hom	0.19
129462	D84239	Hs.111732	IgG Fc binding protein	0.19
133664	X86693	Hs.75445	hevin	0.2
126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske	0.2
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	0.2
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.2
101367	M12963	Hs.73843	alcohol dehydrogenase 1 (class I); alpha	0.2
132254	L20826	Hs.430	plastin 1 (I isoform)	0.2
105646	AA282147	Hs.5888	ESTs	0.2
132883	AA047151	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	0.21
132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma	0.21
108931	AA147186	Hs.250746	ESTs	0.22
131421	X64177	Hs.2667	metallothionein 1H	0.22
107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.22
103576	Z26317	Hs.2631	desmoglein 2	0.22
105173	AA182030	Hs.8364	ESTs	0.22
134843	H60595	Hs.90061	progesterone binding protein	0.22
102009	U02680	Hs.82643	protein tyrosine kinase 9	0.23
123997	D51171	Hs.78902	voltage-dependent anion channel 2	0.23
106609	AA458652	Hs.32181	ESTs	0.23
101300	L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment	0.23
129717	AA481670	Hs.12150	ESTs; Weakly similar to retinal short-ch	0.23
108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.23
121314	AA402799	Hs.182538	ESTs	0.23
124803	R45480	Hs.164866	cyclin K	0.23
130208	AA620556	Hs.15250	peroxisomal D3;D2-enoyl-CoA isomerase	0.23
132888	AA490775	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	0.23
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	0.23
102239	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	0.23
115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	0.24
130558	H96654	Hs.15984	ESTs; Weakly similar to gene pp21 protei	0.24
122666	AA455052	Hs.99387	ESTs	0.24
134495	D63477	Hs.84087	KIAA0143 protein	0.24
124017	F02202	Hs.100960	ESTs	0.24
106925	AA491261	Hs.37558	Homo sapiens clone 23923 mRNA sequence	0.24
115187	AA261805	Hs.44021	ESTs	0.24
105309	AA233790	Hs.4104	ESTs; Weakly similar to cDNA EST yk386g7	0.24
124457	N50114	Hs.128704	ESTs	0.24
130616	AA233763	Hs.16726	Homo sapiens mRNA; cDNA DKFZp564A132 (fr	0.25
105795	AA369245	Hs.17448	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.25
134579	N23222	Hs.85963	CD36 antigen (collagen type I receptor;	0.25

Table 13: H chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete_Title	Ratio Met/Normal
102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	8.457
111307	N73988	Hs.37477	ESTs; Weakly similar to CGI-141 protein	6.05
103119	X63629	Hs.2877	cadherin 3; P-cadherin (placental)	5.207
131564	AA491465	Hs.28792	ESTs	5.136
119729	W69747	Hs.94806	KIAA1062 protein	4.667
124059	F13673	Hs.99769	ESTs	4.398
123987	C21171	Hs.95497	ESTs; Weakly similar to GLUCOSE TRANSPOR	4.292
128817	N47524	Hs.28491	spermidine/spermine N1-acetyltransferase	3.964
133770	M69197	Hs.242279	haptoglobin-related protein	3.823
130412	AA406554	Hs.241572	golgi autoantigen; golgin subfamily a; 5	3.719
104755	AA024482	Hs.9029	DKFZP434G032 protein	3.702
132676	AA283035	Hs.54813	ESTs	3.645
134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	3.581
124690	R05818	Hs.173830	ESTs	3.446
106949	AA496805	Hs.177425	KIAA0964 protein	3.42
130724	AA370091	Hs.179680	ESTs	3.402
128992	R49693	Hs.107708	ESTs	3.32
133421	AA436560	Hs.7327	claudin 1	3.255
103047	X55990	Hs.73839	ribonuclease; RNase A family; 3 (eosinop	3.229
102990	X51441	Hs.181062	serum amyloid A1	3.149
115429	AA284139	Hs.89295	EST	3.114
129158	J05257	Hs.109	dipeptidase 1 (renal)	3.019
123533	AA608751	Hs.244904	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.011

Table 14: H chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

PkeyY	Ex Accn	UniG_ID	Complete_Title	Ratio Met/Normal
103466	Y00339	Hs.155097	carbonic anhydrase II	0.012
104258	AF007216	Hs.5462	solute carrier family 4; sodium bicarbon	0.025
108999	AA156064	Hs.72115	ESTs	0.034
101046	K01160		Accession not listed in Genbank	0.041
133565	H57056	Hs.204831	ESTs	0.042
101346	L76465	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.043
102095	U11313	Hs.75760	sterol carrier protein 2	0.054
111855	R37362	Hs.21351	ESTs	0.055
130320	U19495	Hs.237356	stromal cell-derived factor 1	0.058
123137	AA487468	Hs.100686	ESTs; Weakly similar to secreted cement	0.06
107222	D51235	Hs.82689	tumor rejection antigen (gp96) 1	0.06
102638	U67319	Hs.9216	caspase 7; apoptosis-related cysteine pr	0.063
128906	AA487557	Hs.10706	ESTs	0.065
129105	AA224351	Hs.108681	ESTs	0.069
110837	N30796	Hs.17424	ESTs; Weakly similar to semaphorin F [H.	0.069
100116	D00654	Hs.77443	actin; gamma 2; smooth muscle; enteric	0.071
116786	H25836	Hs.83429	tumor necrosis factor (ligand) superfami	0.074
130867	J04093	Hs.2056	UDP glycosyltransferase 1	0.075
132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.076
131861	D11925	Hs.184245	KIAA0929 protein Msx2 interacting nuclea	0.081
106674	AA461303	Hs.7946	DKFZP586D1519 protein	0.084
109272	AA195718	Hs.86030	ESTs	0.088
132711	N73702	Hs.238927	ESTs	0.091
106569	AA455983	Hs.117816	sorcin	0.092
104636	AA004415	Hs.106106	ESTs	0.093
118823	N79237	Hs.50813	ESTs; Weakly similar to long chain fatty	0.094
134534	X73501	Hs.84905	H. Sapiens mRNA for cytokeratin 20	0.095
119479	W32094	Hs.55501	ESTs	0.096
113778	W15263	Hs.5422	ESTs	0.098
128482	U83908	Hs.100407	programmed cell death 4	0.102
124653	N92884	Hs.109641	ESTs	0.106
133407	AA093348	Hs.7306	secreted frizzled-related protein 1	0.108
135237	AA454930	Hs.9691	ESTs	0.109
116250	AA480975	Hs.44829	ESTs	0.111
132617	AA171913	Hs.5338	carbonic anhydrase XII	0.112
131273	AA421139	Hs.173542	ESTs	0.113
116710	F10577	Hs.70312	ESTs	0.114
131791	S71043	Hs.32225	immunoglobulin alpha 1	0.114
112483	R66534	Hs.28403	ESTs	0.115
132017	W67251	Hs.37331	Homo sapiens vav 3 oncogene (VAV3) mRNA	0.116
124308	H93575	Hs.227146	Homo sapiens mRNA; cDNA DKFZp564J142 (fr	0.117
114846	AA234929	Hs.44343	ESTs	0.119
116551	D20458	Hs.229071	EST	0.12
105299	AA233511	Hs.194720	ATP-binding cassette; sub-family G (WHIT	0.122
130366	L11708	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.122
133806	M12759	Hs.76325	Human Ig J chain gene	0.122
104776	AA026349	Hs.31412	ESTs	0.125
129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.125
131272	AA423884	Hs.139033	paternally expressed gene 3	0.127
105774	AA348014	Hs.23412	ESTs	0.128
134604	M22995	Hs.865	RAP1A; member of RAS oncogene family	0.128
134711	X04011	Hs.88974	cytochrome b-245; beta polypeptide (chro	0.128
129113	AA147646	Hs.108740	DKFZP586A0522 protein	0.133
123995	D51119	Hs.100090	tetraspan 3	0.133
129168	T90621	Hs.109052	chromosome 14 open reading frame 2	0.133
123891	AA621103	Hs.99216	ESTs; Moderately similar to !!!! ALU SUB	0.135
132694	M60830	Hs.5509	ecotropic viral integration site 2B	0.135
135342	W60097	Hs.99120	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	0.135
131510	AA207114	Hs.27842	ESTs; Weakly similar to similar to 1-acy	0.137
133652	AA287383	Hs.7540	ESTs	0.137
134749	L10955	Hs.89485	carbonic anhydrase IV	0.139
106586	AA456598	Hs.256269	ESTs	0.139

106893	AA489636	Hs.25253	ESTs	0.139	
101070	L02785	Hs.1650	down-regulated in adenoma	0.14	
114293	Z40718	Hs.20196	adenylate cyclase 9	0.14	
113966	W86600	Hs.9842	ESTs	0.141	
101185	L19872	Hs.170087	aryl hydrocarbon receptor	0.145	
131492	AA393876	Hs.1255	nuclear receptor subfamily 2; group F; m	0.145	
133889	AA099391	Hs.211582	myosin; light polypeptide kinase	0.145	
120914	AA377254	Hs.97107	EST	0.147	
118771	N74690	Hs.50547	ESTs	0.149	
105496	AA256323	Hs.25264	DKFZP434N126 protein	0.151	
131011	R41771	Hs.22146	ESTs	0.153	
106210	AA428239	Hs.10338	ESTs	0.154	
114069	Z38161	Hs.197335	plasma glutamate carboxypeptidase	0.154	
133011	AA042990	Hs.171921	sema domain; immunoglobulin domain (Ig);	0.154	
115967	AA446887	Hs.42911	ESTs	0.154	
102571	U60115		Homo sapiens skeletal muscle LIM-protein	0.155	
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	0.155	
132903	AA235404	Hs.5985	Homo sapiens clone 25186 mRNA sequence	0.155	
125832	AA628600	Hs.117587	ESTs	0.155	
130064	T67053	Hs.181125	immunoglobulin lambda gene cluster	0.157	
123264	AA491003	Hs.99824	BCE-1 protein	0.159	
130919	AA291710	Hs.21276	collagen; type IV; alpha 3 (Goodpasture	0.159	
103542	Z11793	Hs.3314	selenoprotein P; plasma; 1	0.161	
101478	M23379	Hs.758	RAS p21 protein activator (GTPase activa	0.162	
108921	AA142913	Hs.71721	ESTs	0.164	
100642	HG2743-HT3926		Caldesmon 1, Alt. Splice 6, Non-Muscle	0.167	
132109	AA599801	Hs.40098	ESTs	0.167	
115719	AA416997	Hs.59622	ESTs	0.169	
128915	C02386	Hs.107139	ESTs	0.171	
117634	N36421	Hs.107854	ESTs; Weakly similar to SODIUM- AND CHLO		0.172
129462	D84239	Hs.111732	IgG Fc binding protein	0.174	
131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.176	
130343	AA490262	Hs.15485	ESTs; Weakly similar to APICAL-LIKE PROT	0.177	
115764	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	0.177	
122261	AA436830	Hs.98902	ESTs	0.179	
106605	AA457718	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr		0.179
109991	H09813	Hs.12896	KIAA1034 protein	0.181	
101300	L40391	Hs.6445	Homo sapiens (clone s153) mRNA fragment	0.181	
123080	AA485303	Hs.205126	polymeric immunoglobulin receptor	0.182	
130016	AA055811	Hs.143131	transmembrane glycoprotein	0.186	
122666	AA455052	Hs.99387	ESTs	0.188	
105453	AA252893	Hs.9001	ESTs	0.189	
108980	AA151676	Hs.33455	peptidyl arginine deiminase; type II	0.19	
100248	D31888	Hs.78398	KIAA0071 protein	0.192	
130036	AA195260	Hs.206738	ESTs; Moderately similar to !!!! ALU SUB	0.192	
110882	N36001	Hs.17348	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.193	
131676	C20785	Hs.30514	ESTs	0.195	
111029	N54792	Hs.24697	cytidine monophosphate-N-acetylneuramini	0.196	
131257	AA256042	Hs.24908	ESTs	0.196	
133348	T23517	Hs.7149	ESTs	0.196	
133784	AA214305	Hs.76173	ESTs	0.196	
113863	W68388	Hs.21288	ESTs; Weakly similar to KIAA0704 protein	0.197	
103158	X67235	Hs.118651	hematopoietically expressed homeobox	0.198	
102347	U37518	Hs.83429	tumor necrosis factor (ligand) superfami	0.2	
111351	N90223	Hs.23392	ESTs	0.2	
123495	AA599850	Hs.106747	ESTs; Weakly similar to similar to BPTI/	0.2	
123802	AA620448	Hs.61408	Homo sapiens clone 24760 mRNA sequence	0.2	
129243	H88033	Hs.109727	KIAA0733 protein	0.2	
130219	R77539	Hs.15285	ESTs	0.2	
131171	H04644	Hs.167619	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.2	
133746	U44378	Hs.75862	MAD (mothers against decapentaplegic; Dr	0.2	
116459	AA621399	Hs.64193	ESTs	0.201	
109613	F03031	Hs.27519	ESTs	0.202	
133435	T23983	Hs.7365	ESTs	0.202	
103002	X52001	Hs.1408	endothelin 3	0.204	
125153	W38294		Accession not listed in Genbank	0.204	
131919	AA121266	Hs.34641	ESTs	0.204	
100749	HG3521-HT3715		Ras-Related Protein Rap1b	0.205	
105085	AA147537	Hs.4811	ESTs	0.208	
124571	N67470	Hs.173074	DKFZP564O1863 protein	0.21	
129519	AA298786	Hs.112242	ESTs	0.21	
116724	F13665	Hs.65641	ESTs	0.21	
132932	T15482	Hs.6093	ESTs	0.21	
113803	W42789	Hs.31446	ESTs	0.211	
110792	N24899	Hs.6630	ESTs	0.212	
105178	AA187490	Hs.21941	ESTs	0.212	

107295	T34527	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.212
115262	AA279112	Hs.88594	ESTs	0.213
115839	AA429038	Hs.40541	ESTs	0.213
103211	X73079	Hs.205126	polymeric immunoglobulin receptor	0.214
108604	AA099820	Hs.49696	ESTs	0.215
105173	AA182030	Hs.8364	ESTs	0.217
108539	AA084677	Hs.54558	ESTs; Weakly similar to protein B [H.sap	0.217
109984	H09594	Hs.10299	ESTs	0.217
133536	Y00264	Hs.177486	amyloid beta (A4) precursor protein (pro	0.217
129965	T71333	Hs.13854	ESTs	0.219
114542	AA055768	Hs.122576	ESTs	0.219
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	0.22
101809	M86849		Homo sapiens connexin 26 (GJB2) mRNA, co	0.222
105795	AA369245	Hs.17448	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.222
132119	H99211	Hs.40334	ESTs	0.222
132733	R25385	Hs.123654	KIAA0824 protein	0.222
109415	AA227219	Hs.110826	trinucleotide repeat containing 9	0.222
113083	T40530	Hs.8241	ESTs; Weakly similar to heat shock prote	0.223
107053	AA600147	Hs.5741	ESTs; Weakly similar to NADH-cytochrome	0.224
103653	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.225
104613	AA001049	Hs.24713	Homo sapiens mRNA; cDNA DKFZp586G0123 (f	0.225
126180	R18070	Hs.3712	ubiquinol-cytochrome c reductase; Rieske	0.227
132015	D11900	Hs.3731	ESTs	0.227
130616	AA233763	Hs.16726	Homo sapiens mRNA; cDNA DKFZp564A132 (fr	0.227
132883	AA047151	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	0.23
123169	AA488892	Hs.104472	ESTs; Weakly similar to Gag-Pol polyprot	0.233
115187	AA261805	Hs.44021	ESTs	0.234
116787	H28581	Hs.15641	ESTs	0.234
113195	T57112		yc20g11.s1 Stratagene lung (#937210) Hom	0.235
130707	W45457	Hs.203559	ESTs	0.235
124803	R45480	Hs.164866	cyclin K	0.235
116844	H64938	Hs.38331	ESTs	0.235
102759	U81607	Hs.788	A kinase (PRKA) anchor protein (gravin)	0.238
130584	AA009839	Hs.180841	tumor necrosis factor receptor superfami	0.238
133240	D31161	Hs.68613	ESTs	0.238
132952	AA425154	Hs.61426	ESTs	0.239
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	0.24
131734	D62965	Hs.31297	ESTs	0.24
111890	R38678	Hs.12365	ESTs	0.241
102325	U35139	Hs.50130	necdin (mouse) homolog	0.244
104968	AA084602	Hs.29669	ESTs	0.244
105674	AA284755	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	0.244
120519	AA258585	Hs.129887	cadherin 19 (NOTE: redefinition of symbo	0.244
134675	AA250745	Hs.87773	protein kinase; cAMP-dependent; catalyti	0.244
130642	M63438	Hs.156110	Immunoglobulin kappa variable 1D-8	0.245
134418	R78190	Hs.82933	ESTs; Weakly similar to cDNA EST EMBL:T0	0.245
115137	AA257976	Hs.56156	ESTs	0.245
131713	X57809	Hs.181125	immunoglobulin lambda gene cluster	0.246
108931	AA147186	Hs.250746	ESTs	0.246
106609	AA458652	Hs.32181	ESTs	0.248
115559	AA393810	Hs.41067	ESTs	0.25
133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec	0.25
134088	D43636	Hs.79025	KIAA0096 protein	0.25
134487	R38185	Hs.83954	Homo sapiens unknown mRNA	0.25

Table 15: I chip – Met vs Normal query – up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	Title	Ratio Met/Normal
319379	T91443	Hs.193963	ESTs	18.71
321920	N63915		EST cluster (not in UniGene)	11.9
314522	AI732331	Hs.187750	ESTs; Moderately similar to !!!! ALU CLA	7.23
315720	AW291875	Hs.163900	ESTs	6.06
308010	AI439190	Hs.181165	eukaryotic translation elongation factor	5.76
313774	AW136836	Hs.144583	ESTs	5.01
300734	AW205197	Hs.240951	ESTs	3.98
337895			CH22_EM:AC005500.GENSCAN.56-2	3.98
312339	AA524394		EST cluster (not in UniGene)	3.66
331644	T99544	Hs.173734	ESTs; Weakly similar to !!!! ALU CLASS B	3.53
324643	AI436356	Hs.130729	ESTs	3.52
324302	AA543008	Hs.136806	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.41
314912	AI431345	Hs.161784	ESTs	3.33
319403	T98413		EST cluster (not in UniGene)	3.32
308676	AI761036		EST singleton (not in UniGene) with exon	3.27
331858	AA421163	Hs.163848	ESTs	3.22
315178	AW362945	Hs.162459	ESTs	3.21
321354	AA078493		EST cluster (not in UniGene)	3.18
337898			CH22_EM:AC005500.GENSCAN.56-5	3.16
322682	AI110679		EST cluster (not in UniGene)	3.15
313197	AI738851	Hs.222487	ESTs	3.1
308991	AI879831		EST singleton (not in UniGene) with exon	3.08
310016	AW449612	Hs.152475	ESTs	3.05

Table 16: I chip – Met vs Normal query – down in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex_Accn	UniG_ID	title	Ratio Met/Normal
303041	AF127035		EST cluster (not in UniGene) with exon h	0.02
302360	AJ010901	Hs.198267	mucin 4; tracheobronchial	0.03
301948	AA344647	Hs.116724	aldo-keto reductase family 1; member B11	0.03
336091			CH22_FGENES.689_3	0.04
333657			CH22_FGENES.241_2	0.04
333658			CH22_FGENES.241_4	0.04
333737			CH22_FGENES.261_1	0.05
333656			CH22_FGENES.240_4	0.05
302347	AF039400	Hs.194659	chloride channel; calcium activated; fam	0.06
336084			CH22_FGENES.688_13	0.06
330385	AA449749	Hs.31386	ESTs; Highly similar to secreted apoptos	0.06
304487	AA434241		EST singleton (not in UniGene) with exon	0.07
302292	AF067797		EST cluster (not in UniGene) with exon h	0.07
334030			CH22_FGENES.320_2	0.07
332859			CH22_FGENES.27_2	0.07
333654			CH22_FGENES.240_2	0.07
303270	AL120518	Hs.105352	ESTs	0.08
320352	Y13323	Hs.145296	disintegrin protease	0.08
333637			CH22_FGENES.229_2	0.08
324094	AA382603		EST cluster (not in UniGene)	0.08
320590	U67058	Hs.168102	Human proteinase activated receptor-2 mR	0.08
330622	X63597	Hs.2996	sucrase-isomaltase	0.08
331441	H75860	Hs.39720	ESTs	0.08
308601	AI719930		EST singleton (not in UniGene) with exon	0.09
323770	AA722425		EST cluster (not in UniGene)	0.09
335188			CH22_FGENES.507_3	0.09
333730			CH22_FGENES.258_1	0.09
304480	AA430373		EST singleton (not in UniGene) with exon	0.09
336081			CH22_FGENES.688_10	0.1
332071	AA598594	Hs.112475	ESTs	0.1
318538	N28625	Hs.74034	caveolin 1; caveolae protein; 22kD	0.1
311331	AI679622	Hs.32225	immunoglobulin alpha 1	0.1
319668	NM_002731		EST cluster (not in UniGene)	0.11
332567	N23730	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	0.11
319395	AW062570	Hs.13809	ESTs	0.11
315594	AI983437	Hs.155145	ESTs	0.11
321539	N98619	Hs.62461	ARP2 (actin-related protein 2; yeast) ho	0.12
333647			CH22_FGENES.235_2	0.12
333588			CH22_FGENES.206_2	0.12
321286	AI380940		EST cluster (not in UniGene)	0.12
320727	U96044		EST cluster (not in UniGene)	0.13
335687			CH22_FGENES.596_2	0.13
324611	AA743462	Hs.165337	ESTs	0.14
335115			CH22_FGENES.496_2	0.14
324660	AA541644	Hs.186044	ESTs	0.14
337951			CH22_EM:AC005500.GENSCAN.94-1	0.14
302332	AI833168	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.14
300921	AW293224	Hs.232165	ESTs	0.14
333646			CH22_FGENES.234_2	0.14
335116			CH22_FGENES.496_3	0.14
320211	AL039402	Hs.125783	DEME-6 protein	0.15
336092			CH22_FGENES.689_6	0.15
330673	D57823	Hs.92962	Sec23 (S. cerevisiae) homolog A	0.16
303042	AF129532		EST cluster (not in UniGene) with exon h	0.16
337954			CH22_EM:AC005500.GENSCAN.96-3	0.16
336645			CH22_FGENES.26-1	0.16
335651			CH22_FGENES.590_2	0.16
314499	AL044570	Hs.147975	ESTs	0.17
336124			CH22_FGENES.701_9	0.17
315199	AA877996	Hs.125376	ESTs	0.17
324525	AW044647	Hs.196284	ESTs	0.17
320825	NM_004751		EST cluster (not in UniGene)	0.18

302049	AA377072	Hs.129792	Homo sapiens Chromosome 16 BAC clone CIT	0.18
336083			CH22_FGENES.688_12	0.18
333653			CH22_FGENES.239_2	0.18
323243	W44372		EST cluster (not in UniGene)	0.19
316610	AW087973	Hs.126731	ESTs	0.19
315033	AI493046	Hs.146133	ESTs	0.19
330551	U39840	Hs.105440	hepatocyte nuclear factor 3; alpha	0.19
333642			CH22_FGENES.231_2	0.19
301281	AA843986	Hs.190586	ESTs	0.2
333626			CH22_FGENES.224_2	0.21
303792	C75094	Hs.199839	ESTs; Highly similar to NG22 [H.sapiens]	0.21
332325	T79428	Hs.191264	ESTs	0.21
321223	AA431366		EST cluster (not in UniGene)	0.21
333635			CH22_FGENES.228_2	0.22
314645	AI808999	Hs.207570	ESTs	0.22
322929	AI365585	Hs.146246	ESTs	0.22
324718	AI557019	Hs.116467	ESTs	0.22
335652			CH22_FGENES.590_3	0.22
307783	AI347274		EST singleton (not in UniGene) with exon	0.22
331344	AA357927	Hs.70208	ESTs	0.22
336088			CH22_FGENES.688_17	0.23
320802	D83824	Hs.185055	BENE protein	0.23
335692			CH22_FGENES.596_7	0.23
333593			CH22_FGENES.210_2	0.23
335667			CH22_FGENES.590_18	0.24
314853	AA729232	Hs.153279	ESTs	0.24
320244	AA296922	Hs.129778	gastrointestinal peptide	0.24
300601	AI762130	Hs.165619	ESTs	0.24
305080	AA641485		EST singleton (not in UniGene) with exon	0.25
335189			CH22_FGENES.507_4	0.25

Table 17: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met
101006	J04132	Hs.97087	CD3Z antigen; zeta polypeptide (TiT3 com	7.28
114173	Z39050	Hs.21963	ESTs	6.13
130284	X82206	Hs.153961	ARP1 (actin-related protein 1; yeast) ho	5.77
100787	HG3872-HT4142		Immunoglobulin Gamma Heavy Chain, V(6)Djc Regions (Gb:U13200)	5.63
132461	AA405775	Hs.49005	hypothetical protein	5.62
133806	M12759	Hs.76325	Human Ig J chain gene	5.46
133747	D86972	Hs.75863	KIAA0218 gene product	5.45
123328	AA496968	Hs.105403	EST	5.28
132671	X76302	Hs.54649	putative nucleic acid binding protein RY	5.25
132018	AA293194	Hs.3737	ESTs	5.22
100186	D17516	Hs.4748	adenylate cyclase activating polypeptide	5.14
107155	AA621202	Hs.7946	DKFZP586D1519 protein	5.1
103566	Z22555	Hs.180616	CD36 antigen (collagen type I receptor;	5.06
113355	T79203	Hs.14480	ESTs	4.99
129040	U38864	Hs.108139	zinc finger protein 212	4.96
130214	H78003	Hs.15266	ESTs	4.93
129550	AA480991	Hs.113025	ESTs	4.92
129704	W81301	Hs.12064	ubiquitin specific protease 22	4.91
116425	AA609574	Hs.51483	ESTs	4.77
105166	AA179787	Hs.30570	polyglutamine binding protein 1	4.65
118765	N74442	Hs.183696	ESTs	4.6
108999	AA156064	Hs.72115	ESTs	4.57
112756	R93908	Hs.35258	ESTs	4.54
111655	R16884	Hs.187462	ESTs	4.48
119392	T90672	Hs.238859	ESTs	4.42
131957	AA609008	Hs.183232	ESTs	4.41
129275	D82061	Hs.109993	Ke6 gene; mouse; human homolog of	4.4
113634	T95085	Hs.125182	ESTs	4.4
127187	AA297138	Hs.207422	ESTs	4.32
101147	L13266	Hs.105	glutamate receptor; ionotropic; N-methyl	4.3
134901	S78873	Hs.90875	RAB interacting factor	4.26
100896	HG4593-HT4998		Sodium Channel 1	4.24
100687	HG3115-HT3291		Golli-Mbp (Gb:L18862)	4.21
129758	AA599552	Hs.183770	Homo sapiens mRNA; cDNA DKFZp566P2346 (f	4.19
105440	AA252243	Hs.22851	ESTs	4.16
131551	AA127867	Hs.28608	ESTs	4.15
113761	T99373	Hs.189786	ESTs	4.09
105897	AA401091		ESTs	4.07
129495	AA382529	Hs.239676	ESTs	4.06
103436	X98206		H.sapiens mRNA for UV-B repressed sequen	4.03
104673	AA007633	Hs.20010	ESTs	4.03
128886	L36720	Hs.106880	bystin-like	4.02
100702	HG3236-HT3413		Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)	3.99
123547	AA608820	Hs.124085	KIAA0921 protein	3.98
134877	AA455241	Hs.90527	ESTs	3.97
123650	AA609332	Hs.180696	ESTs	3.94
106482	AA451672	Hs.108824	ESTs; Weakly similar to cDNA EST yk415c1	3.94
101909	S69265		Homo sapiens mRNA for PLE21 protein; com	3.93
108390	AA075070		zm86b6.s1 Stratagene ovarian cancer (#93 LYMPHOCYTE ANTIGEN LY-6A.2/LY-6E.1 PREC	3.93
135403	U06643	Hs.99923	lectin; galactoside-binding; soluble; 7	3.89
121038	AA398536	Hs.97365	ESTs	3.88
128496	T83496	Hs.100610	ESTs	3.86
108785	AA128946		ESTs	3.86
119838	W79499	Hs.58580	ESTs	3.85
130109	L12060	Hs.1497	retinoic acid receptor; gamma	3.84
134538	U79288	Hs.85053	KIAA0513 gene product	3.83
110310	H38209	Hs.32728	EST	3.81
110433	H49425	Hs.32992	ESTs	3.78
111834	R36138	Hs.152458	ESTs	3.76
130903	N27086	Hs.21068	ESTs	3.74
105142	AA164851	Hs.15380	ESTs; Weakly similar to HERV-E envelope	3.73

130248	U84569	Hs.153452	chromosome 21 open reading frame 2	3.73
130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA	3.73
123378	AA521043	Hs.185832	ESTs	3.73
103985	AA313880		EST185737 Colon carcinoma (HCC) cell lin	3.73
112397	R60822	Hs.26805	EST	3.72
100980	J03069	Hs.72931	v-myc avian myelocytomatosis viral oncog	3.72
102609	U64863	Hs.158297	programmed cell death 1	3.7
108974	AA151402	Hs.46531	ESTs	3.7
130192	Y12661	Hs.171014	VGF nerve growth factor inducible	3.69
131318	X51699	Hs.2558	bone gamma-carboxyglutamate (gla) protei	3.68
113759	T99364	Hs.16074	Homo sapiens mRNA; cDNA DKFZp564I153 (fr	3.66
133712	L19267	Hs.198836	dystrophia myotonica-containing WD repea	3.65
134229	R15108	Hs.8037	ESTs	3.65
134241	AA300265	Hs.80540	KIAA0195 gene product	3.65
124699	R06413	Hs.112278	arrestin; beta 1	3.62
107343	U03115	Hs.103945	Human V beta T-cell receptor (TCRBV) gen	3.62
128511	AA425636	Hs.10082	potassium intermediate/small conductance	3.62
105466	AA253412	Hs.21489	ESTs	3.61
131377	R41389	Hs.26159	ESTs	3.6
119135	R49548	Hs.169681	death effector domain-containing	3.6
132982	L02326	Hs.198118	immunoglobulin lambda-like polypeptide 2	3.59
128514	H84261	Hs.100843	ESTs; Weakly similar to similar to GTP-b	3.56
102396	U41804	Hs.54411	putative T1/ST2 receptor binding protein	3.55
134945	R50247	Hs.91600	ESTs	3.55
134913	X60483	Hs.91031	H4 histone family; member D	3.54
102053	U07664	Hs.37035	homeo box HB9	3.52
121569	AA412686	Hs.97955	ESTs	3.52
132560	AA005315	Hs.204524	ESTs; Weakly similar to KIAA0747 protein	3.51
118456	N66580	Hs.161496	EST; Weakly similar to HC1 ORF [M.muscul	3.51
111518	R08160	Hs.222529	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.51
116795	H38858	Hs.251783	EST	3.5
130377	AA378316	Hs.155182	KIAA1036 protein	3.5
121774	AA421758	Hs.98361	ESTs	3.49
123413	AA521448	Hs.103845	ESTs	3.49
133798	AA444115	Hs.76277	ESTs; Weakly similar to salivary proline	3.49
135183	X93996	Hs.239663	myeloid/lymphoid or mixed-lineage leukem	3.48
132479	AA477715	Hs.4953	golgi autoantigen; golgin subfamily a; 3	3.47
117191	H99394	Hs.40339	EST	3.47
130942	X87852	Hs.21432	H.sapiens mRNA for SEX gene	3.46
130700	D55696	Hs.18069	protease; cysteine; 1 (legumain)	3.43
131301	T17386	Hs.164501	ESTs	3.43
100818	HG4018-HT4288		Opioid-Binding Cell Adhesion Molecule	3.43
103393	X94612	Hs.41749	protein kinase; cGMP-dependent; type II	3.43
131337	AA228116	Hs.170204	KIAA0551 protein	3.42
133403	X68688	Hs.72991	zinc finger protein 33b (KOX 31)	3.42
124728	R16231	Hs.106620	Homo sapiens clone 23950 mRNA sequence	3.41
123168	AA488881	Hs.105218	EST	3.39
123324	AA496932	Hs.105399	KIAA0809 protein	3.38
106947	AA496685	Hs.37936	suppressor of variegation 3-9 (Drosophil	3.38
116717	F11065	Hs.79363	ESTs	3.36
102794	U88629	Hs.173334	ELL-RELATED RNA POLYMERASE II; ELONGATIO	3.34
117503	N31963	Hs.44286	ESTs	3.33
112220	R50295	Hs.25703	ESTs	3.33
106340	AA441792	Hs.22857	chord domain-containing protein 1	3.33
106308	AA436186	Hs.30662	ESTs	3.32
130894	D16105	Hs.210	leukocyte tyrosine kinase	3.31
120039	W92548	Hs.94985	ESTs	3.31
131428	U17838	Hs.26719	PR domain containing 2; with ZNF domain	3.3
113285	T66830	Hs.182712	ESTs	3.3
109458	AA232648	Hs.87068	ESTs	3.29
132134	AA242904	Hs.40637	proline-rich Gla (G-carboxyglutamic acid	3.29
118964	N93330	Hs.54937	Homo sapiens clone 24722 unknown mRNA; p	3.29
127621	AI218205	Hs.116204	ESTs	3.29
135149	U40002	Hs.95351	lipase; hormone-sensitive	3.28
114371	Z41835	Hs.27810	ESTs	3.28
130043	AA055404	Hs.193953	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.27
121347	AA405181	Hs.97972	ESTs	3.25
105754	AA302657	Hs.192028	ESTs	3.25
121327	AA404286	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.25
111204	N68295	Hs.37982	ESTs	3.25
120949	AA397830	Hs.98347	ESTs; Weakly similar to GLIOMA PATHOGENE	3.25
130024	U15197	Hs.241560	Human histo-blood group ABO protein mRNA	3.24
125005	T61449	Hs.193727	ESTs	3.24
121067	AA398662	Hs.97302	ESTs	3.24
120996	AA398281	Hs.143684	ESTs	3.23
117101	H94043	Hs.24341	DKFZP586I1419 protein	3.23

130708	U40490	Hs.18136	nicotinamide nucleotide transhydrogenase	3.23
130270	L40399	Hs.153820	hypothetical protein	3.22
131605	AA256220	Hs.29383	ESTs	3.22
100854	HG4194-HT4464		Sodium/Hydrogen Exchanger 5	3.22
123026	AA481072	Hs.99743	ESTs	3.21
108328	AA070204		zm68b3.s1 Stratagene neuroepithelium (#9	3.2
104259	AF007833	Hs.159265	Homo sapiens kruppel-related zinc finger	3.2
133711	J04130	Hs.75703	small inducible cytokine A4 (homologous	3.2
112261	R52145	Hs.25894	ESTs; Highly similar to hypothetical pro	3.19
119529	W38053		Accession not listed in Genbank	3.19
122386	AA446221	Hs.6092	F-box protein containing leucine-rich re	3.19
109157	AA179161	Hs.73562	ESTs	3.19
119903	W85707	Hs.75936	erythrocyte membrane protein band 4.9 (d	3.18
127452	AA491317		aa65c01.r1 NCI_CGAP_GCB1 Homo sapiens cD	3.18
124229	H62793	Hs.221892	ESTs	3.18
129221	AA417126	Hs.109571	translocase of inner mitochondrial membr	3.17
133185	AA481404	Hs.6686	ESTs	3.16
121479	AA411911	Hs.98110	ESTs	3.16
133872	T79868	Hs.180903	hypothetical protein	3.16
132504	U12897	Hs.5022	imprinted in Prader-Willi syndrome	3.16
103089	X60382	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	3.15
129654	AA019943	Hs.118463	H.sapiens mRNA for unknown liver orphan	3.15
117295	N22360	Hs.43153	ESTs	3.15
107349	U48224	Hs.158321	beaded filament structural protein 2; ph	3.14
103451	X99459	Hs.154782	adaptor-related protein complex 3; sigma	3.14
114854	AA235056	Hs.120244	ESTs	3.14
121044	AA398551	Hs.97374	ESTs	3.13
128582	U22963	Hs.101840	major histocompatibility complex; class	3.13
112598	R78565	Hs.138395	EST	3.13
113170	T54342	Hs.222506	ESTs	3.13
111714	R23146	Hs.23466	ESTs	3.13
111809	R33616	Hs.24688	EST	3.12
115249	AA278961	Hs.71124	ESTs	3.11
103228	X75546	Hs.230	fibromodulin	3.11
129944	L00389	Hs.1361	cytochrome P450; subfamily I (aromatic c	3.11
107927	AA028915	Hs.237709	EST	3.11
130297	H94949	Hs.171955	trophinin-assisting protein (tastin)	3.1
125742	H81181	Hs.183654	ESTs; Weakly similar to unknown [S.cerev	3.1
134802	L35546	Hs.89709	glutamate-cysteine ligase (gamma-glutamy	3.1
112560	R72293	Hs.6179	Homo sapiens mRNA; cDNA DKFZp586K2322 (f	3.1
129266	AA343881	Hs.209061	sudD (suppressor of bimD6; Aspergillus n	3.09
126982	AA211419		small inducible cytokine A5 (RANTES)	3.09
131594	H29723	Hs.29261	ESTs; Weakly similar to serine protease	3.08
134910	AA431320	Hs.9100	ESTs	3.08
103505	Y09912	Hs.33102	transcription factor AP-2 beta (activati	3.08
110525	H57330	Hs.37430	EST	3.07
123276	AA491270	Hs.187946	ESTs	3.06
130519	H91819	Hs.10669	ESTs; Moderately similar to KIAA0400 [H.	3.06
126621	AA192638		zq01h08.r1 Stratagene muscle 937209 Homo	3.05
134327	AF006041	Hs.178743	death-associated protein 6	3.04
103513	Y10209		H.sapiens mRNA for CD3L protein	3.04
131243	R16667	Hs.24752	spectrin SH3 domain binding protein 1	3.04
115187	AA261805	Hs.44021	ESTs	3.04
107543	Z43703	Hs.4552	Homo sapiens HRIHFB2157 mRNA; partial cd	3.04
134051	S67070	Hs.78846	heat shock 27kD protein 2	3.04
113461	T86737	Hs.193536	ESTs	3.03
130490	X57522	Hs.158164	ATP-binding cassette; sub-family B (MDR/	3.03
128843	AA234141	Hs.203004	katanin p80 (WD40-containing) subunit B	3.03
100941	HG862-HT862		Transition Protein 2	3.03
122268	AA436855	Hs.178202	ESTs	3.02
107425	W26719	Hs.30204	ESTs	3.02
130930	U19261		TNF receptor-associated factor 1	3.02
132958	W90398	Hs.6147	KIAA1075 protein	3.02
100973	J02888	Hs.73956	NAD(P)H menadione oxidoreductase 2; diox	3.01
104924	AA058532	Hs.28774	ESTs	3.01
129998	Y10055	Hs.162808	phosphoinositide-3-kinase; catalytic; de	3.01
130023	X13461	Hs.239600	calmodulin-like 3	3.01
129536	M33493	Hs.184504	tryptase; alpha	3
112015	R42836	Hs.23198	ESTs	3
103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial	2.99
100756	HG3565-HT3768		Zinc Finger Protein (Gb:M88357)	2.99
103425	X97301		H.sapiens mRNA for Ptg-11 protein	2.99
118291	N63076	Hs.138746	EST	2.98
125877	H15229		ym30g04.r1 Soares infant brain 1NIB Homo repetitive element ;, mRNA sequence.	2.98
101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi	2.98

102958	X15675	Hs.93174	Human endogenous retrovirus pHE.1 (ERV9)	2.97
121183	AA400138	Hs.97703	ESTs	2.97
119241	T12559	Hs.221382	ESTs	2.96
115067	AA253458	Hs.91299	postmeiotic segregation increased 2-like	2.96
126196	AA084394		zn05g10.s1 Stratagene hNT neuron (#93723	2.96
111642	R16153	Hs.128740	ESTs; Highly similar to DNb-5 [H.sapiens	2.95
100898	HG4638-HT5050		Spliceosomal Protein Sap 49	2.95
129370	AA287879	Hs.110796	ESTs; Moderately similar to GTP-binding	2.94
128915	C02386	Hs.107139	ESTs	2.94
101868	M96233	Hs.82891	glutathione S-transferase M4	2.94
124394	N29724		gamma2-adaptin	2.93
103559	Z19585	Hs.75774	thrombospondin 4	2.93
107882	AA025630	Hs.17801	ESTs; Moderately similar to serine/proli	2.93
134919	T99639	Hs.91142	KH-type splicing regulatory protein (FUS	2.92
110293	H30258	Hs.37165	collagen; type IX; alpha 2	2.92
132433	AA082546	Hs.48516	ESTs	2.92
127347	AA428350		ESTs	2.92
121976	AA429807	Hs.98632	ESTs	2.91
133025	AA135492	Hs.6318	ESTs; Highly similar to peroxisomal shor	2.91
133413	S72043	Hs.73133	metallothionein 3 (growth inhibitory fac	2.91
111694	R22035	Hs.23331	ESTs	2.91
128369	F12681	Hs.205300	ESTs	2.9
102464	U49260	Hs.3828	mevalonate (diphospho) decarboxylase	2.9
135358	C21431	Hs.99486	ESTs; Weakly similar to aralar1 [H.sapie	2.9
108661	AA113287	Hs.65905	ESTs; Weakly similar to PTB-ASSOCIATED S	2.9
102185	U20230		Human guanyl cyclase C gene, partial cds	2.89
122071	AA431787	Hs.98762	EST	2.89
102040	U06088	Hs.159479	galactosamine (N-acetyl)-6-sulfate sulfa	2.89
115689	AA410645	Hs.199014	ESTs	2.88
135110	T15817	Hs.193788	nitric oxide synthase 2A (inducible; hep	2.88
118729	N73717	Hs.161526	EST	2.88
129518	AA369807	Hs.112238	ESTs	2.88
125788	R74309	Hs.44499	small EDRK-rich factor 2	2.87
128650	U57971	Hs.103124	ATPase; Ca++ transporting; plasma membra	2.87
125936	H30751	Hs.182859	lifeguard	2.87
100779	HG3731-HT4001		Immunoglobulin Heavy Chain, Vdjrc Regions (Gb:L23566)	2.87
104451	M13299	Hs.102119	blue cone pigment	2.86
133539	M21574	Hs.74615	platelet-derived growth factor receptor;	2.86
119506	W37833	Hs.55563	ESTs	2.86
126568	AA190515		zp85d12.r1 Stratagene HeLa cell s3 93721	2.86
134184	X53742	Hs.79732	fibulin 1	2.86
127633	AI339609	Hs.152733	potassium voltage-gated channel; Isk-rel	2.86
128716	AA045978	Hs.173611	NADH dehydrogenase (ubiquinone) Fe-S pro	2.86
107135	AA620782	Hs.23247	ESTs	2.85
117748	N47317	Hs.141858	ESTs	2.85
124030	F04143	Hs.151032	Homo sapiens clone 23856 unknown mRNA; p	2.85
135120	AA449841	Hs.108300	NOT3 (negative regulator of transcriptio	2.84
102156	U17977		HSU17977 Humn fibroblast cDNA H sapiens	2.84
129418	AA401401	Hs.11127	PET112 (yeast homolog)-like	2.84
103222	X74795	Hs.77171	minichromosome maintenance deficient (S.	2.84
125145	W38001		Accession not listed in Genbank	2.83
100560	HG2228-HT2305		Crystallin, Beta B	2.83
105370	AA236476	Hs.22791	ESTs; Weakly similar to transmembrane pr	2.83
127036	AI468598		ESTs	2.83
128788	AA029073	Hs.105685	ESTs	2.83
119523	W38041		Accession not listed in Genbank	2.82
126436	N31224	Hs.211579	melanoma adhesion molecule	2.82
126559	R15866	Hs.170263	tumor protein 53-binding protein; 1	2.82
118183	N59287	Hs.48361	EST	2.82
101298	L40387	Hs.118633	2'-5'oligoadenylate synthetase-like	2.81
131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro	2.81
124173	H41281	Hs.107619	ESTs	2.81
102295	U32581		Homo sapiens KIAA0421 mRNA; partial cds	2.81
129719	N66396	Hs.167766	ESTs; Moderately similar to Pro-a2(XI) [	2.81
126573	AA482023	Hs.155218	E1B-55kDa-associated protein 5	2.81
125477	AI270093	Hs.234642	aquaporin 3	2.81
106492	AA451896	Hs.7922	ESTs; Weakly similar to contains similar p19; an RNA polymerase II elongation fa	2.8
132881	T86118	Hs.58875	ESTs	2.8
114733	AA133778	Hs.95734	ESTs	2.79
104618	AA001611	Hs.186494	ESTs	2.79
134137	F10045	Hs.79347	KIAA0211 gene product	2.79
133212	U82979	Hs.67846	leukocyte Ig-like receptor; subfamily B	2.78
100882	HG4460-HT4729		Immunoglobulin Heavy Chain, Vdjc Regions (Gb:L23564)	2.78
104756	AA024622	Hs.15813	solute carrier family 22 (organic cation	2.78
129861	N69507	Hs.129849	DKFZP564M182 protein	2.78

120824	AA347548	Hs.96876	ESTs	2.78	
100684	HG3107-HT3283		Plasma Membrane Calcium Pump Hpmca2a	2.78	
121789	AA423970	Hs.178111	ESTs	2.78	
101647	M59941	Hs.118200	colony stimulating factor 2 receptor; be	2.78	
113722	T97957	Hs.202948	ESTs; Weakly similar to alternatively sp	2.77	
115107	AA256371	Hs.186645	ESTs	2.77	
111464	R05518	Hs.19521	ESTs	2.77	
108446	AA079120		zm95e1.s1 Stratagene colon HT29 (#937221	2.77	
123921	AA621329	Hs.250671	Hu DNA seq frm clone 1163J1 on chr 22q13 prot (similar to mouse Celsr1; rat MEGF	2.77	
134445	M59488	Hs.83384	S100 calcium-binding protein; beta (neur	2.76	
114132	Z38688	Hs.24192	ESTs	2.76	
120500	AA256430	Hs.132525	ESTs	2.76	
101860	M95610	Hs.37165	collagen; type IX; alpha 2	2.76	
134430	H52105	Hs.8309	KIAA0747 protein	2.76	
124152	H27216	Hs.107635	ESTs	2.76	
132268	AA058833	Hs.23445	ESTs; Weakly smlr to similar to M. muscu	2.76	
116257	AA481493	Hs.88537	ESTs	2.76	
102438	U46570	Hs.7733	tetratricopeptide repeat domain 1	2.75	
122393	AA446334	Hs.99064	ESTs	2.75	
107653	AA010210	Hs.47041	ESTs	2.75	
123674	AA609473	Hs.105187	ESTs; Moderately similar to kinesin like	2.75	
129858	T66906	Hs.12970	ESTs	2.75	
130117	U06641	Hs.150207	UDP glycosyltransferase 2 family; polype	2.75	
133464	M13982	Hs.73917	interleukin 4	2.75	
127039	AA233366	Hs.256491	ESTs	2.74	
128318	AA418202	Hs.13810	ESTs	2.74	
123363	AA504818	Hs.171279	ESTs	2.74	
127654	AA649249	Hs.75640	natriuretic peptide precursor A	2.74	
132067	L20860	Hs.178382	glycoprotein Ib (platelet); beta polypep	2.74	
125664	AA948418	Hs.25744	ESTs; Weakly similar to Ydr412wp [S.cere	2.73	
132354	L05187	Hs.211913	small proline-rich protein 1A	2.73	
101568	M33764	Hs.75212	ornithine decarboxylase 1	2.73	
101438	M20777	Hs.159263	Homo sapiens; alpha-2 (VI) collagen	2.73	
116233	AA479082	Hs.61142	ESTs	2.73	
122194	AA435882	Hs.97531	ESTs	2.72	
113995	W88466	Hs.22010	ESTs	2.72	
124251	H68286	Hs.107924	ESTs	2.71	
120583	AA281304	Hs.78614	complement component 1; q subcomponent b	2.71	
134958	U72507	Hs.234216	Human 40871 mRNA partial sequence	2.71	
124280	H85835	Hs.100058	dihydropyrimidinase-like 4	2.71	
130113	M64673	Hs.1499	heat shock transcription factor 1	2.71	
106588	AA456612	Hs.25682	ESTs; Weakly smlr to PHOSPHATIDYLETHANOL	2.71	
132023	F01927	Hs.3743	ESTs; Weakly similar to proline-rich pro	2.7	
112284	R53558	Hs.26052	ESTs	2.7	
107897	AA026240	Hs.61387	ESTs	2.7	
122610	AA453598	Hs.99336	ESTs	2.7	
119070	R27788	Hs.52302	ESTs	2.7	
103491	Y08836		Homo sapiens mRNA for HRX-like protein	2.7	
108225	AA058843	Hs.161620	EST	2.7	
105829	AA398290	Hs.21965	ESTs	2.69	
127749	AI251757	Hs.145234	ESTs	2.69	
128428	AI185718	Hs.143900	ESTs	2.69	
108409	AA075578		zm88h3.s1 Stratagene ovarian cancer (#93	2.69	
114739	AA134923	Hs.103833	ESTs; Weakly similar to predicted using	2.68	
128821	D87002	Hs.135	multiple UniGene matches	2.68	
107412	W26105	Hs.8961	ESTs	2.68	
117012	H85893	Hs.194387	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.68	
135262	AA416551	Hs.9732	ESTs	2.68	
105367	AA236397	Hs.20304	ESTs	2.68	
134771	L13939	Hs.89576	adaptor-related protein complex 1; beta	2.68	
105036	AA128617	Hs.25549	ESTs	2.68	
125093	T92930	Hs.186750	ESTs	2.68	
119340	T61899	Hs.90677	ESTs; Highly similar to CGI-82 protein [	2.67	
132603	H62900	Hs.53066	hsp70-interacting protein	2.67	
113733	T98386	Hs.184548	ESTs	2.67	
123564	AA608902	Hs.112612	ESTs	2.66	
116059	AA454165	Hs.53455	ESTs	2.66	
125803	R79373	Hs.29852	ESTs	2.66	
123012	AA479962	Hs.139636	EST	2.66	
106080	AA418046	Hs.35124	ESTs	2.66	
128809	T59668	Hs.102267	lysyl oxidase	2.66	
104354	H08988	Hs.113759	ESTs	2.66	
107068	AA609028	Hs.8032	ESTs	2.65	
101418	M17754	Hs.1276	BN51 (BHK21) temperature sensitivity com	2.65	
135157	AA460138	Hs.95582	SRY (sex-determining region Y)-box 20	2.65	

123312	AA496258	Hs.99601	ESTs	2.65
130034	C00350	Hs.14454	chromosome 2 open reading frame 1	2.65
103897	AA248870	Hs.55058	ESTs	2.65
117771	N47961	Hs.46794	ESTs	2.65
109980	H09529	Hs.98693	DKFZP586J0917 protein	2.64
121966	AA429653	Hs.98616	EST	2.64
114233	Z39652	Hs.27457	ESTs	2.64
129594	R70379	Hs.115396	Human germline IgD chain gene; C-region;	2.63
102319	U34587	Hs.66578	corticotropin releasing hormone receptor	2.63
111700	R22212	Hs.23361	ESTs	2.63
127365	AA001628	Hs.74335	heat shock 90kD protein 1; beta	2.63
104205	AA496240	Hs.17270	DKFZP434C211 protein	2.63
124559	N66223	Hs.135928	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.63
106351	AA442772	Hs.191987	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.63
121903	AA427605	Hs.258742	myosin-binding protein C; cardiac	2.62
116442	AA620310	Hs.184343	ESTs; Weakly similar to KIAA0585 protein	2.62
127041	F06090		HSC0WG031 normalized infant brain cDNA H	2.62
132860	U93049	Hs.58435	FYN-binding protein (FYB-120/130)	2.62
131591	L22454	Hs.180069	nuclear respiratory factor 1	2.61
118118	N56901	Hs.47995	ESTs	2.61
134809	X52611	Hs.18387	transcription factor AP-2 alpha (activat	2.61
117706	N45091	Hs.46472	ESTs	2.61
127488	AA312179	Hs.178617	ESTs; Weakly similar to CGI-82 protein [	2.61
114891	AA235984	Hs.87469	ESTs	2.6
116426	AA609668	Hs.71657	ESTs	2.6
132589	AA432197	Hs.5260	ESTs; Weakly similar to CGI-08 protein [	2.6
128410	AA452788		zx39g11.r1 Soares_total_fetus_Nb2HF8_9w	2.6
106081	AA418394	Hs.25354	ESTs	2.6
129919	R02003	Hs.191208	ESTs; Weakly similar to weak similarity	2.59
124672	R00307	Hs.188504	ESTs	2.59
122758	AA459013	Hs.99742	X-ray repair complementing defective rep	2.59
125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ	2.59
130052	J00220	Hs.145288	Human Ig active epsilon1 5' UT; V-D-J re	2.59
134878	U28055	Hs.250826	macrophage stimulating; pseudogene 9	2.59
131908	L05624	Hs.3446	mitogen-activated protein kinase kinase	2.59
126470	AA843339	Hs.193168	ESTs; Weakly similar to CGI-52 protein [	2.59
132353	M31651	Hs.46319	sex hormone-binding globulin	2.58
119588	W44559	Hs.142525	ESTs	2.58
131757	D17532	Hs.316	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.58
118114	N56875	Hs.143212	cystatin F (leukocystatin)	2.58
128200	AI279952	Hs.158037	ESTs; Weakly similar to transcription re	2.58
131208	C14586	Hs.24220	Homo sapiens mRNA; cDNA DKFZp566M051 (fr	2.58
124721	R11131	Hs.154966	ESTs	2.57
108706	AA121820		Homo sapiens mRNA for KIAA0842 protein;	2.57
118831	N79592	Hs.50838	ESTs	2.57
115708	AA412212	Hs.44033	ESTs	2.57
107233	D59322	Hs.22595	ESTs	2.57
129559	AA234945	Hs.11360	ESTs	2.57
126953	AA743849	Hs.127286	ESTs	2.56
108165	AA055221	Hs.63168	ESTs	2.56
104069	AA401547	Hs.172694	ESTs	2.56
112146	R46512	Hs.25374	ESTs	2.56
108384	AA074891	Hs.124917	ESTs; Highly similar to KIAA0838 protein	2.56
131779	R49047	Hs.179779	ribosomal protein L37	2.56
111829	R36070	Hs.25079	EST	2.55
103424	X97267	Hs.155975	protein tyrosine phosphatase; receptor t	2.55
100133	D13118	Hs.80986	ATP synthase; H+ transporting; mitochond	2.55
130208	AA620556	Hs.15250	peroxisomal D3;D2-enoyl-CoA isomerase	2.55
124649	N92593	Hs.102907	ESTs	2.55
106511	AA452865	Hs.206713	UDP-Gal:betaGlcNAc beta 1;4- galactosylt	2.55
128467	AA176446	Hs.180428	ESTs; Weakly similar to hypothetical 43.	2.55
113524	T90072	Hs.15060	ESTs	2.55
107821	AA020991	Hs.172856	ESTs	2.55
111900	R39044	Hs.25318	Homo sapiens clone 25194 mRNA sequence	2.54
109908	H05255	Hs.203237	EST	2.54
132069	D87454	Hs.192966	KIAA0265 protein	2.54
130660	T95262	Hs.17538	ESTs	2.54
112983	T23443	Hs.7111	ESTs	2.54
128279	H08885		yi88b08.r1 Soares infant brain 1NIB Homo	2.54
106415	AA447994	Hs.29188	ESTs	2.53
116741	H03268	Hs.181746	EST	2.53
103148	X66362	Hs.2994	PCTAIRE protein kinase 3	2.53
132336	AA342422	Hs.45073	ESTs	2.53
129484	R92488	Hs.111989	ESTs	2.53
110169	H19696	Hs.31612	ESTs; Moderately similar to CAGH4 [H.sap	2.53
116880	H68380	Hs.144174	EST	2.53

133511	X04106	Hs.74451	calpain; small polypeptide	2.53	
126037	M85772	Hs.6066	KIAA1112 protein	2.53	
132678	AA599876	Hs.5486	ESTs	2.53	
128751	AA442274	Hs.183176	ESTs	2.52	
133664	X86693	Hs.75445	hevin	2.52	
126977	AA309665		EST180547 Jurkat T-cells V Homo sapiens	2.52	
120697	AA291522	Hs.97250	EST	2.52	
128571	AA416619	Hs.101661	ESTs	2.52	
104422	H86858	Hs.132909	ESTs	2.52	
122372	AA446008	Hs.99044	EST	2.52	
112154	R46769	Hs.25388	ESTs	2.52	
126900	R16034	Hs.12701	ESTs; Highly similar to plasmolipin [H.s	2.51	
115000	AA251342	Hs.144584	ESTs	2.51	
110632	H72344	Hs.171635	ESTs	2.51	
129154	N23673	Hs.108969	mannosidase; alpha; class 2B; member 1	2.51	
107440	W28069	Hs.251993	ESTs; Weakly similar to similar to zinc	2.51	
105694	AA287109	Hs.37883	ESTs	2.51	
106249	AA430388	Hs.13144	ESTs; Weakly similar to ORF YGR038w [S.c	2.51	
134462	U11037	Hs.83620	sel-1 (suppressor of lin-12; C.elegans)-	2.51	
101800	M85276	Hs.105806	granulysin	2.51	
119884	W81606	Hs.58662	Homo sapiens mRNA; cDNA DKFZp564G212 (fr	2.51	
110289	H29829	Hs.31524	ESTs	2.51	
125506	H54273	Hs.154073	UDP-galactose transporter related	2.51	
102954	X15393	Hs.2813	motilin	2.51	
127851	AI469331	Hs.130497	ESTs; Weakly similar to CHLORIDE CONDUCT	2.5	
126179	AI191445	Hs.143855	ESTs; Highly similar to IROQUOIS-CLASS H	2.5	
129443	W69967	Hs.111497	ESTs; Moderately similar to neuronal pro	2.5	
104480	N41486	Hs.99654	protein-O-mannosyltransferase 1	2.5	
115580	AA398695	Hs.144339	Hu DNA seq frm clone 495O10 on chr 6q26-Prot L37A) pseudogene; last exon of gene for a novel prot smlr to worm E04F6.2; ESTs; STSs and GSSs	2.5	
119595	W45031	Hs.55878	EST	2.5	
103336	X85785	Hs.183	Duffy blood group	2.5	
102792	U87964	Hs.227576	GTP binding protein 1	2.49	
129643	L27584	Hs.250712	calcium channel; voltage-dependent; beta	2.49	
134503	U34880	Hs.84183	diptheria toxin resistance protein reqrd	2.49	
117245	N20989	Hs.42927	ESTs	2.49	
126888	H78745	Hs.1063	small nuclear ribonucleoprotein polypept	2.49	
135313	D63484	Hs.98508	KIAA0150 protein	2.49	
121186	AA400156	Hs.183294	ESTs	2.49	
130651	X04445	Hs.1734	inhibin; alpha	2.49	
134218	AA227480	Hs.80205	pim-2 oncogene	2.49	
104008	AA334630		EST38874 Embryo, 9 week Homo sapiens cDN	2.49	
129705	X78706	Hs.12068	carnitine acetyltransferase	2.49	
127900	AI143912	Hs.121824	ESTs	2.49	
104609	R96417	Hs.107795	ESTs	2.48	
131628	U47292	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	2.48	
132184	U51003	Hs.419	distal-less homeo box 2	2.48	
130450	U70735	Hs.15591	COP9 subunit 6 (MOV34 homolog; 34 kD)	2.48	
101679	M62628	Hs.163271	Human alpha-1 Ig germline C-region membr	2.48	
120858	AA350147	Hs.96940	EST	2.48	
101012	J04444	Hs.697	cytochrome c-1	2.48	
110453	H52133	Hs.33026	ESTs; Weakly similar to similar to Enter	2.48	
133771	M68891	Hs.760	GATA-binding protein 2	2.48	
102944	X14445	Hs.37092	fibroblast grwth fctr 3 (murine mammary	2.48	
113269	T65159	Hs.85044	ESTs	2.48	
107069	AA609045	Hs.11759	ESTs; Weakly similar to !!!! ALU CLASS B	2.48	
100476	HG1019-HT1019		Serine Kinase Psk-H1	2.47	
106457	AA449718	Hs.27801	zinc finger protein 278	2.47	
105718	AA291629	Hs.74335	heat shock 90kD protein 1; beta	2.47	
104925	AA058683	Hs.5548	Homo sapiens clone 23765 mRNA sequence	2.47	
109913	H05527	Hs.31588	ESTs	2.47	
103412	X96698	Hs.42957	methyltransferase-like 1	2.47	
102326	U35246	Hs.226025	vacuolar protein sorting 45A (yeast homo	2.47	
116813	H49911	Hs.93102	ESTs	2.47	
123690	AA609566	Hs.112723	EST	2.47	
124714	R09486	Hs.193118	ESTs	2.47	
126154	AI004105	Hs.14232	ESTs; Moderately similar to KIAA0563 pro	2.47	
118880	N90168	Hs.54593	EST	2.47	
122274	AA437094	Hs.184456	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.46	
129600	N78980	Hs.11567	ESTs; Moderately similar to unknown [H.s	2.46	
121356	AA405437	Hs.93581	Homo sapiens mRNA; cDNA DKFZp586E171 (fr	2.46	
109560	F01778	Hs.8154	ESTs	2.46	
123342	AA504336	Hs.31659	thyroid hormone receptor-associated prot	2.46	
128032	AI150084	Hs.126678	ESTs	2.46	
129101	H90310	Hs.108665	ESTs; Weakly similar to CELL-CYCLE NUCLE	2.46	

131185	M25753	Hs.23960	cyclin B1	2.46
121451	AA411008	Hs.98085	EST	2.46
104328	D81932		HUM424C5B Hu fetal brain (TFujiwara) H s	2.46
126543	AA723810	Hs.69517	ESTs; Highly similar to differentially e	2.45
123600	AA609106	Hs.112644	ESTs	2.45
131020	AA411756	Hs.20594	ESTs; Weakly similar to misato [D.melano	2.45
134191	W28902	Hs.7979	KIAA0736 gene product	2.45
130446	X79510	Hs.155693	protein tyrosine phosphatase; non-recept	2.45
131613	R88228	Hs.29595	JM4 protein	2.45
118864	N89670	Hs.42148	ESTs; Weakly similar to Su(P) [D.melanog	2.45
104232	AB002351	Hs.10587	KIAA0353 protein	2.45
122604	AA453489	Hs.99333	ESTs	2.45
120626	AA285064	Hs.104485	EST	2.45
116655	F03866	Hs.68090	ESTs	2.44
116267	AA485080	Hs.256539	ESTs	2.44
114944	AA243172	Hs.87619	TED protein	2.44
127629	AA293279	Hs.29173	ESTs	2.44
120350	AA211300	Hs.104166	ESTs	2.44
103620	Z47087	Hs.182643	transcription elongation factor B (SIII)	2.44
131420	Z11737	Hs.2664	flavin containing monooxygenase 4	2.44
131312	AA399226	Hs.25527	tight junction protein 3 (zona occludens	2.43
122812	AA461044	Hs.142980	EST	2.43
135100	AA398926	Hs.251108	Homo sapiens mRNA; chromosome 1 specific	2.43
113464	T86931	Hs.16295	ESTs	2.43
100045	M11507		AFFX control: transferrin receptor	2.43
128975	AA092129	Hs.107538	ESTs; Moderately similar to /prediction	2.43
103688	AA011479	Hs.154701	ESTs	2.43
127331	F20186		HSPD05873 HM3 Homo sapiens cDNA clone 05	2.43
107337	T97111	Hs.191235	ESTs; Weakly similar to Ydr324cp [S.cere	2.43
122171	AA435750	Hs.98830	EST	2.43
107601	AA004636	Hs.50223	ESTs	2.43
119800	W73523	Hs.58314	ESTs	2.43
104886	AA053348	Hs.144626	growth differentiation factor 11	2.42
122899	AA469960	Hs.178420	ESTs; Highly similar to WASP interacting	2.42
125933	AI308037	Hs.84120	ESTs; Weakly similar to nucleoporin p62	2.42
121664	AA417291	Hs.97978	ESTs	2.42
125450	AA377194	Hs.238909	ESTs; Weakly similar to POLYPOSIS LOCUS	2.42
114611	AA081374	Hs.108110	DKFZP547E2110 protein	2.42
111595	R11492	Hs.191225	ESTs	2.42
111671	R19368	Hs.229084	EST	2.42
110687	H93005	Hs.177311	ESTs	2.42
103019	X53414	Hs.144567	alanine-glyoxylate aminotransferase (oxa	2.42
119076	R36634	Hs.235534	ESTs	2.42
130589	AA234308	Hs.16441	DKFZP434H204 protein	2.42
125975	AA495891	Hs.152290	ESTs; Highly similar to PACAP type-3/VIP	2.42
106380	AA446188	Hs.16614	ESTs	2.41
121965	AA429652	Hs.104901	EST	2.41
121604	AA416788	Hs.98259	EST	2.41
100885	HG4490-HT4876		Proline-Rich Protein Prb4, Allele	2.41
117807	N48701	Hs.46523	EST	2.41
119840	W79525	Hs.58586	ESTs	2.41
102458	U48861	Hs.54397	cholinergic receptor; nicotinic; beta po	2.41
116152	AA460920	Hs.215683	ESTs; Moderately similar to !!!! ALU SUB	2.41
126741	AA522512	Hs.29759	Homo sapiens mRNA; cDNA DKFZp586L2123 (f	2.41
103381	X92715	Hs.3057	zinc finger protein 74 (Cos52)	2.41
124837	R55630	Hs.233602	KIAA0596 protein	2.41
129322	AA437153	Hs.110407	ESTs; Weakly similar to coded for by C.	2.4
129291	AA281930	Hs.110099	core-binding factor; runt domain; alpha	2.4
124789	R43803	Hs.78110	ESTs; Weakly similar to F17A9.2 [C.elega	2.4
133253	Y00970	Hs.183088	acrosin	2.4
118990	N94447	Hs.55047	EST	2.4
134897	R71427	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	2.4
116572	D45654	Hs.65582	DKFZP586C1324 protein	2.4
104294	D14539	Hs.234774	myeloid/lymphoid or mixed-lineage leukem	2.4
118764	N74440	Hs.205264	ESTs	2.4
117437	N27645		yw5e3.s1 Weizmann Olfactory Epithelium H 3' similar to contains L1.t3 L1 repetit	2.4
111651	R16733	Hs.20499	ESTs	2.39
109583	F02322	Hs.26135	ESTs	2.39
125969	R94247	Hs.193879	ESTs	2.39
130647	AA457216	Hs.214190	interleukin enhancer binding factor 1	2.39
113708	T97467	Hs.18065	ESTs	2.39
133469	L03785	Hs.170482	myosin; light polypeptide 5; regulatory	2.39
118266	N62837	Hs.48647	immunoglobulin-like transcript 7	2.39
121656	AA417248	Hs.98212	ESTs	2.39
126530	AI422841	Hs.180086	ESTs	2.39

123708	AA609648	Hs.207767	EST	2.39	
107875	AA025308	Hs.61182	ESTs	2.39	
111711	R22891	Hs.7093	ESTs	2.39	
131405	U79255	Hs.26468	amyloid beta (A4) precursor protein-bind	2.39	
127454	AA502957	Hs.153590	ESTs	2.39	
132341	AA448419	Hs.45209	ESTs	2.38	
133673	D87673	Hs.75486	heat shock transcription factor 4	2.38	
113213	T58607		ya94a02.s1 Stratagene placenta (#937225)	2.38	
106230	AA429356	Hs.12047	ESTs	2.38	
116692	F09261	Hs.66103	ESTs	2.38	
126197	AA172284	Hs.103657	ESTs; Weakly similar to CH-TOG PROTEIN [	2.38	
115966	AA446866	Hs.71371	ESTs	2.38	
132636	U65785	Hs.5417	oxygen regulated protein (150kD)	2.38	
109965	H09077	Hs.30895	EST	2.38	
130203	L14754	Hs.1521	immunoglobulin mu binding protein 2	2.38	
131332	R50487	Hs.25717	ESTs	2.38	
119105	R42357	Hs.91453	ESTs	2.37	
129253	W69316	Hs.109778	ESTs; Weakly similar to similar to beta-	2.37	
113602	T92558	Hs.17036	ESTs	2.37	
118102	N55272	Hs.145798	ESTs	2.37	
100734	HG3432-HT3620		Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 3, K-Sam Iii	2.37	
111533	R08548	Hs.251651	EST	2.37	
130813	U12259	Hs.198	paired box gene 3 (Waardenburg syndrome	2.37	
119180	R80413	Hs.92520	ESTs	2.37	
109335	AA211443	Hs.86492	ESTs	2.37	
107386	U97698	Hs.159593	mucin 6; gastric	2.36	
122486	AA448328	Hs.115527	ESTs	2.36	
112997	T23548	Hs.167467	ESTs	2.36	
109674	F09051	Hs.21837	ESTs; Weakly similar to KIAA0927 protein	2.36	
128868	AA423827	Hs.106730	hypothetical protein	2.36	
127027	R17261		yg12g07.r1 Soares infant brain 1NIB H sa	2.36	
123099	AA485931	Hs.79	aminoacylase 1	2.36	
115716	AA416767	Hs.43498	ESTs; Weakly similar to ORF YKL201c [S.c	2.36	
130830	D86982	Hs.20060	KIAA0229 protein	2.36	
109051	AA159920	Hs.72322	ESTs	2.36	
130181	R39552	Hs.151608	Homo sapiens clone 23622 mRNA sequence	2.36	
131114	R46233	Hs.23107	ESTs	2.36	
123589	AA609047	Hs.188922	ESTs	2.36	
130872	U03891		phorbolin (similar to apolipoprotein B m	2.36	
131962	H78550	Hs.2780	jun D proto-oncogene	2.36	
130502	M55067	Hs.1583	neutrophil cytosolic factor 1 (47kD; chr	2.36	
121785	AA423883	Hs.142442	ESTs	2.35	
125405	T97171	Hs.121570	ESTs	2.35	
103682	AA000993		ESTs	2.35	
125649	T77395	Hs.194816	stomatin-like protein 1	2.35	
115452	AA285019	Hs.55263	ESTs; Highly similar to mitochondrial di	2.35	
129338	T56800	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	2.35	
106105	AA421268	Hs.149443	putative tumor suppressor	2.35	
134770	R72079	Hs.89575	CD79B antigen (immunoglobulin-associated	2.35	
119422	T99496	Hs.229598	EST	2.35	
109869	H02849	Hs.30345	EST	2.35	
134314	AA263032	Hs.81634	ATP synthase; H+ transporting; mitochond	2.35	
114989	AA251097	Hs.189119	ESTs	2.35	
122619	AA453755	Hs.191515	ESTs	2.35	
133129	AA428580	Hs.65551	ESTs	2.35	
128465	AA416762	Hs.100221	nuclear receptor subfamily 1; group H; m	2.35	
115636	AA402715	Hs.58389	ESTs	2.35	
130836	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.34	
132385	Y10256	Hs.47007	serine/threonine protein-kinase	2.34	
107776	AA018820	Hs.221147	ESTs	2.34	
109791	F10669	Hs.13228	DRE-antagonist modulator; calsenilin	2.34	
124409	N33212	Hs.107197	ESTs	2.34	
131068	AA397916	Hs.22595	ESTs	2.34	
121079	AA398719	Hs.14169	ESTs; Weakly similar to CREB-binding pro	2.34	
124662	N94340	Hs.171835	ESTs; Weakly smlr to PUT PRE-MRNA SPLICI	2.34	
133820	M13686	Hs.177582	surfactant; pulmonary-associated protein	2.34	
129424	M55593	Hs.111301	matrix metalloproteinase 2 (gelatinase A	2.34	
109066	AA161377	Hs.72404	EST	2.34	
100339	D63485	Hs.181359	KIAA0151 gene product	2.34	
100809	HG3991-HT4261		Cpg-Enriched Dna, Clone E18	2.34	
120844	AA349417	Hs.96917	ESTs	2.33	
124927	R96146	Hs.221459	ESTs	2.33	
109779	F10527	Hs.3353	Homo sapiens clone 24940 mRNA sequence	2.33	
101171	L16842	Hs.119251	ubiquinol-cytochrome c reductase core pr	2.33	
110805	N26904	Hs.24048	ESTs; Weakly similar to FK506/rapamycin-	2.33	
125440	AI090982	Hs.31895	ESTs	2.33	

133159	AC000061	Hs.663	cystic fibrosis transmemb conductance re	2.33
101829	M91368	Hs.129763	solute carrier family 8 (sodium/calcium	2.33
126492	AA778565	Hs.142505	ESTs	2.33
102774	U83303	Hs.164021	small inducible cytokine subfamily B (CX	2.33
130480	N50809	Hs.15760	ESTs; Weakly similar to similar to Yeast	2.33
126878	AI424759	Hs.238928	ESTs	2.33
117338	N23889	Hs.43466	ESTs	2.32
118662	N70877	Hs.13055	ESTs	2.32
130354	AA416685	Hs.155001	UNC13 (C. elegans)-like	2.32
106760	AA477330	Hs.12293	ESTs	2.32
124294	H90573	Hs.102298	EST	2.32
119428	W02129	Hs.55242	EST	2.32
132629	Z40942	Hs.5383	ESTs	2.32
127998	AA854161	Hs.143585	ESTs	2.32
132728	AA293334	Hs.5566	ESTs; Highly similar to RAS-RELATED PROT	2.32
120292	AA189116	Hs.96168	ESTs	2.32
107598	AA004528	Hs.169444	ESTs	2.32
128164	AI478174	Hs.144846	ESTs	2.32
105753	AA299789	Hs.15277	ESTs	2.31
131256	AA262340	Hs.24907	coronin; actin-binding protein; 2B	2.31
110891	N38863	Hs.234392	platelet-activating factor acetylhydrola	2.31
116767	H13689	Hs.92530	ESTs	2.31
100545	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	2.31
125264	W88995	Hs.167641	ESTs; Weakly similar to C15H9.5 [C.elega	2.31
118387	N64579		yz51d11.s1 Morton Fetal Cochlea H sapien	2.31
104335	D83847	Hs.183864	elastase 3B	2.31
107464	W42944	Hs.171939	ESTs	2.31
112304	R54798	Hs.26239	ESTs	2.31
134313	AA136100	Hs.6673	trinucleotide repeat containing 15	2.31
116322	AA490900	Hs.58643	ESTs; Highly similar to JAK3B [H.sapiens	2.31
111275	N70970	Hs.35006	ESTs	2.31
100109	AJ000480	Hs.143513	phosphoprotein regulated by mitogenic pa	2.31
109338	AA211717	Hs.86507	ESTs	2.31
134432	AA053022	Hs.8312	ESTs	2.31
129649	AD000092	Hs.182628	Homo sapiens DNA from chr 19p13.2 cosmid EKLF; GCDH; CRTC; and RAD23A genes; gen	2.31
122623	AA453990	Hs.99248	ESTs	2.31
112070	R43976	Hs.236310	EST	2.31
127683	AA668123	Hs.134170	ESTs	2.31
104920	AA057620	Hs.30807	ESTs; Highly similar to dJ186O1.1 [H.sap	2.31
106064	AA417373	Hs.15898	ESTs	2.31
106782	AA478487		ESTs	2.31
126709	AA028159	Hs.47234	ESTs	2.3
105129	AA158386	Hs.186476	ESTs	2.3
105719	AA291644	Hs.36793	ESTs	2.3
121698	AA418399	Hs.10351	KIAA0308 protein	2.3
119069	R27619	Hs.231046	EST	2.3
130388	U72515	Hs.189583	putative protein similar to nessy (Droso	2.3
103444	X98801	Hs.74617	dynactin 1 (p150; Glued (Drosophila) hom	2.3
114604	AA076128		zm18g4.s1 Stratagene pancreas (#93728) H 3' similar to SW:RS1A_HUMAN P3927 4S RI	2.3
103878	AA227635	Hs.202588	ESTs	2.3
105828	AA398276	Hs.11962	ESTs	2.3
119778	W72920	Hs.58244	ESTs	2.3
120401	AA234309	Hs.193011	ESTs	2.3
116290	AA488691	Hs.57969	phenylalanine-tRNA synthetase	2.3
130479	R44163	Hs.12457	Homo sapiens clone 23770 mRNA sequence	2.3
104253	AF002672	Hs.152944	loss of heterozygosity; 11; chromosomal	2.29
132615	H66367	Hs.53358	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.29
121954	AA429598	Hs.98587	ESTs	2.29
101336	L49169	Hs.75678	FBJ murine osteosarcoma viral oncogene h	2.29
127247	AA313802	Hs.6289	growth factor receptor-bound protein 2	2.29
117300	N22565	Hs.43212	ESTs	2.29
122229	AA436198	Hs.103902	ESTs	2.29
125106	T95766	Hs.189760	ESTs	2.29
128083	R16100	Hs.166476	ESTs	2.29
131279	AA089853	Hs.25197	STIP1 homology and U-Box containing prot	2.29
133838	M97796	Hs.180919	inhibitor of DNA binding 2; dominant neg	2.29
111837	R36447	Hs.24453	ESTs	2.29
111435	R01620	Hs.19198	ESTs	2.29
123613	AA609158	Hs.112656	EST	2.29
133560	AA256365	Hs.7486	protein expressed in thyroid	2.29
122896	AA469952	Hs.97899	ESTs; Weakly similar to dal2; len:343; C	2.29
113378	T80627	Hs.14757	ESTs	2.29
127174	AA293204	Hs.139352	ESTs	2.29
120153	Z39582	Hs.65777	EST	2.29

112741	R93080	Hs.35035	ESTs	2.28
132152	AA044784	Hs.4105	Homo sapiens mRNA; cDNA DKFZp586A0618 (f	2.28
109790	F10665	Hs.25031	ESTs	2.28
113776	W04657	Hs.24248	ESTs	2.28
102934	X13451		Hu mRNA for lymphocyte lineage-rstrcted	2.28
126168	AA322034		EST24690 Cerebellum II Homo sapiens cDNA	2.28
126363	N94706		Human Chromosome 16 BAC clone CIT987SK-A	2.28
101427	M19508		Human myeloperoxidase gene, exons 1-4	2.28
132616	AA386264	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mito	2.28
105537	AA258813	Hs.27160	ESTs	2.28
126527	AA548559	Hs.103853	ESTs	2.28
115359	AA281936	Hs.88914	ESTs	2.28
108474	AA079667		zm93d1.s1 Stratagene ovarian cncr (#9372	2.28
120685	AA291066	Hs.105099	ESTs	2.28
126171	AA704771	Hs.191942	ESTs	2.28
112858	T02963	Hs.4454	ESTs	2.28
121817	AA424826	Hs.98475	EST	2.28
107895	AA026150	Hs.61384	ESTs	2.28
131161	Z38223	Hs.23735	potassium voltage-gated channel; subfami	2.28
135173	M72885	Hs.95910	Human G0S2 protein gene; complete cds	2.27
103182	X69819	Hs.99995	intercellular adhesion molecule 3	2.27
113889	W72720	Hs.194347	ESTs	2.27
128984	AA319615	Hs.238030	secretory carrier membrane protein 2	2.27
101531	M29877	Hs.576	fucosidase; alpha-L- 1; tissue	2.27
115916	AA436889	Hs.91910	ESTs	2.27
129892	H96850	Hs.89674	dolichyl-diphosphooligosaccharide-protei	2.27
103035	X54871	Hs.77690	RAB5B; member RAS oncogene family	2.27
126479	T78141		ESTs	2.27
125778	R71976	Hs.161791	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.27
108132	AA053586	Hs.63048	ESTs	2.27
111017	N53965	Hs.256327	ESTs	2.27
127165	AA359719	Hs.127121	ESTs	2.27
126446	AI421309	Hs.118926	DKFZP586K0919 protein	2.26
107864	AA025061	Hs.61246	ESTs	2.26
122277	AA437133	Hs.98936	ESTs	2.26
115604	AA400378	Hs.49391	ESTs	2.26
105061	AA134824	Hs.4865	ESTs	2.26
118549	N68163	Hs.49455	EST	2.26
110509	H56493	Hs.61960	ESTs; Moderately similar to HYPOTHETICAL	2.26
114088	Z38280	Hs.26971	Human Chromosome 16 BAC clone CIT987SK-2	2.26
103225	X74837	Hs.2750	mannosidase; alpha; class 1A; member 1	2.26
125842	AA746654	Hs.5181	proliferation-associated 2G4; 38kD	2.26
104538	R25069	Hs.175681	ESTs	2.26
130304	U09368	Hs.154205	zinc finger protein 140 (clone pHZ-39)	2.26
120680	AA290743	Hs.97242	ESTs	2.26
124062	H00440	Hs.144524	ESTs; Weakly similar to signal transduce	2.26
103289	X80915	Hs.1573	growth differentiation factor 5 (cartila	2.26
109286	AA197273	Hs.191324	ESTs	2.26
128555	U62739	Hs.101408	branched chain aminotransferase 2; mitoc	2.26
129439	AA171694	Hs.111461	ceruloplasmin (ferroxidase)	2.26
109221	AA192755	Hs.85840	ESTs; Weakly similar to stac [H.sapiens]	2.26
109906	H05084	Hs.28077	ESTs; Highly similar to GDP-mannose pyro	2.26
130540	U35234	Hs.159534	protein tyrosine phosphatase; receptor t	2.26
122870	AA465158	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	2.26
120219	Z41124	Hs.66045	EST	2.26
128021	AI001136	Hs.78223	N-acylaminoacyl-peptide hydrolase	2.26
121732	AA421047	Hs.98330	ESTs	2.26
107817	AA020781	Hs.60847	ESTs	2.25
101069	L02648	Hs.84232	transcobalamin II; macrocytic anemia	2.25
103065	X58399	Hs.81221	Human L2-9 transcript of unrearranged im	2.25
118019	N52585	Hs.47517	ESTs	2.25
122220	AA436011	Hs.98187	ESTs	2.25
109161	AA179392	Hs.73601	EST	2.25
128699	K03207	Hs.103972	proline-rich protein BstNI subfamily 4	2.25
101914	S71824	Hs.167988	neural cell adhesion molecule 1	2.25
102697	U74667	Hs.6364	Tat interactive protein (60kD)	2.25
119939	W86753	Hs.82407	ESTs	2.25
127793	AI298835	Hs.30445	ESTs; Weakly similar to transcription re	2.25
104450	L77564	Hs.103978	serine/threonine kinase 22B (spermiogene	2.25
133096	AA136042	Hs.131053	ESTs	2.25
115416	AA283893	Hs.203866	ESTs	2.25
117056	H90322	Hs.41387	EST	2.25
115598	AA400129	Hs.65735	ESTs	2.25
121267	AA401397	Hs.165296	ESTs; Highly similar to kallikrein-like	2.25
104778	AA026397	Hs.11039	Homo sapiens clone 24804 mRNA sequence	2.25
110926	N48252	Hs.135287	ESTs	2.24

102795	U88667	Hs.198396	ATP-binding cassette; sub-family A (ABC1	2.24
118643	N70324	Hs.49840	ESTs	2.24
103304	X82240	Hs.2484	T-cell leukemia/lymphoma 1A	2.24
134814	Z48475	Hs.89771	glucokinase (hexokinase 4) regulatory pr	2.24
125912	AA171719	Hs.5233	eukaryotic translation initiation factor	2.24
134365	R32377	Hs.82240	syntaxin 3A	2.24
117224	N20300	Hs.218707	ESTs	2.24
107169	AA621601	Hs.184446	ESTs; Weakly similar to small GTP-bindin	2.24
133948	M59916	Hs.77813	sphingomyelin phosphodiesterase 1; acid	2.24
101426	M19483	Hs.25	ATP synthase; H+ transporting; mitochond	2.24
119922	W86196	Hs.177384	ESTs	2.24
123361	AA504810	Hs.139649	EST	2.24
123915	AA621298	Hs.112967	ESTs	2.24
123540	AA608792	Hs.112591	EST	2.24
124978	T40560	Hs.221759	ESTs	2.24
102354	U38268		Human cytochrome b pseudogene, partial c	2.24
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha	2.24
102160	U18235	Hs.121561	ATP-binding cassette; sub-family A (ABC1	2.24
107520	X76091	Hs.100007	regulatory factor X; 2 (influences HLA c	2.24
131589	U52100	Hs.29191	epithelial membrane protein 2	2.24
126633	AA206993	Hs.154145	guanine nucl binding protein (G protein)	2.23
130887	AA258379	Hs.155986	angiotensin receptor-like 2	2.23
119894	W84670	Hs.58518	EST	2.23
124544	N63837	Hs.40500	similar to S. cerevisiae RER1	2.23
103104	X61587	Hs.75082	ras homolog gene family; member G (rho G	2.23
110119	H17306	Hs.177229	ESTs	2.23
131411	AA464043	Hs.26506	ESTs; Weakly similar to NY-REN-45 antige	2.23
102346	U37359	Hs.227297	meiotic recombination (S. cerevisiae) 11	2.23
106003	AA411167	Hs.8734	ESTs; Moderately similar to !!!! ALU CLA	2.23
122564	AA452251	Hs.98669	ESTs	2.23
133688	U42031	Hs.7557	FK506-binding protein 5	2.23
132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence	2.23
110038	H11746	Hs.31097	ESTs	2.23
123788	AA620293	Hs.112853	ESTs	2.23
135070	X99350	Hs.93974	forkhead box J1	2.23
104908	AA055841	Hs.154396	ESTs	2.22
128674	AA025001	Hs.169452	ESTs	2.22
100810	HG3992-HT4262		Cpg-Enriched Dna, Clone E35	2.22
120065	W93579	Hs.59478	EST	2.22
122775	AA459692	Hs.112143	ESTs	2.22
125443	H71482	Hs.177592	ribosomal protein; large; P1	2.22
118617	N69666	Hs.183413	ESTs; Moderately similar to !!!! ALU SUB	2.22
128001	AI167814	Hs.166664	ESTs	2.22
128160	AI279080	Hs.149971	ESTs; Moderately similar to !!!! ALU CLA	2.22
106608	AA458644	Hs.27115	ESTs	2.22
103485	Y08409	Hs.248415	thyroid hormone responsive SPOT14 (rat)	2.22
135008	AA173423	Hs.92918	ESTs; Weakly similar to R07G3.8 [C.elega	2.22
110122	H17333	Hs.159837	EST	2.22
128397	AI393421	Hs.14032	ESTs	2.22
110231	H24359	Hs.28733	ESTs	2.22
123188	AA489092	Hs.177726	ESTs	2.22
131903	AA481723	Hs.3436	deleted in oral cancer (mouse; homolog)	2.22
122649	AA454616	Hs.90336	ATPase; H+ transporting; lysosomal (vacu	2.22
133090	AA448228	Hs.6468	ESTs	2.22
108002	AA037664	Hs.55067	ESTs; Weakly similar to T07F12.1 gene pr	2.22
133120	X64559	Hs.65424	tetranectin (plasminogen-binding protein	2.21
114263	Z40073	Hs.6045	ESTs	2.21
125518	R20148	Hs.193851	ESTs	2.21
128613	U78551	Hs.102482	Homo sapiens gallbladder mucin MUC5B mRN	2.21
102773	U83192	Hs.23731	discs; large (Drosophila) homolog 4	2.21
119526	W38049		Accession not listed in Genbank	2.21
126844	AA299325		EST11903 Uterus tumor I Homo sapiens cDN	2.21
105860	AA399251	Hs.180933	ESTs; Weakly similar to methyl-CpG bindi	2.21
126957	AA733145	Hs.194560	ESTs	2.21
108959	AA150107	Hs.81810	ESTs	2.2
131663	AA423926	Hs.30318	ESTs	2.2
127468	H02941	Hs.8888	ESTs	2.2
104483	N42776	Hs.146233	ESTs	2.2
123848	AA620773	Hs.221996	ESTs	2.2
101623	M55905	Hs.75342	malic enzyme 2; NAD(+)-dependent; mitoch	2.2
120872	AA357993	Hs.96996	ESTs	2.2
135033	AA173241	Hs.93454	ESTs	2.2
122286	AA437259	Hs.104944	EST	2.2
114862	AA235174	Hs.50250	ESTs	2.2
100255	D38047	Hs.78466	proteasome (prosome; macropain) 26S subu	2.2
103063	X58234	Hs.123178	translocase of inner mitochondrial membr	2.2

132777	R56898	Hs.56663	ESTs	2.2
133082	AA457129	Hs.6455	RuvB (E coli homolog)-like 2	2.2
127529	AA558980	Hs.191750	ESTs	2.2
114602	AA075642	Hs.103594	deleted in malignant brain tumors 1	2.2
120722	AA293435	Hs.97277	ESTs	2.2
102675	U72512		Human B-cell receptor associated protein	2.2
128551	H09058	Hs.237323	N-acetylglucosamine-phosphate mutase; DK	2.2
112020	R43001	Hs.22298	EST	2.2
123625	AA609216	Hs.112666	EST	2.2
120315	AA194266	Hs.178393	ESTs	2.2
122081	AA431992	Hs.104920	ESTs	2.19
101798	M85220		Accession not listed in Genbank	2.19
111501	R07444	Hs.163118	ESTs	2.19
132832	D63482	Hs.57734	KIAA0148 gene product	2.19
100544	HG2147-HT2217		Mucin 3, Intestinal (Gb:M55405)	2.19
106835	AA482077	Hs.33713	ESTs; Weakly similar to hypothetical pro	2.19
132934	AA076145	Hs.61053	ESTs	2.19
108762	AA127515	Hs.71787	ESTs; Highly similar to 30S ribosomal pr	2.19
120164	Z39733	Hs.158159	FAT tumor suppressor (Drosophila) homolo	2.19
135395	L08096	Hs.99899	tumor necrosis factor (ligand) superfami	2.19
101717	M69013	Hs.1686	guanine nucleotide binding protein (G pr	2.19
121172	AA400013	Hs.97750	EST	2.18
114861	AA235123	Hs.40719	ESTs	2.18
120851	AA349662	Hs.174248	ESTs	2.18
121083	AA398736	Hs.97653	EST	2.18
107171	AA621624	Hs.28088	Homo sapiens clone 24515 mRNA sequence	2.18
128754	D31446	Hs.10488	Breakpoint cluster region protein; uteri	2.18
100149	D13897	Hs.169249	peptide YY	2.18
132405	AA323787	Hs.4770	KIAA1068 protein	2.18
114666	AA112274		zm27g6.s1 Stratagene pancreas (#93728) H element;contains element LTR8 repetitiv	2.18
127008	AA223879		zr10g05.r1 Stratagene NT2 neuronal precu	2.18
110373	H42896	Hs.29438	ESTs	2.18
119354	T66942	Hs.100651	golgi SNAP receptor complex member 2	2.18
130115	M31627	Hs.149923	X-box binding protein 1	2.18
130514	AA161085	Hs.15871	ESTs; Weakly similar to acid phosphatase	2.18
128848	H08077	Hs.217179	ESTs; Weakly similar to T27A1.5 [C.elega	2.18
110161	H19312	Hs.28096	ESTs	2.18
132367	X82224	Hs.46634	cysteine conjugate-beta lyase; cytoplasm	2.18
125882	H45538	Hs.101448	metastasis associated 1	2.17
113837	W57698	Hs.8888	ESTs	2.17
106376	AA444004	Hs.6084	ESTs	2.17
113755	T99075	Hs.18570	ESTs	2.17
107525	X91817	Hs.102866	transketolase-like 1	2.17
119207	R93186	Hs.84298	CD74 antigen (invar polypept of maj hist	2.17
131862	AA236365		3-phosphoglycerate dehydrogenase	2.17
115514	AA297739	Hs.55609	ESTs; Weakly similar to ISOLEUCYL-TRNA S	2.17
112290	R53940	Hs.26016	ESTs	2.17
126136	H83353		yv82f02.r1 Soares melanocyte 2NbHM Homo	2.17
121574	AA412712	Hs.119325	Huntingtin-interacting protein A	2.17
118530	N67900	Hs.118446	ESTs	2.16
132327	AA203285	Hs.44892	ESTs; Weakly similar to dJ733D15.1 [H.sa	2.16
100564	HG2239-HT2324		Potassium Channel Protein (Gb:Z11585)	2.16
129376	AA022622	Hs.13543	ESTs; Weakly similar to hypothetical pro	2.16
135317	X86012	Hs.98602	Human DNA sequence from intron 22 of the 9.5kb repeated region; int22h-1; involv	2.16
114973	AA250845	Hs.87762	ESTs	2.16
107559	AA001504	Hs.59860	ESTs	2.16
111014	N53787	Hs.191117	ESTs	2.16
101250	L34060	Hs.79133	cadherin 8	2.16
110697	H93721	Hs.20798	ESTs	2.16
126843	AA450166	Hs.22641	ESTs; Moderately similar to predicted pr	2.16
108272	AA063616	Hs.43773	ESTs	2.16
125012	T66935	Hs.104859	ESTs	2.16
111639	R16101	Hs.140834	EST	2.15
123157	AA488443	Hs.100426	DKFZP564A063 protein	2.15
102315	U34252	Hs.2533	aldehyde dehydrogenase 9 (gamma-aminobut	2.15
131897	AA287623	Hs.3426	GTPase; human homolog of E. coli essenti	2.15
121528	AA412253	Hs.238909	ESTs; Weakly similar to POLYPOSIS LOCUS	2.15
122806	AA460707	Hs.106397	ESTs	2.15
125727	H00958	Hs.181641	ESTs	2.15
133279	AA069571	Hs.6957	Homo sapiens clone 24616 mRNA sequence	2.15
103219	X74570	Hs.75268	sialyltransferase 4C (beta-galactosidase	2.15
120881	AA362144	Hs.104601	EST	2.15
134060	D42039	Hs.78871	KIAA0081 protein	2.15
106598	AA457140	Hs.11411	DKFZP566O084 protein	2.15

	125576	R66208		yi30h03.r1 Soares placenta Nb2HP H sapie contains Alu repetitive element;contain	2.15
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb	2.15
	101490	M25629	Hs.123107	kallikrein 1; renal/pancreas/salivary	2.15
5	129708	AA417181	Hs.120858	ESTs	2.14
	100627	HG2702-HT2798		Serine/Threonine Kinase (Gb:Z25424)	2.14
	121703	AA418671	Hs.104807	ESTs	2.14
	106809	AA479704	Hs.220324	Humn DNA seq frm clone 283E3 on chr 1p36	
				Female Reproductive tract MIFR1; -2; MM	2.14
10	129525	F03873	Hs.112306	Homo sapiens clone 24955 mRNA sequence;	2.14
	100478	HG1067-HT1067		Mucin (Gb:M22406)	2.14
	118593	N69020	Hs.207689	EST	2.14
	114047	W94427	Hs.3807	ESTs; Weakly similar to PHOSPHOLEMMAN PR	2.14
	128823	AA478207	Hs.10632	ESTs; Moderately similar to sex-determin	2.14
15	100534	HG1980-HT2023		Tubulin, Beta 2	2.14
	105757	AA321146	Hs.30596	ESTs	2.14
	109617	F03192	Hs.26789	ESTs; Weakly similar to dJ162H14.1 [H.sa	2.14
	121547	AA412448	Hs.104777	ESTs	2.14
	119420	T98291	Hs.102484	glutathione S-transferase A3	2.14
20	120274	AA177051		nc02a02.s1 NCI_CGAP_Pr3 Homo sapiens cDN repetitive element;contains element LTR	2.14
	132933	AA598702	Hs.6101	bone morphogenetic protein 6	2.14
	133405	X07881	Hs.73031	proline-rich protein BstNI subfamily 3	2.14
	119811	W73922	Hs.49047	ESTs	2.14
25	134536	AA457735	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.14
	105125	AA157799	Hs.6980	aldo-keto reductase family 7; member A2	2.14
	101398	M15881	Hs.1137	uromodulin (uromucoid; Tamm-Horsfall gly	2.14
	132751	AA397901	Hs.55993	ESTs	2.13
	115777	AA424142	Hs.39384	putative secreted ligand homologous to f	2.13
30	123193	AA489228	Hs.136956	ESTs	2.13
	116875	H67749	Hs.161022	EST	2.13
	107271	D60607	Hs.34931	EST	2.13
	134551	R44839	Hs.8526	i-beta-1;3-N-acetylglucosaminyltransfera	2.13
	113413	T83739	Hs.186512	ESTs	2.13
35	120522	AA258843	Hs.258748	ESTs	2.13
	119965	W87738	Hs.59039	EST	2.13
	131283	AA101601	Hs.183986	herpesvirus entry mediator B (poliovirus	2.13
	107347	U43628	Hs.102598	mucosal vascular addressin cell adhesion	2.13
	116490	C14265	Hs.66450	ESTs	2.13
40	100563	HG2239-HT2324		Potassium Channel Protein (Gb:Z11585)	2.13
	110441	H50302	Hs.19845	ESTs; Highly similar to protein phosphat	2.13
	101035	J05158	Hs.73858	carboxypeptidase N; polypeptide 2; 83kD	2.13
	132500	AA047297	Hs.50107	ESTs; Moderately similar to CDO [H.sapie	2.13
	129807	L34820	Hs.5299	aldehyde dehydrogenase 5 family; member	2.13
45	106250	AA430466	Hs.28890	ESTs	2.13
	113569	T91086	Hs.162070	EST	2.13
	122911	AA470087	Hs.239726	ESTs	2.13
	107452	W28988	Hs.250746	ESTs	2.12
	111824	R35661	Hs.25006	EST	2.12
50	132831	U53442	Hs.57732	mitogen-activated protein kinase 11	2.12
	110244	H26742	Hs.25367	ESTs; Weakly similar to ALR [H.sapiens]	2.12
	128918	H85347	Hs.107164	spectrin; beta; non-erythrocytic 1	2.12
	133728	M10901	Hs.75772	nuclear receptor subfamily 3; group C; m	2.12
	122476	AA448211	Hs.99164	ESTs	2.12
55	132004	L37360	Hs.37054	ephrin-A3	2.12
	113971	W86760	Hs.220682	ESTs	2.12
	103386	X92972	Hs.80324	protein phosphatase 6; catalytic subunit	2.12
	131120	AA443676	Hs.23133	ESTs; Weakly similar to alcohol sulfotra	2.12
	102186	U20285		G protein pathway suppressor 1	2.12
60	103694	AA018541	Hs.60580	zinc finger protein	2.12
	111995	R42333	Hs.20893	ESTs	2.12
	124436	N39596	Hs.182584	ESTs	2.12
	100306	D50495	Hs.80598	transcription elongation factor A (SII);	2.12
	103084	X59932	Hs.77793	c-src tyrosine kinase	2.11
65	115092	AA255903	Hs.80975	CD39-like 4	2.11
	121579	AA416543	Hs.111981	ESTs	2.11
	127101	AI349351	Hs.118944	ESTs	2.11
	121195	AA400273	Hs.97791	ESTs	2.11
	112721	R91484	Hs.30853	ESTs	2.11
70	113253	T64207	Hs.55296	HLA-B associated transcript-1	2.11
	120838	AA348887	Hs.96907	ESTs	2.11
	114122	Z38582	Hs.12751	ESTs	2.11
	112635	R82298	Hs.29497	ESTs	2.11
	103785	AA095600	Hs.225647	ESTs	2.11
75	128260	AA331445		EST35277 Embryo, 8 week I Homo sapiens c	2.11
	122987	AA479155	Hs.103364	ESTs	2.11

110374	H42983	Hs.227263	ESTs	2.11
116595	D60625	Hs.177656	calmodulin 1 (phosphorylase kinase; delt	2.11
126117	H78617		yu26a08.r1 Soares fetal liver spleen 1NF	2.11
116610	D80448	Hs.45177	ESTs	2.11
111430	R01248	Hs.19165	ESTs	2.11
106700	AA463929	Hs.28701	ESTs	2.11
120181	Z40121	Hs.65870	ESTs; Weakly similar to Pro-Pol-dUTPase	2.1
132545	AA147218	Hs.5105	ESTs	2.1
105005	AA115253	Hs.28805	ESTs	2.1
126702	U54602	Hs.2785	keratin 17	2.1
124096	H10060	Hs.101687	EST	2.1
132720	Z69881	Hs.5541	ATPase; Ca++ transporting; ubiquitous	2.1
121926	AA428559	Hs.104895	ESTs	2.1
125734	AA157445	Hs.227391	DKFZP547E1010 protein	2.1
122368	AA443963	Hs.104964	EST	2.1
116910	H72014	Hs.161031	ESTs; Weakly similar to SYNAPTOTAGMIN I	2.1
113171	T54613	Hs.9761	EST	2.1
134629	U00951	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repea	2.1
105712	AA291293	Hs.25219	ESTs	2.1
106931	AA495918	Hs.26714	ESTs	2.1
114278	Z40424	Hs.27728	ESTs	2.1
116615	D80666	Hs.45203	ESTs	2.09
100189	D21089	Hs.320	xeroderma pigmentosum; complementation g	2.09
119500	W37694	Hs.55561	ESTs	2.09
129605	S72493	Hs.115947	keratin 16 (focal non-epidermolytic palm	2.09
133912	X62744	Hs.77522	major histocompatibility complex; class	2.09
129636	N34942	Hs.11782	ESTs	2.09
106372	AA443941	Hs.4992	tumor suppressing subtransferable candid	2.09
101885	M98539	Hs.8272	prostaglandin D2 synthase (21kD; brain)	2.09
132749	AA235989	Hs.55967	short stature homeobox 2	2.09
135042	X91348	Hs.93522	putative non-coding transcript (DiGeorge	2.09
109404	AA224594	Hs.86941	ESTs	2.09
101333	L47738	Hs.80313	p53 inducible protein	2.09
100114	D00596	Hs.82962	thymidylate synthetase	2.09
130536	T17045	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	2.09
125772	R83903	Hs.78040	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.09
132192	AA247569	Hs.4209	ESTs	2.09
124697	R06273	Hs.186467	ESTs; Moderately similar to !!!! ALU SUB	2.09
127694	AI247780	Hs.117036	ESTs	2.08
127895	AA772600	Hs.187998	ESTs; Weakly similar to ATP-binding cass	2.08
121315	AA402883	Hs.82269	progestagen-associated endometrial prote endometrial alpha-2-globulin; alpha ute	2.08
112150	R46576	Hs.23239	ESTs	2.08
105054	AA133584	Hs.26333	JM1 protein	2.08
113151	T51620	Hs.9326	EST	2.08
118783	N75285	Hs.50593	ESTs; Moderately similar to cytoplasmic	2.08
126748	AA249580	Hs.239975	ESTs; Moderately similar to CDO [H.sapie	2.08
135160	U77643	Hs.95655	secreted and transmembrane 1	2.08
107518	X60152		zinc finger protein 2	2.08
126055	N28990		yx39g04.r1 Soares melanocyte 2NbHM Homo	2.08
116982	H81933	Hs.40317	ESTs	2.08
101756	M77235	Hs.169331	sodium channel; voltage-gated; type V; a	2.08
116935	H75763	Hs.53468	ESTs	2.08
118556	N68408	Hs.194637	Homo sapiens mRNA; cDNA DKFZp564D113 (fr	2.08
129812	L07807	Hs.166161	dynamin 1	2.08
121946	AA429411	Hs.104888	ESTs	2.08
133843	AA489045	Hs.76691	Homo sapiens clone 25100 mRNA sequence;	2.08
122170	AA435744	Hs.163913	ESTs	2.08
122399	AA446449	Hs.231112	EST	2.08
105775	AA348274	Hs.6664	ESTs	2.08
123943	AA621553	Hs.112998	ESTs	2.08
105771	AA347967	Hs.256267	neuroblastoma RAS viral (v-ras) oncogene	2.08
114454	AA021091	Hs.226208	ESTs	2.08
125802	R78852	Hs.151099	ESTs	2.08
131556	AA442853	Hs.2869	cyclin-dependent kinase 5; regulatory su	2.08
118837	N79836	Hs.216338	ESTs	2.08
107345	U26209	Hs.102307	solute carrier family 13 (sodium-depende	2.08
131324	H58690	Hs.25625	ESTs	2.08
105233	AA216759	Hs.191132	ESTs	2.07
112886	T03864	Hs.7436	putative acyltransferase	2.07
120252	AA169400	Hs.152701	DKFZP434F124 protein	2.07
114867	AA235310	Hs.52899	ESTs; Moderately similar to !!!! ALU SUB	2.07
106715	AA464955	Hs.126062	ESTs; Weakly similar to EPIDERMAL GROWTH	2.07
125560	R51281	Hs.13692	ESTs; Highly similar to PROTEIN TSG24 [M	2.07
112270	R53021	Hs.203358	ESTs	2.07
134626	S82198	Hs.8709	caldecrin (serum calcium decreasing fact	2.07

115723	AA417345	Hs.54846	ESTs	2.07	
123895	AA621192	Hs.112949	EST	2.07	
119906	W85818		ESTs; Moderately similar to !!!! ALU SUB	2.07	
108559	AA085161		zn12c5.s1 Stratagene hNT neuron (#937233 IMAGE:54728 3' similar to TR:G1151228 G	2.07	
101246	L33799	Hs.202097	procollagen C-endopeptidase enhancer	2.07	
100663	HG2915-HT3059		Major Histocompatibility Complex, Class I, E (Gb:M20022)		2.07
114178	Z39063	Hs.17930	Humn DNA seq frm clone 1033B10 on chr 6p for GalT3 (beta3-Galactosyltransferase)	2.07	
125672	AA152281	Hs.78601	uroporphyrinogen decarboxylase	2.07	
118052	N53360	Hs.165133	ESTs	2.07	
102387	U41163	Hs.229731	solute carrier family 6 (neurotransmitte	2.07	
127305	AA535148	Hs.255277	ESTs	2.07	
101182	L19711	Hs.76111	dystroglycan 1 (dystrophin-associated gl	2.07	
131111	R33245	Hs.23076	ESTs; Weakly similar to putative [C.eleg	2.07	
112441	R63388	Hs.28412	ESTs	2.06	
117796	N48571	Hs.46689	EST	2.06	
116099	AA456309	Hs.58831	regulator of Fas-induced apoptosis	2.06	
125559	AA307550	Hs.119571	collagen; type III; alpha 1 (Ehlers-Danl	2.06	
135271	AA397763	Hs.97562	ESTs	2.06	
106083	AA418545	Hs.31659	thyroid hormone receptor-associated prot	2.06	
133419	U67369	Hs.73172	growth factor independent 1	2.06	
127816	AA743646	Hs.120604	ESTs	2.06	
127502	AA614422	Hs.183502	ESTs	2.06	
129371	M10321	Hs.110802	von Willebrand factor	2.06	
108417	AA075716		zm89e5.s1 Stratagene ovarian cancer (#93 CLUSTERIN PRECURSOR (HUMAN);, mRNA sequ		2.06
102837	U94585	Hs.13495	requiem; apoptosis response zinc finger	2.06	
124226	H62396	Hs.190266	ESTs	2.06	
102254	U28131		Human HMGI-C chimeric transcript mRNA, p	2.06	
128472	X87212	Hs.10029	cathepsin C	2.06	
107545	Z82022	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosam	2.06	
135311	M36089	Hs.98493	X-ray repair complementing defective rep	2.06	
121727	AA420973	Hs.104234	ESTs	2.06	
131846	U02619	Hs.331	general transcription factor IIIC; polyp	2.06	
120415	AA235810	Hs.182522	ESTs	2.06	
110529	H57686	Hs.37486	ESTs	2.06	
104996	AA112307	Hs.105894	Homo sapiens mRNA; cDNA DKFZp434G231 (fr		2.06
110351	H41222	Hs.196459	ESTs	2.06	
131261	AA223746	Hs.171776	inositol(myo)-1(or 4)-monophosphatase 1	2.06	
110585	H62223	Hs.133526	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.06	
129420	AA234259	Hs.99816	ESTs	2.06	
103796	AA112595	Hs.31146	Human DNA sequence from clone 1042K10 on lyase (EC 4.3.2.2; Adenylosuccinase; AS 3). Contains ESTs; STSs; GS	2.06	
119782	W72982	Hs.58262	ESTs	2.06	
108641	AA112059		ATP synthase; H+ transporting; mitochond	2.06	
134875	U66672	Hs.180513	ATP-binding cassette; sub-family A (ABC1	2.06	
106832	AA482015	Hs.30114	ESTs; Highly similar to C8 [H.sapiens]	2.06	
109403	AA224413	Hs.86937	ESTs	2.06	
115485	AA287667	Hs.188804	ESTs	2.06	
102923	X12517	Hs.1063	small nuclear ribonucleoprotein polypept	2.06	
123320	AA496792	Hs.139572	EST	2.05	
111901	R39066	Hs.17638	ESTs	2.05	
106558	AA455111	Hs.182447	heterogeneous nuclear ribonucleoprotein	2.05	
126885	AA293052	Hs.10101	ESTs; Weakly similar to coded for by C.	2.05	
113429	T85190	Hs.179808	ESTs	2.05	
102270	U30255	Hs.75888	phosphogluconate dehydrogenase	2.05	
103204	X72475	Hs.192989	H.sapiens mRNA for rearranged Ig kappa l	2.05	
106666	AA461072	Hs.37916	ESTs	2.05	
100947	HG907-HT907		Mg44	2.05	
102578	U60666	Hs.57693	testis specific leucine rich repeat prot	2.05	
105827	AA398255	Hs.31520	ESTs	2.05	
122324	AA442830	Hs.98921	EST	2.05	
101025	J04823	Hs.81097	cytochrome c oxidase subunit VIII	2.05	
115861	AA431768	Hs.90259	ESTs; Weakly similar to alpha 1 [H.sapie	2.05	
108081	AA045306	Hs.42996	ESTs	2.05	
133994	X74929	Hs.242463	keratin 8	2.05	
119131	R46700	Hs.129692	ESTs; Moderately similar to !!!! ALU SUB	2.05	
129793	AA300151	Hs.126857	ESTs	2.05	
101653	M60284	Hs.161305	tachykinin receptor 2	2.05	
120300	AA191648	Hs.131476	ESTs	2.05	
106519	AA453415	Hs.8763	Hu DNA sequence from clone 889N15 on chr Thymocyte Marker CTX; the possibly alte	2.05	
114291	Z40690	Hs.123666	Homo sapiens mRNA full length insert cDN	2.05	
105747	AA293719	Hs.30251	ESTs; Weakly similar to GLUCOSE-6-PHOSPH		2.04

125325	AA332944	Hs.8402	adenylate cyclase 3	2.04	
119978	W88623	Hs.59190	EST	2.04	
102449	U48231	Hs.46348	bradykinin receptor B1	2.04	
101454	M21812	Hs.50889	myosin light chain 2	2.04	
116086	AA455904	Hs.86023	ESTs	2.04	
102297	U32674	Hs.198252	G protein-coupled receptor 9	2.04	
130889	D57622	Hs.20985	sin3-associated polypeptide; 30kD	2.04	
100196	D21853	Hs.79768	KIAA0111 gene product	2.04	
120967	AA398111	Hs.97503	ESTs	2.04	
105735	AA293096	Hs.32417	ESTs	2.04	
135031	R41604	Hs.9344	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.04	
104882	AA052954	Hs.29546	ESTs	2.04	
132619	AA404565	Hs.53447	ESTs; Moderately similar to kinesin ligh	2.04	
127993	AA847856	Hs.124565	ESTs	2.04	
116441	AA620299	Hs.91696	ESTs	2.04	
102272	U30610	Hs.41682	killer cell lectin-like receptor subfami	2.04	
119566	W38209		Accession not listed in Genbank	2.04	
116622	D81171	Hs.45208	ESTs; Weakly similar to collagen type VI	2.04	
127182	AA248620	Hs.166011	catenin (cadherin-associated protein); d	2.04	
116870	H67146	Hs.38564	ESTs	2.04	
115448	AA284845	Hs.165051	ESTs	2.04	
127231	AA434584		zw52c03.r1 Soares_total_fetus_Nb2HF8_9w	2.04	
103457	X99728		H.sapiens NDUFV3 gene, exon 3	2.04	
134737	U00802	Hs.89434	drebrin 1	2.04	
117046	H89505		yu81f4.s1 Soares fetal liver spleen 1NFL to contains Alu repetitive element;, mR	2.04	
124579	N68345	Hs.127179	ESTs; Weakly similar to TERATOCARCINOMA-		2.04
112132	R45970	Hs.236349	EST	2.04	
132281	AA133300	Hs.43803	leukocyte-associated Ig-like receptor 2	2.03	
103668	Z83741	Hs.248174	H2A histone family; member M	2.03	
113501	T89107	Hs.13262	ESTs	2.03	
125021	T70060	Hs.163918	ESTs	2.03	
115754	AA420998	Hs.178095	ESTs	2.03	
123405	AA521370	Hs.191708	ESTs	2.03	
102054	U07695	Hs.155227	EphB4	2.03	
115627	AA401910	Hs.119175	ESTs; Weakly similar to ZINC FINGER PROT	2.03	
129252	AA234663	Hs.109773	ESTs	2.03	
103417	X96849		H.sapiens 5' mRNA of PECAM-1 molecule	2.03	
133721	U11863	Hs.75741	amiloride binding protein 1 (amine oxida	2.03	
114176	Z39059	Hs.27267	ESTs; Weakly similar to tetraspan TM4SF	2.03	
123966	C14068	Hs.21806	ESTs; Moderately similar to similar to N	2.03	
134236	D45371	Hs.80485	adipose most abundant gene transcript 1	2.03	
116381	AA598614	Hs.65394	ESTs	2.03	
103711	AA046737	Hs.102792	ESTs	2.03	
109316	AA206914	Hs.86322	EST	2.03	
123793	AA620343	Hs.112858	ESTs	2.03	
128462	M69238	Hs.166172	aryl hydrocarbon receptor nuclear transl	2.03	
117690	N40467	Hs.93834	ESTs	2.03	
113301	T67452	Hs.13104	EST	2.03	
134563	AA173430	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f		2.03
108316	AA070160		zm69f4.s1 Stratagene neuroepithelium (#9	2.03	
135239	AA454599	Hs.19399	Homo sapiens chromosome 19; fosmid 39554	2.03	
120342	AA207105	Hs.45068	Homo sapiens mRNA; cDNA DKFZp434I143 (fr		2.02
103493	Y08976	Hs.234759	H.sapiens mRNA for FEV protein	2.02	
114204	Z39259	Hs.26096	ESTs	2.02	
125425	H62307	Hs.18575	ESTs; Weakly similar to KIAA0246 [H.sapi	2.02	
133027	AA402624	Hs.63236	synuclein; gamma (breast cancer-specific	2.02	
131323	H54036	Hs.25619	death-associated protein kinase 3	2.02	
121515	AA412133	Hs.104696	ESTs	2.02	
129780	AA291526	Hs.124699	ESTs	2.02	
131292	AF005039	Hs.200600	secretory carrier membrane protein 3	2.02	
132973	AA035446	Hs.214361	ESTs	2.02	
103727	AA059415	Hs.6289	growth factor receptor-bound protein 2	2.02	
113174	T54659	Hs.9779	ESTs	2.02	
120964	AA398085	Hs.142390	ESTs	2.02	
134303	AA457242	Hs.8141	etoposide-induced mRNA	2.02	
128118	T81623	Hs.21765	hypothetical protein of unknown functio	2.02	
121087	AA398751	Hs.97304	ESTs	2.02	
102806	U90306		Human iroquois-class homeodomain protein	2.02	
103195	X70940	Hs.2642	eukaryotic translation elongation factor	2.02	
126767	C17148		C17148 Clontech human aorta polyA+ mRNA	2.02	
105179	AA189083	Hs.21974	ESTs; Moderately similar to mBOCT [M.mus	2.02	
116797	H40486		yn87a08.s1 Soares adult brain N2b5HB55Y 3' similar to contains Alu repetitive e	2.02	
133268	AA099404	Hs.69307	ESTs	2.02	
123951	AA621721	Hs.231130	EST	2.02	

115463	AA286819	Hs.69485	ESTs; Weakly similar to similar to other	2.02
110603	H65776	Hs.222403	ESTs	2.02
101234	L29277	Hs.142258	signal transducer and activator of trans	2.02
121208	AA400470	Hs.97805	ESTs	2.02
122598	AA453465	Hs.99329	ESTs	2.02
110668	H84882	Hs.33791	ESTs; Weakly similar to K:Cl cotransport	2.02
117137	H96670	Hs.42221	ESTs	2.02
119389	T88826	Hs.90973	ESTs	2.01
102940	X13956	Hs.24998	Human 12S RNA induced by poly(rI); poly(	2.01
100748	HG3517-HT3711		Alpha-1-Antitrypsin, 5' End	2.01
103012	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2;6-bi	2.01
132755	AA609201	Hs.182635	ESTs	2.01
130842	H39589	Hs.20159	ESTs; Highly similar to CGI-92 protein [	2.01
133599	M64788	Hs.75151	RAP1; GTPase activating protein 1	2.01
117250	N21081	Hs.15299	HMBA-inducible	2.01
115124	AA256666	Hs.39156	ESTs	2.01
128155	AA926843	Hs.143302	ESTs	2.01
130574	AA379087	Hs.16178	apoptosis antagonizing transcription fac	2.01
132601	R78838	Hs.54943	fracture callus 1 (rat) homolog	2.01
117428	N27366	Hs.43933	EST	2.01
121108	AA399053	Hs.97529	EST	2.01
130518	X69550	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	2.01
110606	H66049	Hs.19085	ESTs; Weakly similar to putative p150 [H	2.01
120606	AA282956		zt15h4.s1 NCI_CGAP_GCB1 Homo sapiens cDN SW:CADR_MOUSE P3938 RETINAL-CADHERIN PR	2.01
130070	T47969	Hs.194660	ceroid-lipofuscinosis; neuronal 3; juven	2.01
130331	Z80783	Hs.239884	H2B histone family; member L	2.01
109599	F02602	Hs.6749	ESTs	2.01
131749	W78211	Hs.31547	ESTs; Highly similar to NADH:ubiquinone	2.01
129463	AA376905	Hs.111742	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.01
114880	AA235698	Hs.65862	ESTs	2.01
114745	AA135523	Hs.139064	EST	2.01
115637	AA402727	Hs.76925	ESTs; Highly similar to R31167_2; partia	2.01
109043	AA159605	Hs.72580	ESTs	2.01
128901	Z41411	Hs.107040	ESTs	2.01
124427	N36812	Hs.178663	ESTs	2
100673	HG3033-HT3194		Spliceosomal Protein Sap 62	2
108436	AA078801		zm94a9.s1 Stratagene colon HT29 (#937221	2
123764	AA610019	Hs.112654	ESTs	2
129343	N70791	Hs.180060	ESTs	2
122794	AA460254	Hs.105043	EST	2
128688	AA161469	Hs.103755	receptor-interacting serine-threonine ki	2
115592	AA399543	Hs.48026	ESTs	2
111693	R22007	Hs.23321	EST	2
113353	T79186	Hs.14468	ESTs	2

Table 18: B survivor vs Mets – Up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG ID	Complete Title	Ratio BS/Met
106024	AA412059	Hs.111742	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.17
110930	N48603	Hs.14947	ESTs	0.18
105772	AA347973	Hs.221132	ESTs	0.2
133271	Z48633	Hs.6940	H.sapiens mRNA for retrotransposon	0.2
107109	AA609943	Hs.32793	ESTs	0.24
109593	F02506	Hs.159591	thyroid hormone receptor interactor 8	0.24
123016	AA480103	Hs.111730	ESTs; Weakly similar to alternatively sp	0.25
100739	HG3484-HT3678		Protein Kinase (Gb:M59287)	0.25
130252	U92014	Hs.153527	Human clone 121711 defective mariner tra	0.26
105149	AA169253	Hs.8958	ESTs	0.26
115412	AA283804	Hs.193552	ESTs	0.27
105952	AA405263	Hs.181400	ESTs	0.28
106596	AA456981	Hs.35349	ESTs	0.28
120249	AA167567	Hs.133325	ESTs	0.28
111676	R19414	Hs.166459	ESTs	0.29
111161	N66767	Hs.124145	ESTs	0.29
109364	AA215379	Hs.50418	ESTs	0.29
132316	U28831		Human protein immuno-reactive with anti-	0.3
104030	AA363131	Hs.222992	ESTs; Weakly similar to TRANSFORMATION-S	0.3
109825	F13663	Hs.16798	ESTs	0.3
111110	N63165	Hs.23618	ESTs	0.31
135315	W90583	Hs.9853	ESTs	0.32
104792	AA029288	Hs.29147	ESTs; Highly similar to ZINC FINGER PROT	0.33
123562	AA608893	Hs.190065	ESTs	0.33
116079	AA455286	Hs.54982	ESTs; Weakly similar to !!!! ALU SUBFAMI	0.33
110671	H87770	Hs.153800	ESTs	0.33
108819	AA130986	Hs.193253	ESTs	0.34
115558	AA393806	Hs.1010	regulator of mitotic spindle assembly 1	0.34
104781	AA026617	Hs.21610	ESTs; Highly similar to BAI1-associated	0.34
111236	N69324	Hs.12526	Homo sapiens clone 23903 mRNA sequence	0.34
113341	T77866	Hs.189703	ESTs	0.35
125371	AI084676	Hs.133266	ESTs; Moderately similar to Sqv-7-like p	0.35
115890	AA435853	Hs.44114	ESTs; Weakly similar to CGI-73 protein [	0.35
113571	T91116	Hs.15713	ESTs	0.35
121683	AA417911	Hs.175663	ESTs	0.35
105489	AA256157	Hs.24115	ESTs	0.35
116320	AA490866	Hs.39429	ESTs	0.36
111917	R39882	Hs.21397	ESTs	0.36
127568	T53722		ya91c06.r3 Stratagene placenta (#937225)	0.36
123541	AA608794	Hs.112592	ESTs	0.36
123131	AA487207	Hs.193272	ESTs	0.36
125069	T86914	Hs.194485	ESTs	0.36
114757	AA136725	Hs.161990	ESTs	0.37
132778	AA446695	Hs.5671	Homo sapiens clone 23926 mRNA sequence	0.37
123132	AA487233	Hs.106711	eukaryotic translation initiation factor	0.37
134029	AA378597	Hs.143601	ESTs; Moderately similar to 67A9.b [D.me	0.37
126956	AI434405	Hs.171957	triple functional domain (PTPRF interact	0.38
106869	AA487563	Hs.188813	ESTs	0.38
107818	AA020957	Hs.167948	ESTs	0.38
129974	K00629	Hs.199300	Human kpni repeat mma (cdna clone pcd-k	0.38
129477	D49728	Hs.1119	nuclear receptor subfamily 4; group A; m	0.38
119369	T79020	Hs.245915	ESTs; Weakly similar to kinase-related p	0.39
114021	W91995	Hs.16145	ESTs	0.39
122024	AA431296	Hs.139433	EST	0.39
130014	N50959	Hs.143102	amine oxidase; copper containing 2 (reti	0.39
110163	H19326	Hs.22073	ESTs; Highly similar to J KAPPA-RECOMBIN	0.39
104641	AA004652	Hs.18564	ESTs	0.39
124777	R41933	Hs.140237	ESTs	0.39
125382	AA713494	Hs.194660	ceroid-lipofuscinosis; neuronal 3; juven	0.4
120406	AA234999	Hs.111279	ESTs; Weakly similar to unnamed protein	0.4
132734	R23653	Hs.164250	ESTs	0.4
117001	H84719	Hs.40721	EST	0.4
120905	AA371602	Hs.182930	ESTs; Highly similar to PHOSPHATIDYLINOS	0.4
125488	AA355158	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	0.4

121989	AA430044	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f		0.4
127921	AA806616	Hs.209523	ESTs	0.4	
119830	W74700	Hs.53478	ESTs	0.41	
106292	AA435571	Hs.148560	ESTs	0.41	
102762	U82303	Hs.123080	Homo sapiens unknown protein mRNA; parti	0.41	
113518	T89731		ye11f06.s1 Stratagene lung (#937210) H s to contains Alu repetitive element;cont	0.41	
100635	HG2724-HT2820		Oncogene Tls/Chop, Fusion Activated	0.41	
113319	T70356	Hs.193141	ESTs; Weakly similar to coding sequence	0.41	
121319	AA402935	Hs.194242	ESTs; Weakly similar to !!!! ALU CLASS B	0.42	
111818	R34382	Hs.24779	ESTs	0.42	
104883	AA052959	Hs.177409	ESTs; Highly similar to dJ1119D9.2 [H.sa	0.42	
129258	W95592	Hs.251946	ESTs; Moderately similar to POLYADENYLAT	0.42	
130576	T86475	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr		0.43
106354	AA443271	Hs.26764	KIAA0546 protein	0.43	
108841	AA132524	Hs.70614	ESTs	0.43	
113922	W80741	Hs.37890	ESTs	0.43	
120997	AA398285	Hs.97598	EST	0.43	
108158	AA054597	Hs.221935	ESTs	0.43	
124516	N58185	Hs.131830	ESTs	0.43	
114477	AA032013	Hs.144260	EST	0.43	
104290	C16652	Hs.107205	Homo sapiens mRNA; cDNA DKFZp434L2221 (f		0.43
126700	AI318412	Hs.108258	actin binding protein; macrophin (microf	0.44	
110887	N38770	Hs.4283	ESTs	0.44	
116141	AA460420	Hs.44949	ESTs	0.44	
110689	H93046	Hs.15571	ESTs	0.44	
115314	AA280583	Hs.256501	ESTs	0.44	
110904	N39453	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (fr		0.44
109482	AA233375	Hs.78085	ESTs	0.44	
102284	U31449	Hs.11881	transmembrane 4 superfamily member 4	0.44	
118654	N70582	Hs.49892	ESTs	0.44	
115334	AA281244	Hs.65300	ESTs	0.44	
113149	T51588		ESTs; Moderately similar to !!!! ALU SUB	0.44	
113721	T97931	Hs.18190	EST	0.44	
111299	N73808	Hs.24936	ESTs	0.44	
103778	AA094107	Hs.7187	ESTs; Weakly similar to similar to glyco	0.44	
113204	T57865	Hs.10310	EST	0.44	
100315	D50857	Hs.82295	dedicator of cyto-kinesis 1	0.44	
115254	AA279024	Hs.194437	ESTs	0.44	
125500	H46104	Hs.244624	ESTs	0.44	
117387	N26011	Hs.53810	ESTs	0.45	
135113	W42450	Hs.206833	ESTs	0.45	
124517	N58204	Hs.199945	ESTs	0.45	
120379	AA227849	Hs.238380	Human endogenous retroviral protease mRN	0.45	
119205	R91954	Hs.153699	ESTs	0.45	
128266	T70341	Hs.131897	ESTs	0.45	
104106	AA422123	Hs.42457	ESTs	0.45	
115864	AA432080	Hs.81200	ESTs	0.45	
113771	W02695	Hs.18714	ESTs	0.45	
126515	AI124649	Hs.252708	Homo sapiens mRNA; cDNA DKFZp586O031 (fr		0.45
127823	AA524806	Hs.78869	transcription elongation factor A (SII);	0.45	
116665	F04405	Hs.223654	EST	0.45	
106355	AA443272	Hs.27836	ESTs	0.45	
132693	AA621429	Hs.55075	KIAA0410 gene product	0.45	
107388	W01587	Hs.173319	ESTs	0.45	
110688	H93021	Hs.182937	peptidylprolyl isomerase A (cyclophilin	0.46	
116893	H69569	Hs.191316	EST	0.46	
105375	AA236542	Hs.9512	ESTs; Moderately similar to !!!! ALU SUB	0.46	
115601	AA400277	Hs.48849	ESTs	0.46	
106896	AA489707	Hs.29896	ESTs; Weakly similar to proline-rich pro	0.46	
111770	R27975	Hs.187469	ESTs	0.46	
115663	AA405838	Hs.40507	ESTs	0.46	
131404	AA504744	Hs.26461	ESTs; Weakly similar to gc-rich sequence	0.46	
108622	AA101828	Hs.189956	ESTs	0.46	
128286	AI025771	Hs.144090	ESTs	0.46	
105760	AA338960	Hs.28170	ESTs	0.46	
100020			AFFX control: BioB-3	0.46	
105209	AA205072	Hs.227743	KIAA0980 protein	0.47	
111975	R41724	Hs.149566	ESTs	0.47	
114688	AA121403	Hs.144331	ESTs	0.47	
116994	H83918	Hs.40528	ESTs	0.47	
118401	N64762	Hs.49053	EST	0.47	
110997	N52540	Hs.74316	desmoplakin (DPI; DPII)	0.47	
123791	AA620331	Hs.245351	EST	0.47	
109858	H02266	Hs.167451	ESTs	0.47	
115470	AA287122	Hs.48391	ESTs	0.47	

130606	AA402109	Hs.16593	ESTs	0.47
116067	AA454827	Hs.124823	ESTs	0.47
125881	AA775807	Hs.150741	2';3'-cyclic nucleotide 3' phosphodieste	0.47
124028	F04112	Hs.177178	ESTs	0.47
108995	AA155574	Hs.172702	ESTs	0.47
125102	T95105	Hs.173772	ESTs	0.47
110421	H48462	Hs.36093	ESTs; Weakly similar to reverse transcri	0.47
105658	AA282914	Hs.10176	ESTs	0.47
129046	AA195678	Hs.108258	actin binding protein; macrophin (microf	0.47
113639	T95128	Hs.17529	ESTs	0.48
132575	AA045365	Hs.5188	ESTs; Weakly similar to 60S RIBOSOMAL PR	0.48
132592	AA129390	Hs.5285	ESTs	0.48
107619	AA004955	Hs.60015	ESTs	0.48
118664	N70907	Hs.230619	EST	0.48
127612	AA917801	Hs.116076	ESTs	0.48
112319	R55615	Hs.26432	ESTs; Weakly similar to finger protein H	0.48
113635	T95087	Hs.15543	ESTs	0.48
119344	T62969	Hs.193348	ESTs	0.48
121080	AA398720	Hs.177953	ESTs	0.48
133686	X83378	Hs.211614	chloride channel 6	0.48
130395	R54534	Hs.87889	helicase-moi	0.49
127530	AA563806	Hs.145728	ESTs	0.49
132971	AA033951	Hs.61700	ESTs	0.49
127132	AA721156	Hs.190440	ESTs	0.49
129980	T72661	Hs.13969	ESTs	0.49
105323	AA234112	Hs.29075	ESTs	0.49
114439	AA018937	Hs.128629	ESTs	0.49
107632	AA007242	Hs.60179	EST	0.49
130952	AB002296	Hs.21560	Human mRNA for KIAA0298 gene; complete c	0.49
127595	AA927308	Hs.130464	ESTs	0.49
124276	H83465	Hs.221934	ESTs	0.49
125935	H30721	Hs.30172	ESTs	0.49
131275	U45974	Hs.25156	Human phosphatidylinositol (4;5) bisphos	0.49
131196	C20633	Hs.24129	ESTs	0.49
125505	AI127843	Hs.155071	ESTs	0.5
113327	T71776	Hs.12097	ESTs	0.5
104709	AA017146	Hs.34579	ESTs; Moderately similar to !!!! ALU SUB	0.5
115772	AA423972	Hs.8154	ESTs	0.5
118296	N63150	Hs.48723	ESTs	0.5
131453	C20596	Hs.26985	KIAA0457 protein	0.5
104734	AA019528	Hs.32677	ESTs	0.5
119358	T70550	Hs.193651	ESTs; Weakly similar to alternatively sp	0.5

Table 19: B survivor vs Mets – Up in B survivor

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met
333601			CH22_FGENES.213_4	5.5
325300			CH.11_hs gi|5866908	4.67
333642			CH22_FGENES.231_2	4.64
333591			CH22_FGENES.208_4	4.46
332859			CH22_FGENES.27_2	4.39
304013	AW518573	Hs.156110	Immunoglobulin kappa variable 1D-8	4.23
333791			CH22_FGENES.274_10	4.18
327641			CH.04_hs gi|5867890	4.03
321172	H49160	Hs.133472	ESTs	3.9
334125			CH22_FGENES.334_4	3.88
333646			CH22_FGENES.234_2	3.88
326554			CH.19_hs gi|5867308	3.84
333650			CH22_FGENES.238_3	3.82
333647			CH22_FGENES.235_2	3.79
333626			CH22_FGENES.224_2	3.68
314671	AW236550	Hs.131914	ESTs	3.68
310847	AI420523	Hs.161282	ESTs	3.67
333657			CH22_FGENES.241_2	3.65
338522			CH22_EM:AC005500.GENSCAN.395-36	3.64
329464			CH.Y_hs gi|6456788	3.6
328868			CH.07_hs gi|6381930	3.6
333637			CH22_FGENES.229_2	3.59
329737			CH.14_p2 gi|6065779	3.5
317828	AI791749	Hs.128896	ESTs	3.44
330520	M96995	Hs.6289	growth factor receptor-bound protein 2	3.44
339271			CH22_BA354I12.GENSCAN.11-2	3.44
314927	AI735482	Hs.159580	ESTs	3.42
334782			CH22_FGENES.432_7	3.42
313138	AW138842	Hs.196669	ESTs	3.4
332650	H51596	Hs.5541	ATPase; Ca++ transporting; ubiquitous	3.38
338648			CH22_EM:AC005500.GENSCAN.460-6	3.38
325677			CH.14_hs gi|5867017	3.34
312639	H50648	Hs.213221	ESTs; Weakly similar to !!!! ALU SUBFAMI	3.33
326545			CH.19_hs gi|5867307	3.32
318364	R44616	Hs.138280	ESTs; Moderately similar to !!!! ALU SUB	3.3
308385	AI625428		EST singleton (not in UniGene) with exon	3.26
328569			CH.07_hs gi|6004480	3.26
328582			CH.07_hs gi|6006033	3.24
310975	AI492857	Hs.170940	ESTs	3.24
336883			CH22_FGENES.322-2	3.21
324425	AW236939	Hs.172154	ESTs	3.2
337870			CH22_EM:AC005500.GENSCAN.48-3	3.19
306624	AI001043		EST singleton (not in UniGene) with exon	3.17
319091	Z45264		EST cluster (not in UniGene)	3.16
335247			CH22_FGENES.516_8	3.12
324945	AA088768		EST cluster (not in UniGene)	3.1
319468	R06504		EST cluster (not in UniGene)	3.09
301635	AI590720	Hs.192662	ESTs; Weakly similar to ZINC FINGER PROT	3.08
321215	AW378128	Hs.120243	ESTs; Weakly similar to CGI-56 protein [	3.04
328507			CH.07_hs gi|5868473	3.03
330266			CH.05_p2 gi|6671885	3.02
326249			CH.17_hs gi|5867263	3.01
325649			CH.14_hs gi|6588011	2.99
304575	AA496437		EST singleton (not in UniGene) with exon	2.98
304559	AA488050		EST singleton (not in UniGene) with exon	2.97
338412			CH22_EM:AC005500.GENSCAN.341-25	2.96
308707	AI769997		EST singleton (not in UniGene) with exon	2.95
313027	N34307	Hs.184003	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.95
306590	AI000246		EST singleton (not in UniGene) with exon	2.95
306183	AA922622		EST singleton (not in UniGene) with exon	2.94
308611	AI735372	Hs.203820	EST; Moderately similar to TRANSLATIONAL	2.94
332454	T63265	Hs.11186	ESTs; Weakly similar to transformation-r	2.94

	330061			CH.17_p2 gi|6721261	2.94
	317671	AW138139	Hs.244598	ESTs	2.93
	338705			CH22_EM:AC005500.GENSCAN.480-4	2.93
	333737			CH22_FGENES.261_1	2.9
5	337756			CH22_EM:AC000097.GENSCAN.109-3	2.9
	333572			CH22_FGENES.189_1	2.89
	335349			CH22_FGENES.539_2	2.89
	328835			CH.07_hs gi|5868339	2.89
	319886	AA984628		EST cluster (not in UniGene)	2.88
10	311247	AI655313	Hs.197692	ESTs	2.87
	303887	R72672	Hs.193484	ESTs; Weakly similar to Similarity with	2.86
	337564			CH22_C65E1.GENSCAN.1-7	2.85
	333225			CH22_FGENES.107_3	2.84
	314938	AA515635		EST cluster (not in UniGene)	2.83
15	305803	AA846052		EST singleton (not in UniGene) with exon	2.83
	305264	AA679505		EST singleton (not in UniGene) with exon	2.83
	332646	AA386264	Hs.5337	isocitrate dehydrogenase 2 (NADP+); mito	2.81
	338508			CH22_EM:AC005500.GENSCAN.391-1	2.81
	308097	AI475411		EST singleton (not in UniGene) with exon	2.81
20	301130	AW194167	Hs.149418	ESTs; Weakly similar to salivary proline	2.8
	325571			CH.12_hs gi|6552439	2.8
	307054	AI148181	Hs.176835	EST	2.8
	337456			CH22_FGENES.777-2	2.79
	317870	AI797066	Hs.201995	ESTs	2.79
25	303171	AA065003	Hs.64179	hypothetical protein	2.78
	333717			CH22_FGENES.253_3	2.76
	303778	AW505368		EST cluster (not in UniGene) with exon h	2.76
	304918	AA602697		EST singleton (not in UniGene) with exon	2.76
	319373	R00371		EST cluster (not in UniGene)	2.75
30	336072			CH22_FGENES.685_4	2.74
	306023	AA897764		EST singleton (not in UniGene) with exon	2.74
	336127			CH22_FGENES.701_15	2.74
	337355			CH22_FGENES.728-1	2.73
	337885			CH22_EM:AC005500.GENSCAN.54-3	2.73
35	308506	AI686791	Hs.119598	ribosomal protein L3	2.73
	300629	AA152119	Hs.155101	ATP synthase; H+ transporting; mitochond	2.73
	333043			CH22_FGENES.70_4	2.72
	327736			CH.05_hs gi|5867940	2.72
	333007			CH22_FGENES.60_4	2.72
40	321966	AL122111		EST cluster (not in UniGene)	2.72
	323179	AW452576	Hs.156875	ESTs	2.72
	332459	AA609625	Hs.112933	Homo sapiens Tax interaction protein 40	2.71
	326224			CH.17_hs gi|5867230	2.71
	329114			CH.X_hs gi|5868650	2.7
45	333577			CH22_FGENES.196_2	2.69
	300413	AW090347	Hs.243443	ESTs	2.67
	304055	R07994		EST singleton (not in UniGene) with exon	2.67
	301013	AI935304	Hs.125262	DKFZP586G1624 protein	2.67
	337848			CH22_EM:AC005500.GENSCAN.33-1	2.66
50	327946			CH.06_hs gi|5868206	2.66
	306300	AA937573		EST singleton (not in UniGene) with exon	2.66
	331071	R01646	Hs.200538	ESTs	2.65
	304841	AA587541		EST singleton (not in UniGene) with exon	2.65
	301321	AI860987	Hs.189097	ESTs	2.65
55	311280	AI767957	Hs.197737	ESTs; Weakly similar to Y38A8.1 gene pro	2.65
	338843			CH22_DJ246D7.GENSCAN.8-1	2.64
	335720			CH22_FGENES.599_23	2.64
	333670			CH22_FGENES.245_4	2.64
	313588	AI803591	Hs.209667	ESTs	2.64
60	335750			CH22_FGENES.602_4	2.63
	333240			CH22_FGENES.111_4	2.63
	332721	R70212	Hs.79630	CD79A antigen (immunoglobulin-associated	2.62
	338747			CH22_EM:AC005500.GENSCAN.511-1	2.62
	303582	AA377444		EST cluster (not in UniGene) with exon h	2.62
65	336898			CH22_FGENES.330-1	2.62
	325835			CH.16_hs gi|6552452	2.62
	301660	F13112		EST cluster (not in UniGene) with exon h	2.61
	335968			CH22_FGENES.652_1	2.61
	336705			CH22_FGENES.63-2	2.6
70	309815	AW292760		EST singleton (not in UniGene) with exon	2.6
	339220			CH22_FF113D11.GENSCAN.6-15	2.6
	308582	AI709056		EST singleton (not in UniGene) with exon	2.6
	334260			CH22_FGENES.367_8	2.6
	309963	AW449073		EST singleton (not in UniGene) with exon	2.6
75	300178	AI282665	Hs.166969	ESTs	2.59
	335690			CH22_FGENES.596_5	2.59

308127	AI492187		EST singleton (not in UniGene) with exon	2.59	
337835			CH22_EM:AC005500.GENSCAN.22-4	2.58	
333251			CH22_FGENES.116_3	2.58	
330319			CH.08_p2 gi|5932415	2.58	
314490	AI758114	Hs.197032	ESTs	2.57	
305934	AA878815	Hs.75442	albumin	2.57	
329665			CH.14_p2 gi|6272129	2.57	
328558			CH.07_hs gi|5868489	2.57	
336094			CH22_FGENES.691_3	2.57	
307899	AI380270		EST singleton (not in UniGene) with exon	2.57	
339312			CH22_BA354I12.GENSCAN.22-10	2.57	
336442			CH22_FGENES.827_8	2.57	
317894	R60848		EST cluster (not in UniGene)	2.56	
330435	HG2689-HT2785		Mucin 5b, Tracheobronchial (Gb:X74955)	2.56	
327304			CH.01_hs gi|5867494	2.56	
308859	AI830787		EST singleton (not in UniGene) with exon	2.55	
302224	AI951549	Hs.161166	KIAA1094 protein	2.55	
304324	AA137045		EST singleton (not in UniGene) with exon	2.54	
338090			CH22_EM:AC005500.GENSCAN.176-3	2.53	
334797			CH22_FGENES.434_5	2.52	
303535	AL043430		EST cluster (not in UniGene) with exon h	2.52	
339037			CH22_DA59H18.GENSCAN.26-5	2.52	
327846			CH.05_hs gi|6531962	2.52	
325271			CH.11_hs gi|5866901	2.52	
312385	R42885	Hs.215555	ESTs	2.51	
302816	AI733918	Hs.204112	ESTs; Weakly similar to alternatively sp	2.51	
316941	AW449871	Hs.124591	ESTs	2.5	
300184	AI285912	Hs.254515	ESTs	2.5	
333762			CH22_FGENES.270_2	2.5	
317028	AA962623	Hs.189144	ESTs; Weakly similar to RENAL SODIUM-DEP	2.5	
326266			CH.17_hs gi|5867264	2.49	
326005			CH.16_hs gi|5867112	2.49	
301971	AJ003125	Hs.120330	a disintegrin-like and metalloprotease (	2.48	
326539			CH.19_hs gi|5867307	2.48	
338896			CH22_DJ32I10.GENSCAN.9-4	2.48	
306773	AI040750		EST singleton (not in UniGene) with exon	2.47	
336279			CH22_FGENES.763_3	2.47	
321017	AL050345	Hs.227637	hypothetical protein	2.47	
306090	AA908609		EST singleton (not in UniGene) with exon	2.47	
333216			CH22_FGENES.104_8	2.46	
338593			CH22_EM:AC005500.GENSCAN.435-2	2.46	
333587			CH22_FGENES.205_2	2.46	
300396	AW295466	Hs.232051	ESTs	2.45	
304693	AA554263		EST singleton (not in UniGene) with exon	2.45	
338934			CH22_DJ32I10.GENSCAN.18-2	2.45	
325751			CH.14_hs gi|6682474	2.45	
334137			CH22_FGENES.337_1	2.45	
333581			CH22_FGENES.200_1	2.45	
302083	AI422807	Hs.134012	C1q-related factor	2.44	
307318	AI208577		EST singleton (not in UniGene) with exon	2.44	
302181	AW374284	Hs.157732	Homo sapiens chromosome 19; cosmid R2689	2.44	
337425			CH22_FGENES.761-1	2.44	
336227			CH22_FGENES.730_2	2.44	
314657	AI015953	Hs.125265	ESTs	2.44	
338529			CH22_EM:AC005500.GENSCAN.398-10	2.44	
333680			CH22_FGENES.247_7	2.43	
324834	AJ003258	Hs.250891	ESTs	2.43	
305093	AA642917		EST singleton (not in UniGene) with exon	2.43	
335787			CH22_FGENES.611_3	2.43	
311704	AI655206	Hs.121512	ESTs; Moderately similar to kinesin like	2.43	
329382			CH.X_hs gi|5868868	2.42	
334785			CH22_FGENES.432_10	2.42	
330130			CH.21_p2 gi|6002196	2.42	
327206			CH.01_hs gi|5867447	2.41	
319235	F11330	Hs.177633	ESTs	2.41	
334691			CH22_FGENES.420_4	2.4	
327610			CH.04_hs gi|5867868	2.4	
327646			CH.04_hs gi|5867894	2.4	
337093			CH22_FGENES.465-18	2.4	
335081			CH22_FGENES.488_4	2.4	
333576			CH22_FGENES.193_2	2.4	
337604			CH22_C20H12.GENSCAN.16-5	2.4	
329879			CH.15_p2 gi|6466518	2.4	
328444			CH.07_hs gi|5868420	2.39	
335700			CH22_FGENES.598_1	2.39	
331255	Z41009	Hs.21446	ESTs; Weakly similar to HYPOTHETICAL PRO	2.39	

327927			CH.06_hs gi|5868173	2.39
334354			CH22_FGENES.377_1	2.39
308517	AI689279		EST singleton (not in UniGene) with exon	2.39
303669	AW499648	Hs.233750	copine V	2.39
333648			CH22_FGENES.237_2	2.38
318318	AI653893	Hs.174463	ESTs; Weakly similar to alpha3b subunit	2.38
338336			CH22_EM:AC005500.GENSCAN.310-8	2.38
304125	H40976		EST singleton (not in UniGene) with exon	2.38
304983	AA617786		EST singleton (not in UniGene) with exon	2.38
334935			CH22_FGENES.464_3	2.38
314326	AW170057	Hs.133179	ESTs	2.38
330406	D49490	Hs.76901	for protein disulfide isomerase-related	2.38
307646	AI302236		EST singleton (not in UniGene) with exon	2.38
338911			CH22_DJ32I10.GENSCAN.11-3	2.38
319952	T79532	Hs.225725	ESTs; Moderately similar to CGI-101 prot	2.37
336878			CH22_FGENES.318-5	2.37
338140			CH22_EM:AC005500.GENSCAN.203-6	2.37
300564	AI383878	Hs.225588	ESTs	2.37
304635	AA523976		EST singleton (not in UniGene) with exon	2.37
334091			CH22_FGENES.327_47	2.37
336328			CH22_FGENES.812_7	2.37
325310			CH.11_hs gi|5866864	2.37
338043			CH22_EM:AC005500.GENSCAN.153-2	2.37
307090	AI161024		EST singleton (not in UniGene) with exon	2.37
335768			CH22_FGENES.607_2	2.37
334969			CH22_FGENES.466_2	2.37
333640			CH22_FGENES.230_2	2.36
330002			CH.16_p2 gi|6623963	2.36
338829			CH22_DJ246D7.GENSCAN.5-12	2.36
323808	AW250114		EST cluster (not in UniGene)	2.36
327755			CH.05_hs gi|5867955	2.35
306426	AA975039		EST singleton (not in UniGene) with exon	2.35
336481			CH22_FGENES.830_1	2.35
335163			CH22_FGENES.502_7	2.35
322012	AL137357		EST cluster (not in UniGene)	2.35
337345			CH22_FGENES.723-1	2.35
334625			CH22_FGENES.414_3	2.35
320957	AI878933		EST cluster (not in UniGene)	2.35
334915			CH22_FGENES.457_4	2.35
336295			CH22_FGENES.787_1	2.35
321556	N46402	Hs.14570	ESTs	2.35
338491			CH22_EM:AC005500.GENSCAN.385-2	2.35
335517			CH22_FGENES.571_34	2.34
330639	X90872	Hs.75854	SULT1C sulfotransferase	2.34
310383	AI263102	Hs.145596	ESTs	2.34
331526	N49967	Hs.46624	ESTs	2.34
334396			CH22_FGENES.381_2	2.34
332993			CH22_FGENES.57_2	2.34
327487			CH.02_hs gi|5867785	2.34
335920			CH22_FGENES.636_16	2.33
336463			CH22_FGENES.829_22	2.33
319000	Z44318		EST cluster (not in UniGene)	2.33
332992			CH22_FGENES.57_1	2.33
332920			CH22_FGENES.37_6	2.33
337590			CH22_C20H12.GENSCAN.6-5	2.33
327059			CH.21_hs gi|6531965	2.33
334399			CH22_FGENES.382_5	2.33
300982	AA837754		EST cluster (not in UniGene) with exon h	2.32
327430			CH.02_hs gi|5867754	2.32
326808			CH.20_hs gi|6682504	2.32
309324	AW015373		EST singleton (not in UniGene) with exon	2.32
329779			CH.14_p2 gi|6002090	2.32
330492	M25809	Hs.64173	ATPase; H+ transporting; lysosomal (vacu	2.31
330080			CH.19_p2 gi|6015314	2.31
334342			CH22_FGENES.375_20	2.31
336306			CH22_FGENES.793_5	2.31
336400			CH22_FGENES.823_15	2.31
323735	AA323714		EST cluster (not in UniGene)	2.31
334496			CH22_FGENES.397_12	2.31
336075			CH22_FGENES.687_1	2.31
335566			CH22_FGENES.580_1	2.31
337657			CH22_EM:AC000097.GENSCAN.32-9	2.31
327816			CH.05_hs gi|5867968	2.3
308465	AI672480		EST singleton (not in UniGene) with exon	2.3
330112			CH.19_p2 gi|6015238	2.3
304465	AA421948		EST singleton (not in UniGene) with exon	2.3

308449	AI660854		EST singleton (not in UniGene) with exon	2.3	
328171			CH.06_hs gi|5868071	2.3	
328271			CH.06_hs gi|6552415	2.3	
328803			CH.07_hs gi|6004475	2.3	
330063			CH.19_p2 gi|6165044	2.29	
312281	H11643		EST cluster (not in UniGene)	2.29	
328974			CH.09_hs gi|5868520	2.29	
333859			CH22_FGENES.290_18	2.29	
326253			CH.17_hs gi|5867263	2.29	
325703			CH.14_hs gi|5867028	2.29	
338925			CH22_DJ32I10.GENSCAN.14-3	2.29	
328552			CH.07_hs gi|5868489	2.29	
337244			CH22_FGENES.646-8	2.29	
314770	AI732722	Hs.187694	ESTs	2.29	
324560	AW502208		EST cluster (not in UniGene)	2.29	
310603	AW376860	Hs.156398	ESTs	2.29	
337363			CH22_FGENES.733-2	2.29	
308015	AI440174	Hs.228907	EST; Weakly similar to GUANINE NUCLEOTID		2.28
309206	AI961962		EST singleton (not in UniGene) with exon	2.28	
337455			CH22_FGENES.777-1	2.28	
327605			CH.03_hs gi|6004463	2.28	
301611	W22172	Hs.59038	ESTs	2.28	
317222	AI206964	Hs.130051	ESTs	2.28	
338278			CH22_EM:AC005500.GENSCAN.290-3	2.28	
337291			CH22_FGENES.673-2	2.27	
337913			CH22_EM:AC005500.GENSCAN.59-10	2.27	
306406	AA971973		EST singleton (not in UniGene) with exon	2.27	
332947			CH22_FGENES.47_10	2.27	
321763	W01148		EST cluster (not in UniGene)	2.27	
304424	AA293494		EST singleton (not in UniGene) with exon	2.27	
303782	T64737		EST cluster (not in UniGene) with exon h	2.27	
326943			CH.21_hs gi|6004446	2.27	
324977	R14439	Hs.209194	ESTs	2.27	
325480			CH.12_hs gi|5866957	2.27	
327743			CH.05_hs gi|5867944	2.27	
333221			CH22_FGENES.105_1	2.26	
336498			CH22_FGENES.833_3	2.26	
321583	H84421		EST cluster (not in UniGene)	2.26	
334191			CH22_FGENES.352_6	2.26	
327089			CH.21_hs gi|6531965	2.26	
310001	F18939	Hs.153827	ESTs	2.26	
304056	R08577		EST singleton (not in UniGene) with exon	2.25	
324700	AW504745	Hs.103913	ESTs; Moderately similar to !!!! ALU SUB	2.25	
330637	X86371	Hs.95659	lethal giant larvae (Drosophila) homolog	2.25	
307642	AI302103		EST singleton (not in UniGene) with exon	2.25	
336985			CH22_FGENES.402-6	2.25	
334425			CH22_FGENES.384_13	2.25	
321216	AI078042	Hs.126691	ESTs	2.25	
315785	AW205946	Hs.150319	ESTs	2.25	
305809	AA853998	Hs.124580	EST	2.25	
331334	AA284858	Hs.89134	ESTs	2.25	
317131	AI991125	Hs.189109	ESTs	2.25	
334216			CH22_FGENES.358_1	2.24	
330330			CH.08_p2 gi|5670267	2.24	
326923			CH.21_hs gi|6456782	2.24	
333774			CH22_FGENES.272_5	2.24	
324311	AA443061	Hs.202520	ESTs	2.24	
338551			CH22_EM:AC005500.GENSCAN.413-2	2.24	
306716	AI024916	Hs.251354	ESTs	2.24	
337689			CH22_EM:AC000097.GENSCAN.77-5	2.24	
300079	AI192520	Hs.147178	EST	2.23	
334617			CH22_FGENES.411_16	2.23	
336890			CH22_FGENES.326-10	2.23	
334495			CH22_FGENES.397_10	2.23	
327301			CH.01_hs gi|5867493	2.23	
337856			CH22_EM:AC005500.GENSCAN.41-3	2.23	
307072	AI150424	Hs.146817	EST	2.23	
330515	M85247		H.sapiens dopamine D1A receptor gene, co	2.22	
325943			CH.16_hs gi|5867138	2.22	
338947			CH22_DJ32I10.GENSCAN.21-4	2.22	
317465	AW197361	Hs.131360	ESTs	2.22	
332458	M33493	Hs.184504	tryptase; alpha	2.22	
333195			CH22_FGENES.98_17	2.22	
304837	AA587139		EST singleton (not in UniGene) with exon	2.22	
307602	AI288843	Hs.231239	EST	2.22	
337078			CH22_FGENES.457-1	2.22	

335862			CH22_FGENES.629_7	2.22	
301979	L28168	Hs.121495	potassium voltage-gated channel; Isk-rel	2.22	
335668			CH22_FGENES.590_19	2.22	
305068	AA639618		EST singleton (not in UniGene) with exon	2.21	
329034			CH.X_hs gi|5868561	2.21	
318403	AI131241	Hs.143234	ESTs	2.21	
328058			CH.06_hs gi|5902482	2.21	
335513			CH22_FGENES.571_28	2.21	
330803	AA004699	Hs.150580	putative translation initiation factor	2.21	
331427	H54764	Hs.237339	EST	2.21	
338973			CH22_DJ32I10.GENSCAN.27-6	2.2	
336723			CH22_FGENES.85-3	2.2	
327290			CH.01_hs gi|5867483	2.2	
337240			CH22_FGENES.644-1	2.2	
306201	AA926818		EST singleton (not in UniGene) with exon	2.2	
303659	AA868464	Hs.126263	ESTs; Highly similar to FIBRILLARIN [H.s	2.2	
334517			CH22_FGENES.399_7	2.2	
334189			CH22_FGENES.352_4	2.2	
335199			CH22_FGENES.508_8	2.2	
333705			CH22_FGENES.250_19	2.2	
305794	AA845324		EST singleton (not in UniGene) with exon	2.2	
303273	AA316069		EST cluster (not in UniGene) with exon h	2.2	
313384	W85694	Hs.118335	ESTs	2.2	
329158			CH.X_hs gi|5868687	2.2	
337551			CH22_FGENES.847-8	2.2	
328792			CH.07_hs gi|5868309	2.2	
303737	AW502711		EST cluster (not in UniGene) with exon h	2.19	
324529	AW502466		EST cluster (not in UniGene)	2.19	
323103	Z45529	Hs.92030	ESTs	2.19	
333773			CH22_FGENES.272_4	2.19	
337906			CH22_EM:AC005500.GENSCAN.56-19	2.19	
327129			CH.21_hs gi|6531976	2.19	
305710	AA826544		EST singleton (not in UniGene) with exon	2.19	
335595			CH22_FGENES.581_34	2.19	
323646	AA310926	Hs.154412	ESTs	2.19	
328368			CH.07_hs gi|5868388	2.19	
325802			CH.14_hs gi|6552451	2.19	
337167			CH22_FGENES.562-27	2.19	
305059	AA635756		EST singleton (not in UniGene) with exon	2.18	
321445	AW245524	Hs.121590	ESTs; Weakly similar to ZINC FINGER PROT	2.18	
332790			CH22_FGENES.2_4	2.18	
336750			CH22_FGENES.128-4	2.18	
310999	AI520706	Hs.171012	ESTs	2.18	
329798			CH.14_p2 gi|6523160	2.18	
327012			CH.21_hs gi|5867664	2.18	
304599	AA506638		EST singleton (not in UniGene) with exon	2.18	
335351			CH22_FGENES.539_4	2.18	
310661	AI354717	Hs.223908	ESTs	2.18	
332791			CH22_FGENES.3_1	2.17	
333022			CH22_FGENES.65_1	2.17	
310502	AI458973	Hs.170422	ESTs	2.17	
324963	AA853440		EST cluster (not in UniGene)	2.17	
325275			CH.11_hs gi|5866902	2.17	
328338			CH.07_hs gi|5868377	2.17	
333063			CH22_FGENES.75_6	2.17	
308895	AI858423		EST singleton (not in UniGene) with exon	2.17	
338685			CH22_EM:AC005500.GENSCAN.472-4	2.16	
325655			CH.14_hs gi|5867007	2.16	
332420	H49570	Hs.108074	ESTs; Weakly similar to CEREBELLIN 1 PRE	2.16	
337216			CH22_FGENES.613-10	2.16	
335660			CH22_FGENES.590_11	2.16	
337145			CH22_FGENES.542-2	2.16	
335753			CH22_FGENES.604_2	2.16	
301766	R02224		EST cluster (not in UniGene) with exon h	2.16	
303442	AI953998	Hs.152510	ESTs; Weakly similar to L-SERINE DEHYDRA	2.16	
311009	AI949701	Hs.210589	ESTs	2.16	
307093	AI167606		EST singleton (not in UniGene) with exon	2.16	
300262	AI874402	Hs.170810	ESTs	2.16	
337989			CH22_EM:AC005500.GENSCAN.112-7	2.16	
326263			CH.17_hs gi|5867264	2.16	
319402	W21298		EST cluster (not in UniGene)	2.16	
321010	Y17456	Hs.227150	Homo sapiens LSFR2 gene; last exon	2.16	
301706	AI929150	Hs.241496	ESTs	2.16	
307412	AI241753	Hs.241507	ribosomal protein S6	2.16	
335662			CH22_FGENES.590_13	2.15	
332480	AA092932	Hs.12570	tubulin-specific chaperone d	2.15	

329273			CH.X_hs gi|5868762	2.15
339383			CH22_BA232E17.GENSCAN.3-20	2.15
332795			CH22_FGENES.5_1	2.15
335227			CH22_FGENES.513_13	2.15
326925			CH.21_hs gi|6456782	2.15
332403	AA424199	Hs.106529	ESTs; Highly similar to CGI-65 protein [	2.15
317786	AI859605	Hs.155686	ESTs	2.15
326582			CH.19_hs gi|5867318	2.15
336494			CH22_FGENES.832_11	2.15
329656			CH.14_p2 gi|6448516	2.15
307581	AI284415		EST singleton (not in UniGene) with exon	2.15
335670			CH22_FGENES.591_2	2.14
332452	AA040369	Hs.11170	SYT interacting protein	2.14
309387	AW079943	Hs.156110	Immunoglobulin kappa variable 1D-8	2.14
308427	AI652677	Hs.195055	EST	2.14
322027	NM_004551		EST cluster (not in UniGene)	2.14
301693	Z45023		EST cluster (not in UniGene) with exon h	2.14
334308			CH22_FGENES.373_11	2.14
301131	AW134518	Hs.131807	ESTs	2.13
338495			CH22_EM:AC005500.GENSCAN.387-1	2.13
329600			CH.10_p2 gi|3962481	2.13
307980	AI431696		EST singleton (not in UniGene) with exon	2.13
337260			CH22_FGENES.652-15	2.13
304655	AA527887		EST singleton (not in UniGene) with exon	2.13
303141	AF195951		EST cluster (not in UniGene) with exon h	2.13
327957			CH.06_hs gi|5868210	2.13
334317			CH22_FGENES.374_1	2.13
302870	AF011407		EST cluster (not in UniGene) with exon h	2.13
333806			CH22_FGENES.278_2	2.13
329947			CH.16_p2 gi|5540101	2.13
309602	AW182523		EST singleton (not in UniGene) with exon	2.13
322790	AI700273	Hs.122162	ESTs; Weakly similar to KIAA0557 protein	2.13
337706			CH22_EM:AC000097.GENSCAN.87-11	2.13
306894	AI092731		EST singleton (not in UniGene) with exon	2.13
325530			CH.12_hs gi|6525289	2.12
321087	AL110227	Hs.241533	Homo sapiens mRNA; cDNA DKFZp434J194 (fr	2.12
309853	AW298169	Hs.57553	tousled-like kinase 2	2.12
326822			CH.20_hs gi|6117831	2.12
328776			CH.07_hs gi|5868309	2.12
335112			CH22_FGENES.494_20	2.12
334564			CH22_FGENES.405_4	2.12
333455			CH22_FGENES.157_4	2.12
317395	R55044	Hs.124130	ESTs	2.12
334221			CH22_FGENES.360_1	2.12
331374	AA442134	Hs.70573	ESTs; Weakly similar to HINT PROTEIN [H.	2.12
304473	AA428343	Hs.140	immunoglobulin gamma 3 (Gm marker)	2.12
328907			CH.08_hs gi|5868493	2.12
319448	R05539	Hs.108738	ESTs	2.12
333676			CH22_FGENES.247_3	2.12
324767	AA630931	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	2.12
318585	Z43405		EST cluster (not in UniGene)	2.12
331732	AA251192	Hs.177708	ESTs	2.12
329553			CH.10_p2 gi|3962492	2.12
336910			CH22_FGENES.343-6	2.12
326959			CH.21_hs gi|6469836	2.12
305417	AA725228		EST singleton (not in UniGene) with exon	2.11
301573	AI150328	Hs.226402	ESTs; Weakly similar to mitochondrial ci	2.11
326935			CH.21_hs gi|6004446	2.11
335176			CH22_FGENES.504_6	2.11
337210			CH22_FGENES.603-5	2.11
311284	AW027025	Hs.239262	ESTs	2.11
330240			CH.05_p2 gi|6671858	2.11
327463			CH.02_hs gi|6004455	2.11
332938			CH22_FGENES.41_3	2.11
332785			CH22_FGENES.1_1	2.11
301035	AI358105	Hs.123164	ESTs	2.1
305712	AA826701		EST singleton (not in UniGene) with exon	2.1
318651	AW003150	Hs.240165	ESTs	2.1
302753	M74299		EST cluster (not in UniGene) with exon h	2.1
334635			CH22_FGENES.417_2	2.1
319447	AA456745		EST cluster (not in UniGene)	2.1
301204	AW008544	Hs.239994	ESTs	2.1
333950			CH22_FGENES.303_6	2.1
325947			CH.16_hs gi|5867138	2.1
337683			CH22_EM:AC000097.GENSCAN.76-1	2.1
328962			CH.08_hs gi|6456775	2.1

	336655			CH22_FGENES.34-3	2.1
	336596			CH22_FGENES.163_2	2.1
	330486	M13755	Hs.833	interferon-stimulated protein; 15 kDa	2.1
	314356	AA531607	Hs.125143	ESTs	2.09
5	314976	AA524725	Hs.162108	ESTs	2.09
	336650			CH22_FGENES.29-6	2.09
	339026			CH22_DA59H18.GENSCAN.22-6	2.09
	302395	AW297357	Hs.114606	ESTs	2.09
	323280	AI910263		EST cluster (not in UniGene)	2.09
10	338857			CH22_DJ32I10.GENSCAN.1-1	2.09
	335374			CH22_FGENES.543_12	2.09
	308766	AI808510		EST singleton (not in UniGene) with exon	2.09
	331027	N48584	Hs.6168	KIAA0703 gene product	2.09
	337853			CH22_EM:AC005500.GENSCAN.37-1	2.09
15	302498	NM_002991		EST cluster (not in UniGene) with exon h	2.09
	312607	AI337440	Hs.169375	ESTs	2.09
	314309	Z44049	Hs.184352	ESTs; Weakly similar to cDNA EST EMBL:D3	2.09
	311695	AI142078	Hs.135562	ESTs	2.09
	333280			CH22_FGENES.126_2	2.09
20	333518			CH22_FGENES.173_3	2.09
	337199			CH22_FGENES.583-11	2.09
	337819			CH22_EM:AC005500.GENSCAN.13-9	2.08
	300546	AA214450	Hs.250913	ESTs	2.08
	322577	AA354452	Hs.59075	ESTs; Weakly similar to WD40 protein Cia	2.08
25	336028			CH22_FGENES.672_1	2.08
	300238	AI394673	Hs.254030	ESTs	2.08
	307429	AI243573		EST singleton (not in UniGene) with exon	2.08
	326444			CH.19_hs gi|5867385	2.08
	310641	AI345597	Hs.254727	ESTs	2.08
30	337633			CH22_C20H12.GENSCAN.32-1	2.08
	336008			CH22_FGENES.668_6	2.08
	339030			CH22_DA59H18.GENSCAN.24-1	2.08
	333952			CH22_FGENES.303_8	2.08
	329149			CH.X_hs gi|5868685	2.08
35	335192			CH22_FGENES.507_7	2.08
	308225	AI557713	Hs.177592	ribosomal protein; large; P1	2.08
	330519	M94172	Hs.69949	calcium channel; voltage-dependent; L ty	2.08
	331809	AA402482	Hs.97312	ESTs	2.07
	324837	AJ003669	Hs.246171	ESTs	2.07
40	332608	D00749	Hs.36972	CD7 antigen (p41)	2.07
	327291			CH.01_hs gi|5867483	2.07
	315936	AW069807	Hs.247094	ESTs; Moderately similar to !!!! ALU SUB	2.07
	317917	AI143593	Hs.129419	ESTs	2.07
	328674			CH.07_hs gi|5868254	2.07
45	338654			CH22_EM:AC005500.GENSCAN.460-55	2.07
	320828	AJ012590	Hs.194728	hexose-6-phosphate dehydrogenase (glucos	2.07
	337896			CH22_EM:AC005500.GENSCAN.56-3	2.07
	335310			CH22_FGENES.532_3	2.07
	300076	AW074835	Hs.145223	ESTs	2.07
50	303588	AL046182		EST cluster (not in UniGene) with exon h	2.07
	328848			CH.07_hs gi|6381921	2.07
	318723	C18060		EST cluster (not in UniGene)	2.07
	335352			CH22_FGENES.539_5	2.07
	339316			CH22_BA354I12.GENSCAN.22-15	2.06
55	335873			CH22_FGENES.631_1	2.06
	335261			CH22_FGENES.520_2	2.06
	322032	AL079807		EST cluster (not in UniGene)	2.06
	308771	AI809301		EST singleton (not in UniGene) with exon	2.06
	310024	AI252661	Hs.145224	ESTs	2.06
60	320555	R36212	Hs.235534	ESTs	2.06
	319314	T74062		EST cluster (not in UniGene)	2.06
	334642			CH22_FGENES.417_9	2.06
	335767			CH22_FGENES.607_1	2.06
	336159			CH22_FGENES.707_3	2.06
65	336358			CH22_FGENES.818_1	2.06
	334687			CH22_FGENES.419_12	2.06
	339389			CH22_BA232E17.GENSCAN.4-7	2.06
	335898			CH22_FGENES.635_6	2.06
	328847			CH.07_hs gi|6381920	2.06
70	313431	W91884		EST cluster (not in UniGene)	2.06
	313270	AI374993	Hs.159611	ESTs	2.06
	339211			CH22_FF113D11.GENSCAN.6-6	2.06
	333860			CH22_FGENES.290_19	2.06
	308952	AI868157	Hs.224226	EST	2.06
75	305471	AA743947		EST singleton (not in UniGene) with exon	2.06
	300619	AA991438	Hs.233293	ESTs	2.06

302962	AI693349	Hs.228981	EST	2.06	
332446	AA112799	Hs.238756	ESTs; Weakly similar to unknown [H.sapie	2.06	
334972			CH22_FGENES.468_2	2.05	
330196			CH.05_p2 gi|6165140	2.05	
304754	AA579795		EST singleton (not in UniGene) with exon	2.05	
309726	AW248521	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	2.05	
333939			CH22_FGENES.301_5	2.05	
304836	AA587008		EST singleton (not in UniGene) with exon	2.05	
302087	AA324163		EST cluster (not in UniGene) with exon h	2.05	
308424	AI650714		EST singleton (not in UniGene) with exon	2.05	
304347	AA176914		EST singleton (not in UniGene) with exon	2.05	
333141			CH22_FGENES.85_1	2.05	
310573	AW292180	Hs.156142	ESTs	2.05	
337565			CH22_C65E1.GENSCAN.1-11	2.05	
304295	AA084082		EST singleton (not in UniGene) with exon	2.05	
326624			CH.20_hs gi|5867553	2.05	
326443			CH.19_hs gi|5867385	2.04	
339012			CH22_DA59H18.GENSCAN.19-2	2.04	
337384			CH22_FGENES.745-1	2.04	
332326	T79623	Hs.111787	ESTs	2.04	
303706	AW501525		EST cluster (not in UniGene) with exon h	2.04	
336046			CH22_FGENES.679_8	2.04	
301770	R05887		EST cluster (not in UniGene) with exon h	2.04	
326726			CH.20_hs gi|5867597	2.04	
330485	M11186	Hs.113216	oxytocin; prepro- (neurophysin I)	2.04	
332956			CH22_FGENES.48_13	2.04	
300021	M97935		AFFX control: STAT1	2.04	
306872	AI086920		EST singleton (not in UniGene) with exon	2.03	
302744	L03151		EST cluster (not in UniGene) with exon h	2.03	
338507			CH22_EM:AC005500.GENSCAN.390-11	2.03	
334020			CH22_FGENES.317_1	2.03	
333870			CH22_FGENES.291_3	2.03	
330552	U40223	Hs.248157	pyrimidinergic receptor P2Y; G-protein c	2.03	
335486			CH22_FGENES.570_18	2.03	
339374			CH22_BA232E17.GENSCAN.2-5	2.03	
328384			CH.07_hs gi|5868392	2.03	
334690			CH22_FGENES.420_3	2.03	
310318	AI733942	Hs.145338	ESTs	2.03	
325893			CH.16_hs gi|5867088	2.03	
331373	AA435513	Hs.178170	ESTs; Weakly similar to DUAL SPECIFICITY	2.03	
329784			CH.14_p2 gi|5912597	2.03	
335087			CH22_FGENES.488_11	2.03	
310582	AI336563	Hs.254585	ESTs	2.03	
332611	R06751	Hs.1600	chaperonin containing TCP1; subunit 5 (e	2.03	
339258			CH22_BA354I12.GENSCAN.8-3	2.03	
336851			CH22_FGENES.274-1	2.03	
305596	AA780664	Hs.8734	ESTs; Moderately similar to !!!! ALU CLA	2.03	
330364			CH.X_p2 gi|3126882	2.03	
302940	AL137619		EST cluster (not in UniGene) with exon h	2.03	
317349	AA923657	Hs.126359	ESTs; Weakly similar to !!!! ALU SUBFAMI	2.03	
309869	AW300314		EST singleton (not in UniGene) with exon	2.03	
333422			CH22_FGENES.147_2	2.03	
325233			CH.10_hs gi|6381943	2.03	
330586	U77968	Hs.79564	neuronal PAS domain protein 1	2.03	
336725			CH22_FGENES.88-1	2.02	
334157			CH22_FGENES.340_7	2.02	
303357	AW006352	Hs.159643	ESTs; Weakly similar to MLD [H.sapiens]	2.02	
328533			CH.07_hs gi|5868482	2.02	
309210	AI962817		EST singleton (not in UniGene) with exon	2.02	
327412			CH.02_hs gi|5867750	2.02	
333172			CH22_FGENES.94_7	2.02	
334869			CH22_FGENES.447_3	2.02	
301047	AA971465	Hs.116136	ESTs	2.02	
329394			CH.X_hs gi|6478817	2.02	
301736	F12128		EST cluster (not in UniGene) with exon h	2.02	
335591			CH22_FGENES.581_30	2.02	
338234			CH22_EM:AC005500.GENSCAN.260-7	2.02	
334433			CH22_FGENES.385_8	2.02	
334904			CH22_FGENES.452_18	2.02	
318443	AI939323	Hs.157714	ESTs; Weakly similar to NEUR ACETYLCHOLI	2.02	
300151	AI243445	Hs.189654	ESTs	2.01	
310348	AI478563	Hs.145519	ESTs	2.01	
310898	AI439868	Hs.165742	ESTs	2.01	
332860			CH22_FGENES.27_3	2.01	
301699	AI879117		EST cluster (not in UniGene) with exon h	2.01	
332554	W96450	Hs.23111	phenylalanine-tRNA synthetase-like	2.01	

327994			CH.06_hs gi|5868218	2.01	
315613	AW137420	Hs.192311	ESTs	2.01	
335356			CH22_FGENES.541_3	2.01	
334028			CH22_FGENES.318_7	2.01	
335277			CH22_FGENES.523_3	2.01	
308657	AI749855	Hs.236497	EST; Weakly similar to GLANDULAR KALLIKR		2.01
305913	AA876109		EST singleton (not in UniGene) with exon	2.01	
323681	AW247730	Hs.102548	glucocorticoid receptor DNA binding fact	2.01	
333533			CH22_FGENES.175_20	2.01	
328753			CH.07_hs gi|5868298	2.01	
302397	L01694	Hs.211523	guanine nucleotide binding protein (G pr	2.01	
304643	AA526588		EST singleton (not in UniGene) with exon	2.01	
333065			CH22_FGENES.75_8	2.01	
316192	AA904441	Hs.221286	ESTs	2	
302533	L36149	Hs.248116	chemokine (C motif) XC receptor 1	2	
312988	AA813689	Hs.123436	ESTs	2	
333612			CH22_FGENES.217_7	2	
333615			CH22_FGENES.217_10	2	
316085	AI027959	Hs.132300	ESTs	2	
337936			CH22_EM:AC005500.GENSCAN.85-7	2	
330972	H18467	Hs.118983	ESTs; Weakly similar to diaphanous 1 [H.	2	

Table 20: B survivor vs Mets – Up in Mets

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title

Pkey	Ex Accn	UniG_ID	Complete Title	Ratio BS/Met
316625	AA780307	Hs.122156	ESTs	0.28
316076	AW297895	Hs.116424	ESTs	0.3
315943	AA699756	Hs.117335	ESTs	0.38
317198	AI810384	Hs.128025	ESTs	0.38
320082	AA487678	Hs.189738	ESTs	0.39
313510	AI147291	Hs.154006	ESTs	0.39
323683	AI380045	Hs.225033	ESTs	0.39
318558	AW402677	Hs.90372	ESTs	0.4
310264	AI915771	Hs.148867	ESTs	0.4
314945	AW276866	Hs.192715	ESTs	0.41
313403	W86995	Hs.113157	ESTs	0.42
321505	H73183	Hs.129885	ESTs	0.43
312171	AW444619	Hs.138211	ESTs	0.43
324585	AI823969	Hs.132678	ESTs	0.44
316695	AA809844		EST cluster (not in UniGene)	0.44
319818	AA825819	Hs.136952	ESTs	0.44
337522			CH22_FGENES.819-1	0.45
324714	AA574312	Hs.245737	ESTs	0.45
315060	AA551104	Hs.189048	ESTs	0.46
300548	AI026836	Hs.114689	ESTs	0.47
304483	AA431441		EST singleton (not in UniGene) with exon	0.47
313096	AI422367	Hs.163533	ESTs	0.47
306501	AA987294		EST singleton (not in UniGene) with exon	0.47
329086			CH.X_hs gi|5868604	0.47
320176	AA167566	Hs.133325	ESTs	0.47
320418	AI674461	Hs.199638	ESTs	0.47
302982	W92391	Hs.198222	ESTs; Weakly similar to C2H2-type zinc f	0.48
315609	AW207535	Hs.224012	ESTs	0.48
317056	AA904908	Hs.250643	ESTs	0.48
314361	AL038765	Hs.161304	ESTs	0.49
315169	AI371390	Hs.158667	ESTs	0.49
323743	AA324992	Hs.257168	ESTs	0.49
313903	AW167439	Hs.190651	ESTs	0.49
315061	AA551196	Hs.188952	ESTs	0.49
300969	AI140799	Hs.76230	ribosomal protein S10	0.5
331950	AA454595	Hs.99369	ESTs	0.5
315076	AI623817	Hs.168457	ESTs	0.5
300975	AI283548	Hs.149668	ESTs	0.5

~~TABLE 1-20A~~

Table 1-20A, shows the accession numbers for those pkeys lacking unigeneID's for Tables 1-20. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accesssion
108446	112224_1	AA085383 AA126091 AA074174 AA075373 AA079120 AA070831 AA075978 AA075372 AA128503
108474	116896_1	AA115179 AA079667 AA115897 AA079771
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		AA345406 AI277554 AA134749 AA856624 BE613247 AA299003 AL048138 AA028121 T92510 AI923835 AW020440 AI401594 AI889401 N93290 AA044247 AA028100 AI582845 AA811151 AI741811 AI925878 AA448277 AA172221 AI214783 BE220793 AA022746 AI082882 AA022849 AI928385 AA573472 AI420686 AW072902 AI799493 AI873506 AI468977 AI192079 AI468976 AA044272 AW015701 AW316979 AA933042 AA609017 AI318393 AI424571 AI934945 AA172023 AW050917 AA846180 AA134748 AI003947 AI766769 AW006697 AA653517 AW575680 AI474214 AA401478 U36922 AA927064 AA868000 D62654 T91745 AW500202 AA194764 AA746346 AA130464 AW117498 AA054526 N26432 H02534 H04964 AW303367 BE300931 AI218049 AI208073 AW182749 AA983630 AI147585 AA194765 AA054534 AA922720 AI436585 AI346535 AA134269 AA280923 AA897422 AA019559 AW274010 AA035406 AA917879 H99327 W32908 AI216046 AW496823 AA019414 H82288 W35284 AI936621 AI767113 AA866177 AW367874 H82398 AF032885 AW300151 AW467069 AA809346 AI188507 AI494178 AA872752 AI631631 U02310 NM_002015 AA815006 AI382453 AW197658 AI761654 AI804396 AI382221 AI813640 AI439635 AI523901 AW517242 AI221705 AW298104 AW204560 AW573095 AW028783 AW014650 AI766744 AI808294 AI698758 AI041809 AI766667 AI479103 AA872797 AA769305 AA765080 AA334166 AI472322
131862	3673_14	AI541246 AW055046 BE312897 NM_006623 AF006043 AL038012 BE256739 BE272577 AA143633 AA143643 BE464595 AI312112 H01791 R26319 BE170902 AW131612 F29120 AA455866 AI540181 AI885777 F36716 AI149501 AI246028 AI373003 AL046700 AA455869 W69120 AA146617 AI188256 AI937281 AI806751 AI087240 AI123219 AI589686 AI332501 W69087 AI494321 AA725793 AI222350 AA625736 AA644568 AI472282 AI370905 AA934652 AA913035 AI128576 AW341709 AI269125 AA975139 AI620890 AI969828 AI356660 W95879 F32252 AI218442 AI928601 AI474470 AI245409 AI601111 AA928594 AI809316 F19498 AI373442 AI218893 AA573914 AA906869 AI833041 AA993899 AW250763 AA887142 AA884655 R26108 AI919414 H01042 AA534622 AA723368 AW005753 AI871394 AA661885 BE171317 BE271194 AW249310 T83902 BE246962 BE279817 BE562094 BE513363 AL045369 BE561008 BE267526 BE544065 BE559579 BE561747 T35796 BE250596 BE268704 T31298 BE536521 BE561183 BE269560 BE269944 BE514005 BE561068 BE268145 BE267559 BE559744 BE560930 BE278335 BE513832 BE561017 BE396371 BE562260 BE281009 BE281327 AW410446 BE259628 BE547443 BE311971 T83809 AW249441 BE270204 BE295488 R90868 BE269359 BE397222 BE396694 AW248394 BE397708 BE268174 AW247676 AW248404 AA093721 BE397622 AA093706 T09027 BE408338 BE261454 BE260628 BE295110 AF171237 BE295135 BE407534 BE536635 BE264727 BE296052 BE270265 BE546712 BE298269 BE547732 BE548734 BE253463 BE312238 BE261042 BE545186 BE313055 BE542602 BE538530 BE535215 BE208107 BE513616 BE295982 BE561273 BE560057 BE562005 BE280371 AW247443 BE259311 AA126209 AA171445 AW674121 AA134790 BE018733 AA233357 AA121604 AA114201 BE265626 BE260086 BE313195 BE313434 BE261587 AA223432 AL039212 BE260762 AL046154 BE549057 AA316523 BE259727 BE260759 BE208754 BE019077 AA206899 T33021 BE255340 AA182643 BE258057 BE258040 BE254759 BE544454 AF171236 AA224410 T08700 AL037155 BE279638 W78185 BE545040 BE261376 BE261692 BE259694 AA313254 H09056 AA357719 BE619163 BE018472 BE277966 BE278390 AA353616 AA378769 AA356685 BE564039 BE300236 BE250358 BE543245 AF171235 BE384461 BE408141 AA137039 AI355285 BE535442 AA356783 AW675020 AI810351 W17380 BE074695 AI978750 AA316052 BE278523 BE619725 BE270953 AW026987 R89415 BE271359 BE515234 AW008497 AW386938 AI038839 AI862998 AI719458 AA113414 AI859984 AI870773 AA129452 BE047253 AW673881 AA827034 BE302302 AI572915 AW264575 BE294567 AA805899 AI625116 AA310115 AI460065 AA169760 AA955009 BE302084 AA629846 AA640597 W63787 AI805738 W94207 AA114165 AI240462 BE349066 AA668794 AA134085 AW050730 AA134084 BE540728 AA910015 AW248892 AW247299 AA564678 AI139117 T16008 AI754100 AI091987 AA856537 BE205770 AI199445 AA603509 AW771741 AI126994 AI000820 AI023844 AW250047 AI673263 T35536 AA126049 AI668802 T35470 AA224348 BE247113 AI367665 AA223233 AA206815 AI284773 AA093396 AA113268 T03547 AA234268 AA101404 AA991274 AI275931 AA918855 AA236365 AA226966 AI685723 AI284774 AW248023 AI754314 H09057 AA844271 AI272992 AA315077 AA205718 D57244 AA742550 AA219567 AI927435 AI042620 AW247957 T35545 T15567 R90845 AA719914 AI085499 AI970845
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103163	43223_1	AU077018 X67683
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335236	CH22_2577FG_515_8_LINK_EM	
328025	c_6_hs	
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335265	CH22_2607FG_521_1_LINK_EM	
335266	CH22_2608FG_521_2_LINK_EM	
328053	c_6_hs	
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335284	CH22_2626FG_526_6_LINK_EM	
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328109	c_6_hs	
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305259	AA679225	
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335344	CH22_2691FG_536_3_LINK_EM	
335348	CH22_2695FG_537_4_LINK_EM	
335349	CH22_2696FG_539_2_LINK_EM	
305264	AA679505	
328134	c_6_hs	
335371	CH22_2720FG_543_9_LINK_EM	
335377	CH22_2726FG_543_17_LINK_E	
328171	c_6_hs	
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326943	c21_hs	
326957	c21_hs	
326981	c21_hs	
326997	c21_hs	
305335	AA704235	
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328221	c_6_hs	
328224	c_6_hs	
328228	c_6_hs	
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305361	AA708902	
335451	CH22_2802FG_562_9_LINK_EM	
328236	c_6_hs	
335455	CH22_2806FG_562_15_LINK_E	
328243	c_6_hs	
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328276	c_7_hs
328277	c_7_hs
328282	c_7_hs
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328305	c_7_hs
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335527	CH22_2882FG_572_7_LINK_EM
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328314	c_7_hs
335536	CH22_2891FG_574_2_LINK_EM
305454	AA738413
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335667	CH22_3027FG_590_18_LINK_E
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335783	CH22_3152FG_610_3_LINK_EM
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328607	c_7_hs
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335831	CH22_3204FG_620_5_LINK_EM
335832	CH22_3205FG_620_6_LINK_EM
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328624	c_7_hs
328636	c_7_hs
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305787	AA845035
328662	c_7_hs
335895	CH22_3272FG_635_3_LINK_EM
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337114	CH22_5060FG_494_17_
337121	CH22_5096FG_519_1_
337132	CH22_5112FG_526_3_
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337172	CH22_5192FG_565_2_
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305816	AA854776
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305877	AA865649
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335971	CH22_3350FG_652_4_LINK_DJ
335975	CH22_3354FG_652_9_LINK_DJ
335980	CH22_3360FG_653_2_LINK_DJ
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328770	c_7_hs
335993	CH22_3373FG_656_6_LINK_DJ
335998	CH22_3379FG_656_16_LINK_D
335999	CH22_3380FG_657_1_LINK_DJ
328791	c_7_hs
337203	CH22_5256FG_591_3_
337204	CH22_5261FG_595_1_
307120	AI184343
307140	AI185762
307177	AI188864
305903	AA873085
305925	AA877883
328803	c_7_hs
330002	c16_p2
328810	c_7_hs
328820	c_7_hs
330021	c16_p2
305967	AA886428
328835	c_7_hs
305971	AA886874
328841	c_7_hs
305984	AA887654
328851	c_7_hs
328859	c_7_hs
330057	c17_p2
330058	c17_p2
305999	AA889603
307215	AI193189
307262	AI202100
307318	AI208577
307380	AI222985
307433	AI244895
307437	AI245683

307556	AI281651	
307558	AI281998	
337645	CH22_5960FG__LINK_EM:AC00	
337657	CH22_5976FG__LINK_EM:AC00	
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307588	AI285535	
307592	AI285739	
337685	CH22_6020FG__LINK_EM:AC00	
337695	CH22_6033FG__LINK_EM:AC00	
337697	CH22_6037FG__LINK_EM:AC00	
307606	AI290006	
307629	AI300246	
307642	AI302103	
307643	AI302124	
307646	AI302236	
307703	AI318588	
307728	AI335557	
307752	AI339447	
307799	AI351112	
309005	AI884454	
307864	AI367417	
307877	AI368880	
307899	AI380270	
309108	AI925949	
309169	AI949216	
309181	AI951727	
307904	AI381019	
307912	AI382224	
307918	AI383496	
307954	AI419692	
307961	AI421059	
307992	AI434166	
309206	AI961962	
309233	AI971416	
309245	AI972447	
309247	AI972768	
309275	AI989570	
309324	AW015373	
309333	AW025709	
309343	AW028652	
309351	AW057547	
309403	AW082954	
309533	AW151131	
309592	AW172384	
325271	c11_hs	
325285	c11_hs	
325289	c11_hs	
309600	AW182066	
309605	AW182800	
309759	AW268822	
309767	AW271805	
309815	AW292760	
309859	AW298760	
302681	31257_1	X97550 X97552
302683	31326_1	X85153 T63701
309958	AW444488	
309977	AW451663	
309985	AW452919	
302727	32493_1	L10141 L10151 L10148 L09095
302747	32813_1	AF062275 L03830
304022	T02990	
304055	R07994	
304056	R08577	
304060	T61464	
304125	H40976	
304127	H42981	
304134	H54627	
304195	N35382	
302952	39444_1	AF103179 U82961
302996	41196_1	AF054663 AF124197 R70292
304269	AA069029	
304324	AA137045	
304330	AA157834	
304424	AA293494	
304465	AA421948	

	304467	AA424703	
	304480	AA430373	
	304485	AA434076	
	304487	AA434241	
	304559	AA488050	
	304575	AA496437	
	304605	AA513225	
	304612	AA514207	
	304623	AA521331	
	304635	AA523976	
	304667	AA535602	
	304674	AA541735	
	304675	AA541740	
	304693	AA554263	
	304696	AA554758	
	304707	AA564846	
	304731	AA576085	
	304734	AA576428	
	304745	AA577771	
	304746	AA577793	
	306009	AA894560	
	306012	AA896989	
	306053	AA905312	
	306081	AA908472	
	306090	AA908609	
	304811	AA584361	
	304813	AA584540	
	304817	AA584712	
	304833	AA586504	
	304841	AA587541	
	304887	AA599355	
	306137	AA916176	
	306180	AA922503	
	306183	AA922622	
	306193	AA923457	
	304918	AA602697	
	304968	AA614308	
	306200	AA926816	
	306220	AA928363	
	306221	AA928686	
	306300	AA937573	
	320789	252516_1	R78712 AA603646 R78713
	306351	AA961356	
	330435	41165_1	U63836 AW842139 X74956 U78550 AW840802 X74954 AW388241 AW842709 AF253321 X74955 X74370 AW363799 BE073386 AI791962 AA587390 AW840865
	330436	10605_34	BE259039 W29128 AW410299 X72990 BE246492 NM_005243 X66899 AI909006 AW248151 AL031186 AA012966 BE273549 BE311429 BE253102 Y07848 BE538102 BE256863 BE261240 BE312156 BE618412 BE257322 BE620446 AW806629 AA376777 AA325384 BE256808 BE251039 BE257878 BE275352 AA357169 AW403562 AA204995 AA093259 W95953 BE256279 BE336683 BE252465 BE251266 AA380754 BE294942 AA380941 AA380999 BE297164 BE249995 BE294719 BE295372 AI270673 BE305132 BE563752 BE295357 AI525421 BE263980 AA057505 AA020915 BE266318 BE206948 AI474020 BE296420 BE297374 BE408545 BE019366 BE407372 BE266180 BE279437 R58233 T19567 BE300738 AW381179 AA357571 AW361285 AA436908 AA301019 AA301022 N20202 BE408777 BE548638 BE167415 AA071260 BE088429 BE280092 W23117 T19568 R51681 AW402216 W22784 BE185607 AI457224 BE544120 AL134874 S72620 AA375079 D51319 AW818280 BE514686 AW853024 BE563744 AA300469 T07592 BE622190 BE272834 W21781 BE315450 BE542367 BE393120 AA988441 H55137 BE562296 BE622502 BE395960 AA329733 AA332348 AI768317 AA456866 AI497832 AW878437 AA857042 U18018 BE621418 AI818790 AI949507 BE397693 AI885545 AI858854 AI355147 BE169028 S62138 AW732191 AA856891 BE266060 X71427 BE268557 AF095890 AW001288 AI799634 AI623498 AA071346 BE547662 BE261446 AI564543 BE559759 U35622 BE314249 BE264915 AI638591 AI538385 AW090025 BE384754 AI888689 AW778800 AI925273 AA075797 AW949130 AV660275 AW438697 AI587137 AI524121 AA806249 AW628247 AA808241 AI244388 AI761125 AW117672 AA911782 AI129250 AA654447 H55291 BE258050 BE206162 W95867 AA857187 AI871378 AI660103 AW103827 AI220929 AW149949 BE465561 AI302857 AW168841 D82190 AW249814 AI623432 AI687358 AW951077 R51592 W60458 AI092863 AW474693 D12765 AI911646 D82208 D82187 AW074031 AI358527 AW338497 AA970893 AW072573 AA205364 AI858886 AA012830 AW148763 AI863056 AA548656 BE250325 AI016994 AI864005 BE046122 AI497746 C75340 R58896 D82141 AW168240 C19048 AI741090 D29465 AI222365 AA948288 AI583522 AW572212 AI091290 AA582727 AA579897 AA570629 W60883 AW516989 AL038160 AA577334 AI865872 AA994043 AA922583 AA464778 AA209178 AI829479 AI370235 BE246529 AA384177 AA456255 AI699730 W60654 AL035744 AA862042 R32756 AI886886 AA993087 AI289479 AA627840 AA464184 AI619503 R32755 AW075358 AI432315 AA457024 AA020865 R92132 AA454629 AA746059 AA454643 AA456240 AA826984 BE163738 AI806470 AI991074 AI802560 AA587095 AA558714 AA968521 N87780 AI538246 N71794 AV661738 AI368903 AA362570 AI989445 AI674962 S75762 BE245204 AA975296 D20123 AW005704 AA693328 AA582270 AI918474 AW205707 AI696299 AA220990 AA101538 T29030 H27201 AW262526 AI610530 AA126840 AA126790 X92120 AW367868 BE299644 BE299451 AA476561 BE300044 AA134363 BE295222 AA307504 N42337 AA319098 N39502 AW964461 N57241 BE299049 N86332 R51156 AA085859 T75212 AA133939 AA147129 AA156161 BE543953 BE538848 AA133676 BE299745 AA135050 AA218535 AW406401 AW411287 BE410528 C01410 NM_004083 BE314959 AA836413 AA085862 AW024370 AA471059 AW467508 AA001025 AI828231 AA633221 T95517 AA147038 AA476447 AW027012 AW078627 BE513200 AI192297 AA886279 AW081806 AA316185 AA010506 AI269929 W93139 AI682935 AA609555 AA378028 AI093877 AA999997 AA730698 AI143923 AW575315 AA890550 AA494353 AW576601 AI796336 AA826130 AA609207 AI539618 AI088539 AI089090 AA825505

			AA632978 AA015892 AW204713 AA156495 AA824613 AA133630 N29826 AA527476 AI633352 T27908 AA134364 AA133940 AW043601 H37775 AA772375 AA057871 AA047888 AA054225 H86568 AA001511 H25718 AW189507 AA165589 AA054433 H85549 AA165486 AA058972 AA454911 AA464064 AA493802 AA428253 R85508 AW302469 AI611812 BE162582 F11073 T95518 N26811 AI783929 H40669 AW611745 AI658803 R51042 R45276 AA528386 AA782875 AW880218 AL138391 AA314536 AW949338 AA149466 AA149552 AI346513 AA216776 BE349131 AW007654 AI141803 AA622688 AI185131 AW057635 AA101539 AA627986 H27202 AI536847 W93084 AI973148 AI246788 AW572108 AI469414 AA454835 AA612707 AA430746 AI084991 AA010400 AA856636 AA463928 AI248310 R07170 AA834033 D12244 AI655670 AA054350 AA639480 AI702067 AI475389
330527	14658_-15	S77356	
330833	103550_1	AA046804	AA046821
330855	111881_1	AA070316	AA079318
332099	genbank_AA608983		AA608983
332240	genbank_N54803		N54803

TABLE 1-20B

Table 1-20B, shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Tables 1-20. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332792	Dunham, I. et.al.	Plus	73381-73768
332843	Dunham, I. et.al.	Plus	1142859-1143494
332909	Dunham, I. et.al.	Plus	1946582-1946735
332920	Dunham, I. et.al.	Plus	2007562-2007785
332947	Dunham, I. et.al.	Plus	2431726-2432006
332949	Dunham, I. et.al.	Plus	2436245-2436348
332958	Dunham, I. et.al.	Plus	2516164-2516310
332992	Dunham, I. et.al.	Plus	2699997-2701093
332993	Dunham, I. et.al.	Plus	2701550-2701685
333004	Dunham, I. et.al.	Plus	2759056-2759165
333006	Dunham, I. et.al.	Plus	2762853-2762953
333007	Dunham, I. et.al.	Plus	2763569-2763709
333132	Dunham, I. et.al.	Plus	3358040-3358153
333133	Dunham, I. et.al.	Plus	3360058-3360195
333139	Dunham, I. et.al.	Plus	3369495-3369571
333152	Dunham, I. et.al.	Plus	3612171-3612354
333205	Dunham, I. et.al.	Plus	3942727-3943009
333221	Dunham, I. et.al.	Plus	3978070-3978187
333225	Dunham, I. et.al.	Plus	3992229-3992386
333245	Dunham, I. et.al.	Plus	4157587-4157668
333248	Dunham, I. et.al.	Plus	4162041-4162139
333261	Dunham, I. et.al.	Plus	4336597-4337752
333272	Dunham, I. et.al.	Plus	4381561-4382212
333281	Dunham, I. et.al.	Plus	4506230-4506342
333283	Dunham, I. et.al.	Plus	4514226-4514360
333288	Dunham, I. et.al.	Plus	4516841-4516939
333298	Dunham, I. et.al.	Plus	4581537-4581947
333306	Dunham, I. et.al.	Plus	5396233-5396310
333382	Dunham, I. et.al.	Plus	4905796-4905913
333403	Dunham, I. et.al.	Plus	4925140-4925256
333420	Dunham, I. et.al.	Plus	4954302-4954465
333428	Dunham, I. et.al.	Plus	4973869-4974007
333464	Dunham, I. et.al.	Plus	5210762-5211300
333465	Dunham, I. et.al.	Plus	5211385-5211858
333488	Dunham, I. et.al.	Plus	5396233-5396310
333515	Dunham, I. et.al.	Plus	5564299-5564851
333520	Dunham, I. et.al.	Plus	5586133-5586296
333566	Dunham, I. et.al.	Plus	5954226-5954473
333567	Dunham, I. et.al.	Plus	5959139-5959515
333571	Dunham, I. et.al.	Plus	6007916-6008058
333572	Dunham, I. et.al.	Plus	6026896-6027189
333576	Dunham, I. et.al.	Plus	6090345-6090721
333577	Dunham, I. et.al.	Plus	6123950-6124281
333580	Dunham, I. et.al.	Plus	6142935-6143145
333587	Dunham, I. et.al.	Plus	6250599-6250966
333588	Dunham, I. et.al.	Plus	6255445-6255779
333591	Dunham, I. et.al.	Plus	6285884-6286251
333592	Dunham, I. et.al.	Plus	6297731-6297976
333593	Dunham, I. et.al.	Plus	6304132-6304428
333594	Dunham, I. et.al.	Plus	6308990-6309450
333599	Dunham, I. et.al.	Plus	6337885-6338255
333600	Dunham, I. et.al.	Plus	6355629-6355925
333601	Dunham, I. et.al.	Plus	6360075-6360442
333607	Dunham, I. et.al.	Plus	6504431-6504690
333608	Dunham, I. et.al.	Plus	6510834-6511130

333619	Dunham, I. et.al.	Plus	6562799-6562926
333623	Dunham, I. et.al.	Plus	6584559-6584956
333625	Dunham, I. et.al.	Plus	6603020-6603310
333626	Dunham, I. et.al.	Plus	6614174-6614467
333627	Dunham, I. et.al.	Plus	6620584-6620903
333628	Dunham, I. et.al.	Plus	6629004-6629233
333629	Dunham, I. et.al.	Plus	6636915-6637205
333631	Dunham, I. et.al.	Plus	6650904-6651011
333632	Dunham, I. et.al.	Plus	6651520-6651658
333635	Dunham, I. et.al.	Plus	6663683-6663973
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333642	Dunham, I. et.al.	Plus	6708760-6709139
333643	Dunham, I. et.al.	Plus	6728053-6728343
333646	Dunham, I. et.al.	Plus	6739110-6739379
333647	Dunham, I. et.al.	Plus	6772502-6772779
333648	Dunham, I. et.al.	Plus	6787465-6787782
333650	Dunham, I. et.al.	Plus	6796852-6797128
333652	Dunham, I. et.al.	Plus	6809455-6809573
333653	Dunham, I. et.al.	Plus	6811130-6811392
333654	Dunham, I. et.al.	Plus	6816731-6816993
333656	Dunham, I. et.al.	Plus	6822087-6822406
333657	Dunham, I. et.al.	Plus	6831369-6831445
333658	Dunham, I. et.al.	Plus	6835282-6835474
333668	Dunham, I. et.al.	Plus	7011009-7011223
333670	Dunham, I. et.al.	Plus	7027945-7028181
333680	Dunham, I. et.al.	Plus	7071730-7071794
333682	Dunham, I. et.al.	Plus	7076641-7076760
333698	Dunham, I. et.al.	Plus	7205279-7205383
333710	Dunham, I. et.al.	Plus	7230314-7230476
333717	Dunham, I. et.al.	Plus	7308714-7308815
333727	Dunham, I. et.al.	Plus	7373219-7373311
333785	Dunham, I. et.al.	Plus	7775317-7775415
333791	Dunham, I. et.al.	Plus	7795972-7796082
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333875	Dunham, I. et.al.	Plus	8135505-8136179
333879	Dunham, I. et.al.	Plus	8146919-8147062
333891	Dunham, I. et.al.	Plus	8156437-8156709
333918	Dunham, I. et.al.	Plus	8307124-8307215
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333932	Dunham, I. et.al.	Plus	8489124-8489205
333983	Dunham, I. et.al.	Plus	8813593-8813668
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334010	Dunham, I. et.al.	Plus	8996696-8998236
334015	Dunham, I. et.al.	Plus	9055452-9055595
334017	Dunham, I. et.al.	Plus	9139516-9139634
334026	Dunham, I. et.al.	Plus	9196549-9196681
334030	Dunham, I. et.al.	Plus	9288463-9288782
334044	Dunham, I. et.al.	Plus	9373898-9374065
334047	Dunham, I. et.al.	Plus	9428152-9428211
334055	Dunham, I. et.al.	Plus	9662077-9662270
334063	Dunham, I. et.al.	Plus	9731991-9732085
334066	Dunham, I. et.al.	Plus	9739568-9739680
334068	Dunham, I. et.al.	Plus	9746279-9746477
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334106	Dunham, I. et.al.	Plus	10261155-10261841
334109	Dunham, I. et.al.	Plus	10267679-10267864
334111	Dunham, I. et.al.	Plus	10279365-10279531
334115	Dunham, I. et.al.	Plus	10316414-10316608
334118	Dunham, I. et.al.	Plus	10344273-10344384
334120	Dunham, I. et.al.	Plus	10402389-10403196
334135	Dunham, I. et.al.	Plus	10457085-10457183
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334239	Dunham, I. et.al.	Plus	13056569-13056693
334244	Dunham, I. et.al.	Plus	13159198-13159302
334257	Dunham, I. et.al.	Plus	13213243-13213429
334260	Dunham, I. et.al.	Plus	13223819-13223968
334298	Dunham, I. et.al.	Plus	13424763-13425914
334342	Dunham, I. et.al.	Plus	13646844-13646980
334354	Dunham, I. et.al.	Plus	13702598-13702747
334430	Dunham, I. et.al.	Plus	14269664-14270102
334435	Dunham, I. et.al.	Plus	14275597-14275689
334451	Dunham, I. et.al.	Plus	14315572-14315741
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334529	Dunham, I. et.al.	Plus	14788825-14788971
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334590	Dunham, I. et.al.	Plus	15033247-15033753
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334676	Dunham, I. et.al.	Plus	15516334-15516412
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334730	Dunham, I. et.al.	Plus	15967830-15967934
334797	Dunham, I. et.al.	Plus	16383231-16383458
334819	Dunham, I. et.al.	Plus	16758514-16758711
334855	Dunham, I. et.al.	Plus	18402556-18402735
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334914	Dunham, I. et.al.	Plus	19495158-19495275
334915	Dunham, I. et.al.	Plus	19505267-19506101
334935	Dunham, I. et.al.	Plus	20108247-20108373
335019	Dunham, I. et.al.	Plus	20689525-20689582
335036	Dunham, I. et.al.	Plus	20755250-20756375
335049	Dunham, I. et.al.	Plus	20877184-20877309
335081	Dunham, I. et.al.	Plus	21113871-21113937
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335163	Dunham, I. et.al.	Plus	21583508-21583655
335174	Dunham, I. et.al.	Plus	21631301-21631447
335180	Dunham, I. et.al.	Plus	21641226-21641603
335188	Dunham, I. et.al.	Plus	21669118-21669328
335189	Dunham, I. et.al.	Plus	21673403-21673472
335193	Dunham, I. et.al.	Plus	21692208-21692362
335200	Dunham, I. et.al.	Plus	21743499-21743881
335201	Dunham, I. et.al.	Plus	21745249-21745664
335284	Dunham, I. et.al.	Plus	22272583-22272712
335311	Dunham, I. et.al.	Plus	22501602-22501676
335320	Dunham, I. et.al.	Plus	22542132-22542246
335371	Dunham, I. et.al.	Plus	22849529-22849808
335377	Dunham, I. et.al.	Plus	22869909-22870188
335421	Dunham, I. et.al.	Plus	23250433-23250498
335448	Dunham, I. et.al.	Plus	23477532-23477831
335451	Dunham, I. et.al.	Plus	23480611-23480711
335455	Dunham, I. et.al.	Plus	23486127-23486216
335468	Dunham, I. et.al.	Plus	23787245-23787367
335470	Dunham, I. et.al.	Plus	23812877-23813365
335482	Dunham, I. et.al.	Plus	24087956-24088114
335485	Dunham, I. et.al.	Plus	24098953-24099123
335517	Dunham, I. et.al.	Plus	24226461-24226531
335536	Dunham, I. et.al.	Plus	24498783-24499762
335565	Dunham, I. et.al.	Plus	24881886-24882470
335585	Dunham, I. et.al.	Plus	24988240-24988405
335587	Dunham, I. et.al.	Plus	24991457-24991618
335593	Dunham, I. et.al.	Plus	25037253-25037370
335634	Dunham, I. et.al.	Plus	25163837-25164042
335651	Dunham, I. et.al.	Plus	25317560-25317696
335652	Dunham, I. et.al.	Plus	25325625-25325883
335667	Dunham, I. et.al.	Plus	25345735-25345856
335687	Dunham, I. et.al.	Plus	25445952-25446064
335690	Dunham, I. et.al.	Plus	25455442-25455625
335692	Dunham, I. et.al.	Plus	25468557-25468725
335693	Dunham, I. et.al.	Plus	25471363-25471524
335700	Dunham, I. et.al.	Plus	25512222-25512890
335720	Dunham, I. et.al.	Plus	25596542-25596646
335721	Dunham, I. et.al.	Plus	25599118-25599228
335733	Dunham, I. et.al.	Plus	25686486-25686626
335739	Dunham, I. et.al.	Plus	25698550-25698826
335745	Dunham, I. et.al.	Plus	25718164-25718332
335747	Dunham, I. et.al.	Plus	25723304-25723494
335783	Dunham, I. et.al.	Plus	25941882-25942040
335968	Dunham, I. et.al.	Plus	27743843-27744029

335971	Dunham, I. et.al.	Plus	27752808-27753017
335975	Dunham, I. et.al.	Plus	27801321-27801391
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336049	Dunham, I. et.al.	Plus	29124451-29124606
336055	Dunham, I. et.al.	Plus	29166352-29166573
336072	Dunham, I. et.al.	Plus	29269409-29269575
336075	Dunham, I. et.al.	Plus	29343938-29344050
336081	Dunham, I. et.al.	Plus	29372270-29372407
336083	Dunham, I. et.al.	Plus	29379738-29379881
336084	Dunham, I. et.al.	Plus	29380664-29380792
336086	Dunham, I. et.al.	Plus	29385594-29385713
336087	Dunham, I. et.al.	Plus	29387122-29387253
336088	Dunham, I. et.al.	Plus	29389001-29389124
336089	Dunham, I. et.al.	Plus	29401421-29401625
336090	Dunham, I. et.al.	Plus	29413020-29413162
336091	Dunham, I. et.al.	Plus	29415486-29415617
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336128	Dunham, I. et.al.	Plus	30059294-30059367
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336306	Dunham, I. et.al.	Plus	33172949-33173281
336316	Dunham, I. et.al.	Plus	33338776-33338919
336333	Dunham, I. et.al.	Plus	33673947-33677345
336387	Dunham, I. et.al.	Plus	34013939-34014124
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336489	Dunham, I. et.al.	Plus	34239511-34239619
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337219	Dunham, I. et.al.	Plus	26129629-26130053
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337562	Dunham, I. et.al.	Plus	278105-278281
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338705	Dunham, I. et.al.	Plus	25231397-25231551
338747	Dunham, I. et.al.	Plus	26336372-26336460
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339419	Dunham, I. et.al.	Plus	34359680-34359777
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332896	Dunham, I. et.al.	Minus	1631641-1631422
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326423	5867369	Minus	142311-142500
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326603	6056312	Minus	50323-50575
326806	6469835	Plus	101628-102149
326783	6525298	Plus	196378-196863
326668	6552455	Plus	146726-146838
326725	6552456	Minus	223005-223125
326857	6552460	Minus	120142-120345
326763	6598307	Plus	239690-239902
326808	6682504	Minus	65107-65214
326874	6682507	Minus	4643-4888
326876	6682507	Minus	46203-46499
326884	6682511	Plus	33403-33479
326997	5867660	Minus	71389-72147
327009	5867664	Plus	933145-933266
327015	5867664	Plus	1030457-1030534
326942	6004446	Minus	88675-88785
326943	6004446	Minus	89242-89427
326957	6469836	Plus	37529-37694
327049	6531965	Minus	1924026-1924110
327051	6531965	Plus	2222592-2222717
327056	6531965	Plus	2374323-2374751
327059	6531965	Plus	2421032-2421799
327067	6531965	Minus	3726023-3726668
327089	6531965	Plus	5238983-5239187
327037	6531965	Minus	387854-388045
327123	6531971	Minus	23980-24340
327125	6531971	Plus	48884-48975
326981	6588016	Plus	105091-106038
330139	4210430	Plus	112089-112450
330153	4325335	Plus	146951-147475
330130	6002196	Minus	241903-241967
327203	5867447	Plus	36485-36577
327206	5867447	Plus	177855-178031
327259	5867454	Plus	87268-87438
327264	5867461	Plus	47014-47367

327273	5867466	Plus	73451-73549
327274	5867470	Minus	84027-84128
327277	5867473	Minus	165616-165715
327278	5867473	Minus	166350-166439
327289	5867481	Plus	49296-49536
327304	5867494	Plus	20664-20850
327315	5867508	Minus	78409-79245
327246	5867547	Plus	136212-136325
327155	5867549	Plus	90343-90876
327159	5867550	Minus	8219-8331
327334	5902477	Minus	142655-142745
327341	6017016	Minus	122906-123014
327185	6117805	Minus	3287-3451
327309	6456757	Minus	10219-10457
327263	6525274	Minus	153814-154920
327362	6552412	Minus	62459-62805
327413	5867750	Plus	101410-101508
327418	5867750	Minus	153453-153547
327430	5867754	Plus	1320-1403
327431	5867754	Plus	1853-1958
327472	5867775	Plus	74628-74937
327487	5867785	Minus	146220-146326
327379	5867795	Plus	1368-1820
327461	6004455	Plus	209031-209210
327532	6469818	Plus	71994-72137
330170	6648220	Plus	103280-103849
330166	6648220	Plus	86542-86867
327544	5867797	Minus	18105-18332
327564	5867811	Plus	13850-14018
327566	5867811	Plus	33383-33901
327581	5867825	Plus	5318-5434
327585	5867825	Plus	85660-85764
327605	6004463	Plus	199214-199579
327710	5867860	Minus	131012-131790
327610	5867868	Minus	174109-174278
327624	5867871	Minus	37699-37788
327641	5867890	Plus	13583-13702
327646	5867894	Minus	3043-3258
327614	6525283	Plus	3634-4001
327736	5867940	Minus	37781-37887
327739	5867942	Minus	182187-182548
327740	5867943	Plus	25716-26077
327743	5867944	Minus	155930-156098
327755	5867955	Minus	61969-62145
327772	5867964	Minus	26185-26285
327774	5867964	Minus	127659-127899
327823	5867968	Minus	170359-170433
327827	5867968	Minus	201918-202048
327833	5867968	Minus	303618-303732
327805	5867968	Plus	19952-20019
327809	5867968	Plus	54610-54761
327816	5867968	Minus	79202-79552
327790	5867977	Plus	19822-19985
327791	5867977	Plus	22491-22610
327793	5867979	Plus	18874-19254
327845	6531962	Plus	193402-193549
327846	6531962	Plus	195216-195373
330204	6013606	Plus	86663-86811
330189	6165182	Minus	26732-26991
330239	6671857	Plus	117484-118092
330266	6671885	Minus	129505-129832
330275	6671904	Plus	103585-103716
330280	6671910	Plus	2109-2377
330286	6671913	Minus	31050-31171
327999	5867994	Plus	94710-94841
328109	5868020	Minus	353895-354525
328098	5868020	Minus	261745-261920
328134	5868039	Plus	72354-72487
328171	5868071	Plus	101102-101224
328221	5868099	Minus	37489-37829
328224	5868101	Plus	105563-105832
328228	5868105	Minus	21488-21596
328236	5868117	Plus	13864-14371
327864	5868130	Plus	59139-59358
327888	5868149	Minus	51964-52120
327899	5868156	Minus	102288-102697

327925	5868172	Minus	118396-118490
327927	5868173	Plus	50989-51246
327937	5868192	Minus	33127-33485
327946	5868206	Plus	44102-44319
327982	5868216	Plus	30307-30527
327990	5868218	Minus	36225-36503
328015	5902482	Minus	477679-478113
328016	5902482	Minus	507572-508519
328025	5902482	Minus	931937-932171
328031	5902482	Plus	1176372-1177283
328053	5902482	Minus	2709850-2710010
328243	6056292	Plus	1-243
328271	6552415	Plus	39015-39098
328592	5868227	Minus	252407-252565
328570	5868231	Plus	89210-89816
328607	5868233	Minus	246798-246944
328620	5868241	Minus	15651-15788
328624	5868246	Minus	120666-120836
328791	5868309	Plus	171592-171929
328810	5868327	Plus	101730-101914
328820	5868330	Plus	90446-90602
328835	5868339	Plus	88053-88461
328282	5868353	Plus	72692-72819
328314	5868371	Minus	288397-288505
328328	5868375	Plus	169210-169407
328420	5868411	Plus	53612-53886
328428	5868417	Plus	13599-13780
328436	5868417	Plus	203760-203904
328444	5868420	Plus	65393-66103
328462	5868433	Plus	49649-49768
328467	5868434	Minus	15954-16073
328474	5868446	Minus	128777-128970
328484	5868454	Minus	21974-22140
328504	5868471	Plus	47064-47217
328506	5868471	Plus	60716-60830
328507	5868473	Minus	199637-199990
328544	5868486	Plus	145659-145829
328552	5868489	Plus	47328-47607
328557	5868489	Plus	138094-138161
328558	5868489	Plus	143648-144108
328276	6004471	Plus	13282-13450
328277	6004471	Minus	279901-280181
328662	6004473	Plus	1184773-1184855
328636	6004473	Plus	192484-192543
328803	6004475	Minus	291716-291948
328305	6004478	Minus	34730-34851
328569	6004480	Plus	232896-233243
328581	6006033	Minus	121249-121400
328582	6006033	Minus	134177-134282
328768	6017031	Minus	223741-224238
328770	6017031	Minus	363933-364166
328841	6381920	Minus	5214-5479
328851	6381923	Plus	2502-2606
328859	6381928	Plus	69045-69138
328860	6381928	Plus	83265-83366
328863	6381929	Minus	29313-29506
328868	6381930	Plus	112825-112993
328876	6525286	Plus	94053-94185
328886	6588003	Plus	31068-31429
328888	6588003	Minus	111901-111999
328936	5868500	Minus	1352202-1352259
328938	5868500	Plus	1522923-1522986
328971	6478806	Minus	23976-24105
330338	5457162	Plus	48406-48518
330327	5919194	Plus	121561-121683
330319	5932415	Plus	49095-50132
328974	5868520	Plus	31557-31668
328981	5868527	Minus	105677-105764
328989	5868535	Plus	182088-182198
330363	3126882	Minus	61838-61901
330370	6580495	Plus	10826-11669
329041	5868564	Plus	141592-141785
329078	5868597	Plus	326798-326860
329097	5868624	Plus	12002-12170
329107	5868626	Plus	101063-101190
329114	5868650	Minus	23792-23910

329116	5868650	Minus	43389-43493
329164	5868691	Plus	62305-62517
329187	5868713	Plus	29909-30175
329201	5868718	Plus	79266-79539
329221	5868727	Minus	105837-105894
329246	5868732	Minus	250541-250792
329254	5868733	Plus	4133-4214
329326	5868806	Plus	155884-155992
329330	5868806	Minus	340278-340403
329382	5868868	Plus	41401-41655
329384	5868869	Minus	116524-116662
329386	6004484	Plus	160502-161110
329140	6017060	Plus	290842-290905
329182	6056331	Minus	662206-663423
329018	6249620	Plus	103950-104034
329319	6381976	Plus	721390-721470
329392	6478815	Plus	109786-109854
329029	6525302	Plus	281445-282490
329401	6682544	Plus	21342-24014
329406	6682547	Plus	47249-47395
329411	6682549	Minus	84558-84835
329429	5868882	Minus	97008-97091
329436	5868883	Plus	230265-230528
329464	6456788	Minus	4437-4538

TABLE 21:
310 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO NORMAL COLON TISSUE

Table 21 shows 310 genes up-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal colon tissue level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Genes up mets vs normal

Pkey	ExAccn	UnigeneID	Unigene Title	R1	
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.72	
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	16.36	
409041	AB033025	Hs.50081	KIAA1199 protein	13.94	
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	13.90	
432314	AA533447	Hs.312989	ESTs	12.24	
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.60	
443162	T49951	Hs.9029	DKFZP434G032 protein	9.52	
436385	BE551618	Hs.144097	ESTs	9.20	
418662	AI801098	Hs.151500	ESTs	9.00	
433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	8.90	
412093	BE242691	Hs.14947	ESTs	8.74	
442369	AI565071	Hs.159983	ESTs	8.40	
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.39	
435937	AA830893	Hs.119769	ESTs	8.22	
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.22	
432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	7.96	
440524	R71264	Hs.16798	ESTs	7.94	
424878	H57111	Hs.221132	ESTs	7.88	
430433	AA478883	Hs.273766	ESTs	7.82	
410245	C17908	Hs.194125	ESTs	7.78	
417315	AI080042	Hs.336901	ribosomal protein S24	7.76	
430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	7.76	
432435	BE218886	Hs.282070	ESTs	7.74	
426818	AA554827	Hs.289115	DKFZp434A0131 protein	7.58	
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	7.56	
444838	AV651680	Hs.208558	ESTs	7.54	
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	7.48	
446682	AW205632	Hs.211198	ESTs	7.26	
421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	7.19	
440116	AI798851	Hs.283108	hemoglobin, gamma G	7.12	
450230	AW016607	Hs.201582	ESTs	7.08	
456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	7.04	
421814	L12350	Hs.108623	thrombospondin 2	6.89	
440774	AI420611	Hs.127832	ESTs	6.86	
428065	AI634046	Hs.157313	ESTs	6.78	
422330	D30783	Hs.115263	epiregulin	6.72	
413950	AA249096	Hs.32793	ESTs	6.67	
438011	BE466173	Hs.145696	splicing factor (CC1.3)	6.62	
421057	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	6.58	
428698	AA852773	Hs.334838	KIAA1866 protein	6.40	
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	6.38	
425787	AA363867	Hs.155029	ESTs	6.38	
435812	AA700439	Hs.188490	ESTs	6.32	
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	6.28	
418875	W19971	Hs.233459	ESTs	6.22	
407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.17	
408243	Y00787	Hs.624	interleukin 8	6.12	
434936	AI285970	Hs.183817	ESTs	6.12	

412088	AI689496	Hs.108932	ESTs	6.04	
450377	AB033091	Hs.74313	KIAA1265 protein	6.00	
407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	5.98	
408296	AL117452	Hs.44155	DKFZP586G1517 protein	5.94	
456999	AA319798	Hs.298581	eukaryotic translation elongation factor	5.90	
432559	AW452948	Hs.257631	ESTs	5.88	
423349	AF010258	Hs.127428	homeo box A9	5.84	
436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	5.84	
453204	R10799	Hs.191990	ESTs	5.84	
429183	AB014604	Hs.197955	KIAA0704 protein	5.78	
427882	AA640987	Hs.193767	ESTs	5.72	
447033	AI357412	Hs.157601	ESTs	5.70	
428054	AI948688	Hs.266619	ESTs	5.66	
414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	5.64	
442806	AW294522	Hs.149991	ESTs	5.64	
418259	AA215404	Hs.137289	ESTs	5.60	
434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	5.60	
419999	AI760942	Hs.191754	ESTs	5.58	
431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.58	
422790	AA809875	Hs.25933	ESTs	5.56	
440980	AL042005	Hs.1117	tripeptidyl peptidase II	5.48	
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.46	
438578	AA811244	Hs.164168	ESTs	5.44	
410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	5.42	
426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	5.42	
450164	AI239923	Hs.30098	ESTs	5.40	
438899	AF085833	Hs.135624	ESTs	5.38	
432945	AL043683	Hs.8173	hypothetical protein FLJ10803	5.36	
437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	5.34	
419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	5.33	
407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	5.30	
447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	5.26	
419682	H13139	Hs.92282	paired-like homeodomain transcription fa	5.26	
421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	5.22	
443373	AI792868	Hs.135365	ESTs	5.22	
412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	5.21	
443651	W22152	Hs.282929	ESTs	5.21	
411274	NM_002776	Hs.69423	kallikrein 10	5.17	
421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	5.17	
426981	AL044675	Hs.173081	KIAA0530 protein	5.14	
431319	AA873350	Hs.302232	ESTs	5.10	
434966	AA657494		gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens	5.10	
418830	BE513731	Hs.88959	hypothetical protein MGC4816	5.08	
428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	5.07	
408784	AW971350	Hs.63386	ESTs	5.04	
411975	AI916058	Hs.144583	ESTs	5.02	
409760	AA302840		gb:EST10534 Adipose tissue, white I Homo	4.97	
420717	AA284447	Hs.271887	ESTs	4.96	
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.95	
434442	AA737415	Hs.152826	ESTs	4.94	
441328	AI982794	Hs.159473	ESTs	4.92	
438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.92	
451277	AK001123	Hs.26176	hypothetical protein FLJ10261	4.92	
438406	BE273296	Hs.254467	Homo sapiens cDNA FLJ13255 fis, clone OV	4.90	
424950	AA602917	Hs.156974	ESTs	4.88	
436823	AW749865	Hs.293645	ESTs, Weakly similar to I38022 hypotheti	4.87	
444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.82	
444301	AK000136	Hs.10760	asporin (LRR class 1)	4.80	
445390	AI222165	Hs.144923	ESTs	4.80	
439608	AW864696	Hs.301732	hypothetical protein MGC5306	4.78	
450506	NM_004460	Hs.418	fibroblast activation protein, alpha	4.78	
432682	AI376400	Hs.159588	ESTs	4.76	
426086	T94907	Hs.188572	ESTs	4.76	
435981	H74319	Hs.188620	ESTs	4.74	
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.72	
435756	AI418466	Hs.33665	ESTs	4.72	
447982	H22953	Hs.137551	ESTs	4.72	
449509	AA001615	Hs.84561	ESTs	4.72	
407946	AA226495	Hs.154292	ESTs	4.70	
426215	AW963419	Hs.155223	stanniocalcin 2	4.70	
414783	AW069569	Hs.278270	unactive progesterone receptor, 23 kD	4.68	
417601	NM_014735	Hs.82292	KIAA0215 gene product	4.68	
438461	AW075485	Hs.286049	phosphoserine aminotransferase	4.68	
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	4.68	
426501	AW043782	Hs.293616	ESTs	4.67	
409024	AW883529	Hs.173830	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.67	

439848	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	4.66	
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	4.66	
442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	4.62	
409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.62	
432409	AA806538	Hs.130732	KIAA1575 protein	4.60	
452220	BE158006	Hs.212296	ESTs	4.60	
442577	AA292998	Hs.163900	ESTs	4.58	
434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	4.58	
414271	AK000275	Hs.75871	protein kinase C binding protein 1	4.58	
433854	AA610649	Hs.333239	ESTs	4.56	
431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	4.53	
434220	AI174777	Hs.283039	Homo sapiens PRO2492 mRNA, complete cds		4.50
457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	4.50	
449941	AW450536	Hs.209260	ESTs	4.48	
415116	AA160363	Hs.269956	ESTs	4.47	
414386	X00442	Hs.75990	haptoglobin	4.47	
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	4.44	
423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)		4.44
449618	AI076459	Hs.15978	KIAA1272 protein	4.44	
428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	4.42	
430573	AA744550	Hs.136345	ESTs	4.42	
430929	AA489166	Hs.156933	ESTs	4.40	
433530	BE349534	Hs.281789	ESTs	4.40	
446099	T93096	Hs.17126	hypothetical protein MGC15912	4.40	
447082	T85314	Hs.42644	thioredoxin-like	4.39	
407168	R45175	Hs.117183	ESTs	4.38	
417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.38	
408380	AF123050	Hs.44532	diubiquitin	4.36	
431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	4.36	
406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	4.34	
419317	AA236282	Hs.172318	ESTs	4.32	
450295	AI766732	Hs.210628	ESTs	4.32	
423578	AW960454	Hs.222830	ESTs	4.31	
419553	N34145	Hs.250614	ESTs, Moderately similar to ZN91_HUMAN Z	4.31	
429512	AA453987	Hs.144802	ESTs	4.30	
426848	H72531	Hs.36190	ESTs	4.30	
429831	AA564489	Hs.137526	ESTs	4.30	
433735	AA608955	Hs.109653	ESTs	4.30	
450546	AA010200	Hs.175551	ESTs	4.27	
421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	4.27	
413243	AA769266	Hs.193657	ESTs	4.26	
433230	AW136134	Hs.220277	ESTs	4.22	
439717	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	4.20	
439362	AI954880	Hs.134604	ESTs	4.19	
450157	AW961576	Hs.60178	ESTs	4.17	
451690	AW451469	Hs.209990	ESTs	4.17	
418661	NM_001949	Hs.1189	E2F transcription factor 3	4.16	
443135	AI376331	Hs.156103	ESTs	4.16	
443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S		4.16
407765	AW076027	Hs.257711	ESTs, Moderately similar to ALU8_HUMAN A	4.14	
428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	4.14	
447519	U46258	Hs.339665	ESTs	4.14	
439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.12	
450219	AI826999	Hs.224624	ESTs	4.12	
431451	AA761378	Hs.192013	ESTs	4.11	
432917	NM_014125	Hs.279812	PRO0327 protein	4.10	
431328	AA502999	Hs.291591	ESTs	4.09	
425992	AA367069	Hs.100636	ESTs	4.08	
404571				4.06	
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.06	
421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	4.06	
432731	R31178	Hs.287820	fibronectin 1	4.06	
433588	AI056872	Hs.133386	ESTs	4.06	
434658	AI624436	Hs.310286	ESTs	4.06	
444040	AF204231	Hs.182982	golgin-67	4.06	
444984	H15474	Hs.132898	fatty acid desaturase 1	4.06	
438543	AA810141	Hs.192182	ESTs	4.05	
413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo		4.04
434575	AI133446	Hs.299964	Homo sapiens clone FLB7723 PRO2055 mRNA,		4.04
430256	AA470152	Hs.192195	ESTs	4.04	
424839	AA740632	Hs.120850	ESTs, Weakly similar to ALU1_HUMAN ALU S		4.02
429048	AI372949	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	4.02	
449429	AA054224	Hs.59847	ESTs	4.02	
410762	AF226053	Hs.66170	HSKM-B protein	4.00	
418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens		4.00
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.00	

429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotactin)	4.00
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.00
435008	AF150262	Hs.162898	ESTs	4.00
431361	AW971375	Hs.292921	ESTs	3.97
444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.96
434701	AA460479	Hs.321707	KIAA0742 protein	3.96
413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	3.95
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.92
428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	3.91
435714	AA699325	Hs.269880	ESTs	3.86
447514	AI809314	Hs.208501	ESTs, Weakly similar to B34087 hypotheti	3.86
453818	BE256832	Hs.10711	hypothetical protein FLJ13449	3.85
433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	3.85
440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	3.85
417819	AI253112	Hs.133540	ESTs	3.84
409596	BE244200	Hs.55075	KIAA0410 gene product	3.83
423129	L44396	Hs.124106	Homo sapiens cDNA FLJ11941 fis, clone HE	3.83
453884	AA355925	Hs.36232	KIAA0186 gene product	3.83
431193	AW749505	Hs.296770	KIAA1719 protein	3.81
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	3.80
425568	AW963118	Hs.161784	ESTs	3.78
441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.77
428079	AA421020	Hs.208919	ESTs	3.77
412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	3.76
435354	AA678267	Hs.117115	ESTs	3.75
436535	AW295687	Hs.254420	ESTs	3.74
420439	AW270041	Hs.193053	eukaryotic translation initiation factor	3.72
436090	AI640635	Hs.116468	EST	3.71
416265	AA177088	Hs.190065	ESTs	3.70
417715	AW969587	Hs.86366	ESTs	3.67
435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.67
438607	AW080237	Hs.252884	ESTs	3.66
408194	AA601038	Hs.191797	ESTs, Weakly similar to S65657 alpha-1C-	3.65
417211	T97617	Hs.269092	ESTs	3.60
435538	AB011540	Hs.4930	low density lipoprotein receptor-related	3.59
410390	AA876905	Hs.125286	ESTs	3.58
438818	AW979008	Hs.222487	ESTs	3.57
431416	AA532718	Hs.178604	ESTs	3.57
433517	AW022133	Hs.189838	ESTs	3.56
428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	3.56
432954	AI076345	Hs.214199	ESTs	3.53
434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	3.53
421933	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.52
422082	AA016188	Hs.111244	hypothetical protein	3.52
437135	AL038624	Hs.208752	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.49
424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.49
434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	3.49
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.48
417670	R07785		gb:yf15c06.r1 Soares fetal liver spleen	3.48
431615	AW295859	Hs.235860	ESTs	3.48
429355	AW973253	Hs.292689	ESTs	3.45
430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	3.45
432929	AW207166	Hs.191265	ESTs	3.44
437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	3.44
445674	BE410347	Hs.13063	transcription factor CA150	3.42
408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.42
408908	BE296227	Hs.250822	serine/threonine kinase 15	3.41
432235	AA531129	Hs.190297	ESTs	3.41
453985	N44545	Hs.251865	ESTs	3.41
415736	AA827082	Hs.291872	ESTs	3.38
430220	BE378277	Hs.152230	ESTs	3.37
426510	AW861225	Hs.194637	BANP homolog, SMAR1 homolog	3.37
412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.36
411573	AB029000	Hs.70823	KIAA1077 protein	3.33
413816	AW958181	Hs.189998	ESTs	3.32
428057	AI343641	Hs.185798	ESTs	3.32
436280	AI690734	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.31
449365	AW968261	Hs.118913	ESTs, Moderately similar to T46371 hypot	3.31
440659	AF134160	Hs.7327	claudin 1	3.30
436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypotheti	3.29
433862	D86960	Hs.3610	KIAA0205 gene product	3.29
424624	AB032947	Hs.151301	Ca2+dependent activator protein for secr	3.29
439955	AW203959	Hs.149532	ESTs	3.28
417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	3.28
436150	AW510927	Hs.125243	ESTs	3.27
414900	AW452420	Hs.248678	ESTs	3.26

439349	AI660898	Hs.195602	ESTs	3.25	
428255	AI627478	Hs.187670	ESTs	3.24	
436217	T53925	Hs.107	fibrinogen-like 1	3.24	
429083	Y09397	Hs.227817	BCL2-related protein A1	3.24	
422244	Y08890	Hs.113503	karyopherin (importin) beta 3	3.22	
430178	AW449612	Hs.152475	ESTs	3.21	
413810	AW197644	Hs.19107	ESTs	3.20	
428728	NM_016625	Hs.191381	hypothetical protein	3.20	
437151	AA745618	Hs.194637	BANP homolog, SMAR1 homolog	3.19	
427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.19	
438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.19	
439943	AW083789	Hs.124620	ESTs	3.18	
439280	AI125436	Hs.48752	ESTs	3.18	
452336	AA960961	Hs.305953	zinc finger protein 83 (HPF1)	3.17	
433713	AW976511	Hs.112592	ESTs	3.16	
414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	3.14	
407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.14
432722	AA830532	Hs.326150	ESTs	3.14	
419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	3.11	
449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.11
418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	3.09	
409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	3.08	
436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.08	
406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	3.07	
408242	AA251594	Hs.43913	PIBF1 gene product	3.07	
444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	3.06	
459407	N92114		gb:za22h11.r1 Soares fetal liver spleen	3.05	
433972	AI878910	Hs.3688	cisplatin resistance-associated overexpr	3.04	
427704	AW971063	Hs.292882	ESTs	3.03	
440255	AI932285	Hs.160569	ESTs	3.03	
424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S		3.03
413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.02
433944	AL117518	Hs.3686	KIAA0978 protein	3.01	
440428	BE560954		gb:601347719F1 NIH_MGC_8 Homo sapiens cD		3.00

TABLE 21A

Table 21A shows the accession numbers for those pkeys lacking unigeneID's for Table 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409760	115373_1	AA302840 T93016 T92950 AA077551
413497	1373771_1	BE177661 H06215 BE144709 BE144829
417670	1692163_1	R07785 T85948 T86972
418876	179960_1	AA740616 AA654854 AA229923
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
423974	233842_1	AL118754 AA333202 H38001
430068	312849_1	AA464964 M85405 AA947566
432340	345248_1	AA534222 AA632632 T81234
433586	370470_1	T85301 AW517087 AA601054 BE073959
434280	382816_1	BE005398 AA628622 AA994155
434966	396504_1	AA657494 AI582663 AI581639
438962	467390_1	BE046594 BE046667 AA828585 AI207343
439848	477806_1	AW979249 D63277 AA846968
440428	49370_-1	BE560954
440638	499025_1	AI376551 T87714 AA897445
456332	179104_1	AA228357 AW841786 AW841716

TABLE 21B

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404571	7249169	Minus	112450-112648

TABLE 22: 177 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO NORMAL COLON TISSUE

Table 22 shows 177 genes down-regulated in colon cancer derived liver metastases compared to normal colon tissue. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" normal colon tissues was less than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" normal adult tissue level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Genes down mets vs. normal

Pkey	ExAccn	UnigeneID	Unigene Title	R1
425196	AL037915	Hs.155097	carbonic anhydrase II	0.03
414522	AW518944	Hs.76325	step II splicing factor SLU7	0.03
409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.03
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	0.03
424326	NM_014479	Hs.145296	disintegrin protease	0.04
414798	AI286323	Hs.97411	hypothetical protein MGC12335	0.04
432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.04
425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	0.05
437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.05
447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	0.05
414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.06
428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	0.06
432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.07
431727	AW293464	Hs.162031	ESTs	0.07
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	0.07
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.08
412047	AA934589	Hs.49696	ESTs	0.08
412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.08
422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.08
450684	AA872605	Hs.25333	interleukin 1 receptor, type II	0.09
418935	T28499	Hs.89485	carbonic anhydrase IV	0.09
433658	L03678	Hs.156110	immunoglobulin kappa constant	0.09
422260	AA315993	Hs.105484	regenerating gene type IV	0.09
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	0.09
426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	0.09
441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.10
440624	AF017987	Hs.7306	secreted frizzled-related protein 1	0.10
420929	AI694143	Hs.296251	programmed cell death 4	0.10
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.10
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	0.10
414802	AI793107	Hs.27018	Ris	0.10
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.11
421996	AW583807	Hs.1460	glucagon	0.11
423371	AU076819	Hs.1650	solute carrier family 26, member 3	0.11
406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	0.11
414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	0.11
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	0.11
424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	0.12
426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	0.12
453967	AW009077	Hs.232947	ESTs	0.12
425920	AL049977	Hs.162209	claudin 8	0.13
408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodieste	0.13
457407	AA505035	Hs.195651	ESTs	0.13
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.14
422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	0.14
409196	NM_001874	Hs.334873	carboxypeptidase M	0.14
416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.14
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	0.14

457982	AW856093	Hs.183617	ESTs	0.14
407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.14
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	0.14
424885	AI333771	Hs.82204	ESTs	0.14
423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.14
444237	AA336878	Hs.9842	Human DNA sequence from clone RP4-788L20	0.14
445848	AA774824	Hs.13377	Homo sapiens clone 23649 and 23755 unkno	0.14
451062	AL110125	Hs.25910	Homo sapiens mRNA; cDNA DKFZp564C1416 (f	0.14
436485	X59135	Hs.156110	immunoglobulin kappa constant	0.14
423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.15
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.15
427506	AK000134	Hs.179100	hypothetical protein FLJ20127	0.15
430712	AW044647	Hs.196284	ESTs	0.15
421666	AL035250	Hs.1408	endothelin 3	0.16
425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	0.16
429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	0.16
433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.16
450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	0.16
417820	D87449	Hs.82635	UDP-glucuronic acid/UDP-N-acetylgalactos	0.16
406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	0.16
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	0.16
436327	AA813075	Hs.120181	ESTs	0.16
408873	AL046017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	0.16
429524	AB033037	Hs.205293	KIAA1211 protein	0.16
447023	AA356764	Hs.17109	integral membrane protein 2A	0.17
424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.17
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	0.17
432563	NM_013261	Hs.198468	peroxisome proliferative activated recep	0.17
406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.17
451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.17
447726	AL137638	Hs.19368	matrilin 2	0.17
409549	AB029015	Hs.54886	phospholipase C, epsilon 2	0.17
433334	AI927208	Hs.231958	matrix metalloproteinase 28	0.17
425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.17
407360	X13075		gb:Human 2a12 mRNA for kappa-immunoglobu	0.17
430627	U61148	Hs.247685	atonal homolog 1 (Drosophila)	0.17
418807	NM_004944	Hs.88646	deoxyribonuclease I-like 3	0.18
453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.18
422994	AW891802	Hs.296276	ESTs	0.18
432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.18
400417	X72475		-	0.18
443506	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.18
428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.18
451928	AI823801	Hs.30315	CTCL tumor antigen se57-1	0.18
429576	BE242628	Hs.209061	sudD (suppressor of bimD6, Aspergillus n	0.18
422106	D84239	Hs.111732	Fc fragment of IgG binding protein	0.19
430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.19
452852	AK001972	Hs.30822	hypothetical protein FLJ11110	0.19
421904	BE143533	Hs.109309	hypothetical protein FLJ20035	0.19
417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	0.19
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	0.19
452802	AU076403	Hs.323468	electron-transferring-flavoprotein dehyd	0.19
450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	0.19
420061	AW024937	Hs.29410	ESTs	0.19
426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.19
408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.19
437682	AA476652	Hs.94952	Homo sapiens cDNA: FLJ23371 fis, clone H	0.19
449110	H56112		gb:yq95f07.r1 Soares fetal liver spleen	0.19
446727	AB011095	Hs.16032	KIAA0523 protein	0.19
408395	BE072425	Hs.44579	hypothetical protein FLJ20199	0.20
423541	AA296922	Hs.129778	gastrointestinal peptide	0.20
410850	AW362867	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	0.20
412420	AL035668	Hs.73853	bone morphogenetic protein 2	0.20
423942	AF209704	Hs.135723	glycolipid transfer protein	0.20
421832	NM_016098	Hs.108725	HSPC040 protein	0.20
459046	AA910339	Hs.26216	LOC50627	0.20
421360	AA297012	Hs.103839	erythrocyte membrane protein band 4.1-li	0.20
438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m	0.20
403047				0.20
421712	AK000140	Hs.107139	hypothetical protein	0.20
427333	AF067797	Hs.176658	aquaporin 8	0.20
421964	X73079	Hs.288579	polymeric immunoglobulin receptor	0.20
438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	0.21
445200	AA084460	Hs.12409	somatostatin	0.21
404854				0.21
426390	AA377299	Hs.90431	ESTs	0.21

403381				0.21
449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalyti	0.21
457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.21
435730	AB020635	Hs.4984	KIAA0828 protein	0.21
431518	AA743462	Hs.165337	ESTs	0.21
412589	R28660	Hs.24305	ESTs	0.21
432584	AA928829	Hs.47099	hypothetical protein FLJ21212	0.21
426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	0.21
429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.21
414429	R51494	Hs.71818	ESTs	0.22
439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	0.22
406697	M21388	Hs.123017	Human unproductively rearranged Ig mu-ch	0.22
406663	U24683	Hs.302063	immunoglobulin heavy constant mu	0.22
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	0.22
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	0.22
430107	AA465293	Hs.105069	ESTs	0.22
424273	W40460	Hs.144442	phospholipase A2, group X	0.22
419559	Y07828	Hs.91096	ring finger protein	0.22
413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	0.22
407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	0.22
433906	AI167816	Hs.43355	ESTs	0.22
446203	Z47553	Hs.14286	flavin containing monooxygenase 5	0.22
403740				0.22
405701				0.22
413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	0.22
419577	L36531	Hs.91296	integrin, alpha 8	0.23
451820	AW058357	Hs.337353	ESTs	0.23
424897	D63216	Hs.153684	frizzled-related protein	0.23
422880	AF228704	Hs.121524	glutathione reductase	0.23
430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	0.23
430753	AI432401	Hs.2659	fibrinogen-like 2	0.23
409060	AI815867	Hs.50130	necdin (mouse) homolog	0.23
412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	0.24
414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	0.24
417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	0.24
414589	AA149791	Hs.68864	ESTs, Weakly similar to phosphatidylseri	0.24
427167	AI239607	Hs.99196	hypothetical protein MGC11324	0.24
440630	BE561430	Hs.239388	Human DNA sequence from clone RP1-304B14	0.24
423044	AA320829	Hs.97266	protocadherin 18	0.24
441931	BE564830	Hs.23744	hypothetical protein FLJ12899	0.24
443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.24
405441				0.24
407241	M34516		gb:Human omega light chain protein 14.1	0.24
415165	AW887604	Hs.78065	complement component 7	0.24
426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	0.24
410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	0.24
436032	AA150797	Hs.109276	latexin protein	0.24
414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	0.24
414197	W44877	Hs.55501	ESTs	0.24
406836	AW514501	Hs.156110	immunoglobulin kappa constant	0.24
437083	AW082597	Hs.244862	ESTs	0.25
421709	AA159394	Hs.107056	CED-6 protein	0.25
426512	AW511656	Hs.170177	Meis1 (mouse) homolog	0.25

TABLE 22A

Table 22A shows the accession numbers for those pkeys lacking unigeneID's for Tables 21A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
449110	798430_1	H56112 H58047 AI630710 N58742

TABLE 22B

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
403381	9438267	Minus	26009-26178
403740	7630882	Plus	86504-87227
404854	7143420	Plus	14260-14537
405441	7408124	Plus	100952-101283
405701	4263751	Plus	93243-93364

TABLE 23: 175 GENES UP-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 23 shows 175 genes up-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 3.0. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Genes up liver metastases vs Duke's B survivors

Pkey	ExAccn	UnigeneID	Unigene Title	R1
426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	9.06
432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	7.96
424878	H57111	Hs.221132	ESTs	7.88
428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	7.48
407284	AI539227	Hs.214039	hypothetical protein FLJ23556	7.45
439943	AW083789	Hs.124620	ESTs	7.00
442369	AI565071	Hs.159983	ESTs	7.00
415116	AA160363	Hs.269956	ESTs	6.98
433517	AW022133	Hs.189838	ESTs	6.70
437176	AW176909	Hs.42346	calcineurin-binding protein calsarcin-1	6.68
440524	R71264	Hs.16798	ESTs	6.62
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	6.38
448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	6.28
412088	AI689496	Hs.108932	ESTs	6.04
417670	R07785		gb:yf15c06.r1 Soares fetal liver spleen	5.95
440774	AI420611	Hs.127832	ESTs	5.91
426086	T94907	Hs.188572	ESTs	5.90
436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	5.84
453204	R10799	Hs.191990	ESTs	5.84
407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	5.67
432435	BE218886	Hs.282070	ESTs	5.61
434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	5.60
421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	5.54
407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.51
440980	AL042005	Hs.1117	tripeptidyl peptidase II	5.48
443651	W22152	Hs.282929	ESTs	5.42
412668	AA456195	Hs.10056	hypothetical protein FLJ14621	5.29
444838	AV651680	Hs.208558	ESTs	5.24
433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.11
430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	5.11
434966	AA657494		gb:nt66f04.s1 NCI_CGAP_Pr3 Homo sapiens	5.10
426897	AW976570	Hs.97387	ESTs	5.08
432954	AI076345	Hs.214199	ESTs	5.07
431416	AA532718	Hs.178604	ESTs	5.00
420717	AA284447	Hs.271887	ESTs	4.96
424950	AA602917	Hs.156974	ESTs	4.94
438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.92
419999	AI760942	Hs.191754	ESTs	4.89
435812	AA700439	Hs.188490	ESTs	4.86
418662	AI801098	Hs.151500	ESTs	4.79
428065	AI634046	Hs.157313	ESTs	4.77
407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	4.75
435981	H74319	Hs.188620	ESTs	4.74
419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	4.73
432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	4.72
447982	H22953	Hs.137551	ESTs	4.72

449509	AA001615	Hs.84561	ESTs	4.72
407946	AA226495	Hs.154292	ESTs	4.70
438607	AW080237	Hs.252884	ESTs	4.68
438406	BE273296	Hs.254467	Homo sapiens cDNA FLJ13255 fis, clone OV	4.62
426818	AA554827	Hs.289115	DKFZp434A0131 protein	4.62
452220	BE158006	Hs.212296	ESTs	4.60
436823	AW749865	Hs.293645	ESTs, Weakly similar to I38022 hypotheti	4.60
433854	AA610649	Hs.333239	ESTs	4.56
413816	AW958181	Hs.189998	ESTs	4.52
428079	AA421020	Hs.208919	ESTs	4.52
421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	4.50
417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.48
423974	AL118754		gb:DKFZp761P1910_r1 761 (synonym: hamy2)	4.44
449618	AI076459	Hs.15978	KIAA1272 protein	4.44
431615	AW295859	Hs.235860	ESTs	4.44
418876	AA740616		gb:ny97f11.s1 NCI_CGAP_GCB1 Homo sapiens	4.43
428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	4.42
430573	AA744550	Hs.136345	ESTs	4.42
430929	AA489166	Hs.156933	ESTs	4.40
446099	T93096	Hs.17126	hypothetical protein MGC15912	4.40
439362	AI954880	Hs.134604	ESTs	4.36
421999	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006	4.35
434220	AI174777	Hs.283039	Homo sapiens PRO2492 mRNA, complete cds	4.33
432925	AA878324	Hs.192734	ESTs	4.32
417819	AI253112	Hs.133540	ESTs	4.30
426848	H72531	Hs.36190	ESTs	4.30
429831	AA564489	Hs.137526	ESTs	4.30
433735	AA608955	Hs.109653	ESTs	4.30
418884	AA230228	Hs.59197	ESTs	4.28
413243	AA769266	Hs.193657	ESTs	4.26
431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	4.23
428054	AI948688	Hs.266619	ESTs	4.22
413967	AW204431	Hs.117853	ESTs, Weakly similar to I38022 hypotheti	4.22
433230	AW136134	Hs.220277	ESTs	4.22
421057	T58283	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone H	4.22
423578	AW960454	Hs.222830	ESTs	4.21
439717	W94472	Hs.59529	ESTs, Moderately similar to ALU1_HUMAN A	4.20
443696	AW607444	Hs.134622	ESTs	4.20
432722	AA830532	Hs.326150	ESTs	4.18
435756	AI418466	Hs.33665	ESTs	4.14
428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	4.14
439451	AF086270	Hs.278554	heterochromatin-like protein 1	4.12
445943	AW898533	Hs.181574	ESTs	4.12
450219	AI826999	Hs.224624	ESTs	4.12
431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	4.11
432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.10
443148	AI034357	Hs.211194	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.08
450177	AI698091	Hs.107845	ESTs	4.08
420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.06
421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	4.06
432731	R31178	Hs.287820	fibronectin 1	4.06
433588	AI056872	Hs.133386	ESTs	4.06
434658	AI624436	Hs.310286	ESTs	4.06
444040	AF204231	Hs.182982	golgin-67	4.06
429512	AA453987	Hs.144802	ESTs	4.06
443349	AI052572	Hs.269864	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
439867	AA847510	Hs.161292	ESTs	4.04
425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	4.02
431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.00
432125	AW972667	Hs.287510	Homo sapiens cDNA FLJ12300 fis, clone MA	4.00
435468	AW362803	Hs.166271	ESTs	3.97
412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	3.95
446682	AW205632	Hs.211198	ESTs	3.95
441328	AI982794	Hs.159473	ESTs	3.92
455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	3.90
438996	AW748336	Hs.168052	KIAA0421 protein	3.86
418303	AA215701	Hs.186541	ESTs, Weakly similar to I38022 hypotheti	3.85
444816	Z48633	Hs.283742	H.sapiens mRNA for retrotransposon	3.84
429355	AW973253	Hs.292689	ESTs	3.83
438578	AA811244	Hs.164168	ESTs	3.83
432945	AL043683	Hs.8173	hypothetical protein FLJ10803	3.83
435318	T97301	Hs.18026	ESTs	3.82
449941	AW450536	Hs.209260	ESTs	3.80
424915	R42755	Hs.23096	ESTs	3.76
449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.76
416265	AA177088	Hs.190065	ESTs	3.75

413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	3.74
412093	BE242691	Hs.14947	ESTs	3.74
413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.73
431915	AK000777	Hs.272197	Homo sapiens cDNA FLJ20770 fis, clone CO	3.68
434442	AA737415	Hs.152826	ESTs	3.63
434959	AW974949	Hs.186564	ESTs, Weakly similar to I38022 hypotheti	3.63
427704	AW971063	Hs.292882	ESTs	3.62
426510	AW861225	Hs.194637	BANP homolog, SMAR1 homolog	3.60
435714	AA699325	Hs.269880	ESTs	3.60
432598	AI341227	Hs.157106	ESTs	3.57
438543	AA810141	Hs.192182	ESTs	3.55
422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.54
418259	AA215404	Hs.137289	ESTs	3.54
428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	3.49
419457	AA243146	Hs.209334	ESTs, Moderately similar to S23A_HUMAN P	3.47
439312	AA833902	Hs.270745	ESTs	3.47
408784	AW971350	Hs.63386	ESTs	3.45
456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	3.45
424762	AL119442	Hs.183684	eukaryotic translation initiation factor	3.44
442884	AI076570	Hs.134053	ESTs	3.44
421023	AW449855	Hs.96557	Homo sapiens cDNA FLJ12727 fis, clone NT	3.43
434575	AI133446	Hs.299964	Homo sapiens clone FLB7723 PRO2055 mRNA,	3.42
430433	AA478883	Hs.273766	ESTs	3.39
419317	AA236282	Hs.172318	ESTs	3.38
448710	T62926	Hs.304184	ESTs	3.37
439322	H72245	Hs.188635	ESTs	3.37
430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	3.35
411755	BE327036	Hs.117494	ESTs	3.33
427882	AA640987	Hs.193767	ESTs	3.28
438899	AF085833	Hs.135624	ESTs	3.28
436535	AW295687	Hs.254420	ESTs	3.25
434936	AI285970	Hs.183817	ESTs	3.22
451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susce	3.18
447514	AI809314	Hs.208501	ESTs, Weakly similar to B34087 hypotheti	3.18
413672	BE156536		gb:QV0-HT0368-310100-091-h10 HT0368 Homo	3.16
435073	AA664078		gb:ac04a05.s1 Stratagene lung (937210) H	3.13
450295	AI766732	Hs.210628	ESTs	3.13
419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.13
434495	AW352170	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	3.12
408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.12
456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.12
421489	AI922821	Hs.32433	ESTs	3.12
436090	AI640635	Hs.116468	EST	3.11
450230	AW016607	Hs.201582	ESTs	3.11
438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.09
418720	AI381687	Hs.39526	ESTs	3.09
433102	AI343966	Hs.158528	ESTs	3.08
436150	AW510927	Hs.125243	ESTs	3.05
440116	AI798851	Hs.283108	hemoglobin, gamma G	3.04
414900	AW452420	Hs.248678	ESTs	3.04
435937	AA830893	Hs.119769	ESTs	3.02
424848	AI263231	Hs.327090	EST	3.02
435354	AA678267	Hs.117115	ESTs	3.00

TABLE 23A

Table 23A show the accession numbers for those pkeys lacking unigeneID's for tables 1-20A, 21A, 22A, and 23A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
413497	1373771_1	BE177661 H06215 BE144709 BE144829
413672	1382512_1	BE156536 BE156439 BE156700 BE156449 BE156653 BE156533 BE156524 BE156670 BE156721 BE156723
417670	1692163_1	R07785 T85948 T86972
418876	179960_1	AA740616 AA654854 AA229923
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
423974	233842_1	AL118754 AA333202 H38001
432340	345248_1	AA534222 AA632632 T81234
434966	396504_1	AA657494 AI582663 AI581639
435073	399701_1	AA664078 AW363313 AA805009
438962	467390_1	BE046594 BE046667 AA828585 AI207343
455778	1364506_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
456332	179104_1	AA228357 AW841786 AW841716

TABLE 24: 34 GENES DOWN-REGULATED IN COLON CANCER DERIVED LIVER METASTASES COMPARED TO COLON CANCER PRIMARY TUMOR SAMPLES CLASSIFIED AS DUKE'S B SURVIVOR

Table 24 shows 34 genes down-regulated in colon cancer derived liver metastases compared to colon cancer primary tumor samples classified as Duke's B stage with a positive survival outcome (Duke's B survivor). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer derived liver metastases to "average" Duke's B survivor was greater than or equal to 0.25. The "average" colon cancer derived liver metastases level was set to the 50th percentile. The "average" Duke's B survivor level was set to the 50th percentile.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Genes down liver metastases vs Duke's B survivors

Pkey	ExAccn	UnigeneID	Unigene Title	R1
414522	AW518944	Hs.76325	step II splicing factor SLU7	0.05
416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.07
409153	W03754	Hs.50813	hypothetical protein FLJ20022	0.07
414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	0.11
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	0.11
424326	NM_014479	Hs.145296	disintegrin protease	0.11
428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	0.12
417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	0.12
422260	AA315993	Hs.105484	regenerating gene type IV	0.12
425196	AL037915	Hs.155097	carbonic anhydrase II	0.13
433336	AF017986	Hs.31386	secreted frizzled-related protein 2	0.13
450685	L15533	Hs.423	pancreatitis-associated protein	0.14
407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	0.15
414798	AI286323	Hs.97411	hypothetical protein MGC12335	0.16
452852	AK001972	Hs.30822	hypothetical protein FLJ11110	0.17
447513	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A	0.17
423541	AA296922	Hs.129778	gastrointestinal peptide	0.17
425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	0.18
406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	0.18
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	0.18
428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	0.19
414812	X72755	Hs.77367	monokine induced by gamma interferon	0.20
452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	0.20
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	0.21
408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	0.21
453064	R40334	Hs.89463	potassium large conductance calcium-acti	0.21
431727	AW293464	Hs.162031	ESTs	0.22
433658	L03678	Hs.156110	immunoglobulin kappa constant	0.22
442064	AI422867	Hs.88594	ESTs	0.22
417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	0.22
430280	AA361258	Hs.237868	interleukin 7 receptor	0.23
452877	AI250789	Hs.32478	ESTs	0.23
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	0.24
402408				0.24

TABLE 24B

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402408	9796239	Minus	110326-110491

TABLE 25:

Table 25 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 26. Seq ID No links the nucleic acid and protein sequence information in Table 26 to Table 25.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
Seq.ID.No.:	Sequence Identification Number found in Table 26

Pkey	ExAccn	UnigeneID	Unigene Title	Seq ID No.
426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1-4
419145	N99638		gb	5 & 6
426818	AA554827	Hs.340046	DKFZp434A0131 protein	7 & 8
421057	T58283		Homo sapiens cDNA	9
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	10 & 11
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	12 & 13
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	14 &15
443162	T49951	Hs.9029	DKFZP434G032 protein	16 &17
436385	BE551618	Hs.144097	ESTs	18-20
447033	AI357412	Hs.157601	ESTs	21 & 22
439608	AW864696	Hs.301732	hypothetical protein MGC5306	23-27
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	28 & 29
442577	AA292998	Hs.163900	ESTs	30 & 31
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	32 & 33
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	34 & 35
457407	AA505035	Hs.345911	ESTs	36
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	37 & 38
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	39 & 40

TABLE 25A

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
409041		10962_2 AB033025 AL359061 AL045836 AI751521 AI752804 AI752650 AA853580 AI752290 AA853460 AI752769 AA852309 AA853785 AA853219 AW068503 AI752069 AL049389 AW068368 BE439518 W52813 BE141833 AI940574 AI750606 AL109718 AA242845 AA315795 AA307741 AW954603 AI752070 AA350794 AI752649 AA307755 AW951677 AA298896 BE439692 AA852453 AW068826 AW853984 AA418236 AA639417 AW290917 AI750592 AI752768 AL045837 AI926513 AW262903 BE439819 AI459360 AW339074 AW295181 AW029483 AI750945 AI750659 AI752525 AI147688 BE440122 AI751522 AI473816 AI752291 AI694639 AI925816 AA599476 AA242752 AW021892 AI755098 AW469299 AW769363 AA853579 AI784082 AA852454 AI925501 AA976657 AW150473 AW166734
417332	166755_1	AW972717 AA523805 AI962905 AI373245 AW235545 AI812045 AW589434 AI826824 AW572339 AI377551 AA195718 AI868470
419145	182217_1	N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815
421057	198849_1	T58283 AA765038 AA283052 H99396 AA814751 AI032674 N81016 N81017 BE222349 AA830545
424566	2408_1	M16801 NM_000901 D57171 AL041328 AF068623 AI201179 AA151766 AA568349 AI698649 AI692765 BE327401 AA744953 AA744951 AW361986 AV651840 T29894 AW945146 AW945145 W24096 AI183952 AI458972 AW190993 AI765359 AI634663 AI741201 AW418944 AI767551 AA679687 AW772342 AW629508 BE504300 AI251790 AI522294 AA724341 AW615402 AI537570 AA470665 AI458375 AW768901 AA447079 T23537 AI783744 R44301 D56621 N91919 AA149749
426101	26088_1	AL049987 AW362842 T78981 AA247541 AI217018 AW961515 AA632986 AA663108 BE326465 AW872412 AI024689 AA453725 BE150456 AA229448 AA442638 AA442648 AI916737 AA460220 AA868553 AI827987 AI005467 R31132 AI742087 AA442379 N56349 AW769479 AI860142 AI917507 AA813604 AI860141 AI459289 AA522837 AI354470 AI921333 BE466760 AW971193 AW103830 AW277065 AW020895 AI187977 N28268 AI084517 R95914 AA833517 AA563934 AA437299 AA436880 AA447794 AA812876 AA663178 R31089 AI472712 R64648 AA600372 AA229164 AA703066 AW270324 AI191725 AA551512 AA493776
426818	272427_1	AA554827 AA701001 AW972954 AL039129 AA385540 AA911663
429970	31134_1	AK000072 AW840683 AW843764 AW844444 AW844515 AW603469 AW862395 AI860838 AW511708 AF127035 NM_012128 AK000138
430378	3170_1	Z29572 AW976377 AA286871 AA633372 AA987627 AA743176 AI865358 AJ006884 AF031845 Z14955
431958	3394_1	X63629 NM_001793 BE175433 BE153414 BE153425 AW364593 BE315317 AW950190 AA314252 BE142943 AW365220 AW368405 BE004269 AW366568 AL040609 AI829273 AI591168 BE146183 AI631060 AI830793 W78081 W92295 AI927422 BE009313 AI371793 AW993031 AI204659 AA535113 AW993030 AI190281 AA555159 AW269637 AW993146 AI149268 AA425217 AW473194 AI890930 AA551993 AI952106 W92308 AI827275 W45400 AI952328 AW609233 AA774611 AA551779 AI913967 AI798658 AI537658 AW517535 AA632236 AW339148 AW589522 AA836945 AA961263 AW015821 AW272946 C00249 W40333 BE143121
436385	418907_1	BE551618 AI207338 BE220568 AI261568 AW841737 AA714722 AA946891 AI033239
439608	47438_3	AW864696 AW338889 AI342866 AA084522 AI244150 AI610339 AA425635 AA764930 AA976965 AW805766 AA057765 AW805845 AW802595 AA262971 AI969620 N75323 BE549060 AW805725 AA025809 N80776 N64595 AW073372 AA025493 AI819475 AW028879 AW189496 AA442907 AW410368 AI911629 N71276 AW316922 AW805838 AA043880 AW189184 AA449756 AA748153 AA705608 AI910643 AA279492 BE160119 AW805761 AA026262 AA782207 AW057652 AW805768 H21998 AW194254 AW275178 AA449040 AA279582 N76314 N54348
442577	54549_1	AA292998 AW238350 AI676059 AW074092 BE566458 AW078677 AW514801 AW073701 AW170620 AI523736 AI580870 AI923975 AI393326 AI700229 AW450814 AW628452 AI671457 AA937534 AI889694 AW339423 AW291875 AA551874 AI682314 AI926227 AA397375
443162	5613_1	T49951 AA025326 H04839 AA393303 R63101 W57657 W25628 AI961431 R71165 N39940 H01548 H01759 AA641624 AI634930 AA595296 AW994770 AW994747 BE047247 W38159 AA858133 AI701944 AW386273 AA676625 R24676 R79410 AA922863 AI151319 H01013 AA024482 W02674 H01456 AI150858 AW135972 AW631167 AI270332 H04750 T49622 AA004543 R63061 AI093066 AI247539 H01225 H03388 AW472933 AA382448 AI219287 N27194 AW389613 AA649738 AW994764 AW389614 R25176 AA897262 R71626 AA909471 R71240 AW811917 R76109 AI202312 AI866010 R76162 AL117538 R79411 T58656 AW994674
446619	685_1	AU076643 AA594604 AA346866 R18197 AA345192 AA337773 AA089791 R84435 AA337838 AW392167 AA075190 D55416 AW150360 AW366257 AA579816 H93048 AW385689 AW385697 AI186216 AW581197 AL037509 AB019562 AA232626 R97905 AW368019 AA242891 AW888502 AI798331 AW385635 AW581221 T96947 H87989 AA369511 AA075191 R80742 AA366406 W92752 H45586 AI864016 AW888497 BE004992 AI384110 AI624256 AI627593 W92728 AI682719 AA948208 AA171734 N40517 J04765 AA379957 AA362403 NM_000582 AF052124 AA300290 AA333447 AA343721 AW889543 BE566767 R76601 R18015 AA100531 AA489963 AA101296 AA363513 AA344088 AA336750 T77505 D56440 AL110351 AL110331 F12195 R20175 AA336664 H17766 AA363538 AA363590 D28760 AW578517 AA363531 AI814667 AA846899 AA366253 AW951285 AA297992 AA327756 AW361609 AW815455 AW815427 AW815428 D54182 AW852200 AA171630 W27018 AW815864 AW379995 AW378222 AW362610 BE566022 AW021023 C17352 D58435 AA345409 AI623991 AW020967 AI924770 AI799443 AW946393 AA991239 AI571617 AI935181 AI923999 AI826895 AI860319 AW189873 AW270353 AW023584 AI813811 R99929 AW339056 AA913152 AI636352 AI829394 AW151077 AW192580 AI570119 AI086391 AW021764 AW519154 AI375193 AW268678 BE465690 AW019983 AW268654 AI573138 AI141809 AI954553 AI559242 AA568945 AA886417 AW338527 AI635881 BE465666 AI921239 AA968537 AI956027 AA911981 AI827661 AW511046 BE619780 AI922227 AI811870 AW190131 AW129220 AW512906 AI290757 AI819088 AI623771 AA775616 BE349419 AI126375 H88773 AI241758 AW275157 AI337848 AI613425 AI631387 AA922631 AI273483 AI982898 AW168957 AI446481 BE501588 BE048264 AI499922 AW023812 BE220523 AW973846 BE349276 AI141091 AA976060 AW973845 AA101270 AI582472 AW613675 AI139360 AI282627 AI276044 N22345 AI261875 AA634136 AI824468 AW887693 N27107 R21504 AI042223 N22067 AW196871 AI581019 BE004973 AA252035 N22087 AA570717 H11250 AI804026 AA368098 AA021512 H08842 N26275 AA176368 AI758758 AA570371 AA232574 BE221177 AW190221 AW471386 M78225 AI422140 AI624521 AA719775 AA300291 AA568657 AI871430 BE465630 N71862 T72587 W92721 H88774 D54383 AW103693 AW089986 AI382689 R42363 R44962 T98770 AA357374 AW022074 AI356207 T29241 AW089431 AI933875 N66267 N67352 AA121786 AA363910 F09824 T95618 N66888 R80550 AI280667 AW196719

			R59299 AW021049 H73469 AI954311 BE439454 AW079450 AW973850 AA348338 AW896006 AW268145 AA853631 H17650 R39537 N66873 N67240 H06298 AI784199 R44260 AA904118 AA911756 F04544 AA807809 AA665210 AI696448 T29719 AA837240 T64844 H08926
	447033	704603_1	AI357412 AI870708 AI590539 W07459
5	449032	7945_1	AA045573 AA279920 R20139 AA372783 AW963629 H21473 R78318 W74359 AA022505 AA369091 AW084075 AA503638 AV660815 AI216262 AA779843 BE219825 AF125534 AW972129 AI919099 AI621283 AI300590 AI953701 AA331415 AW610546 AW793050 AI953679 AW793047 AW610543 AI671103 AW292105 AW024112 R77947 W76339 AA305111 AA132523 AA227467 H21401 AW366572 AW024129 AI701886 AI654744 BE042803 AI347173 AW866053 AW662710 R36639 AI469777 AA962733 AI865366 AA501998 AW866054 BE178974
10	457407	333252_1	AA505035 AW235098 AI634028

Table 26

Seq ID NO: 1 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

```
1      11     21     31     41     51
|      |      |      |      |      |
CAATATAGTA CAATAACTAT TTGCATGACA TTTACATCGG ATATTATGAG TGATCTAGAG   60
TTGATATGAA GTATATGGGA GGATGTGCAA AGGTGATGTG CAAATACTAT GTCATTTTAT  120
AGGGGGGACT TGAGTATCCT TTGTTACCCT CAGGAGATCC TGAAACCAGT CCCCCATGGA  180
TACTGAGGGC TGACTGTATA GTCCTATCCT CACGGAACTT TCATTCTAAT GGGGGAAGAC  240
TGACTATAAA CAAAATATAT GTAATAGGTG GTGGTAAGTA CCGTGGAGAA GTAACAAATG  300
GGGCAAAGTG AGTTATACAG CTCCATTCTT AGAAACCTTG GAGTACTTTT CTTAGTTTAT  360
ACTCGTGGTG GTTTCCTTTT GTCTCCTTTA TTACATGGGA CTCTGACATG TGCCCATAGC  420
TAGGGTGACA GTAGGATCTA CCCGATAGTA GGGTGGCAGT AGGATCTACC CAAAAAGCGT  480
CCTGCTGATA CAGGACCAAA GCATCCTGTT GTTCTCGAGC CTATAAAAAG AGCTAATGGT  540
GTTGCTTCTC TTAACTGTGG CCTCCTACAC TGTGTTTTGG ATGATTGGTG ATGTCTTGGA  600
TATTCTGTTT CTTTGGAACT TTGAATATAC AACACTTTAC TAGGGAATTA GCAATGGAAG  660
CAGAGCAAAG ATGTACAGAG GAAACAATGC GTAACTCTGA TGGAATTGAA GTCATGAGGC  720
AGCAGAGAGC TTAAATTACA GCTTTAAAAA TTTTTATTTT TTAGAGGGAA TTTACTTGGG  780
AGTAACAGCA GTAATAGTTA ACGGAGCCAG AATGCTTGAG TCATATAATT GCAAAGCAGA  840
GTTGGGAGCA ACAGATGCTA AAGAGTAGTT GCTGTAGTTC CTCTTTGGGT CGTAGGAGCA  900
GTTGTCATAT TACTATATAG CTACTGCATG AAGAAGAGTT CTTAGTGAGG CCTGGGTGAA  960
CAGCTCTTCT TAGTATTCTG TGTGACCCCA TTTGACCTTT TAACAAATCC CTAAGTAAAT 1020
AAATAGCCCC TCAGGAAAAC TAAGTTTTTC TCTGCTGTTT TTTTGCTTGA GAGAGCTATA 1080
ACTGTAATAG ACTTATATTT CTGAACATTT TAGTGCTTGC CAATATTTGG TAATATTTAT 1140
GTTTCCTATA TTTGTAATGA ACATTCTTCT TCCGGTACAT TTTTTGTTAA ATTATTGTTT 1200
GATGGATAAA AGTTCACCTT TTATTGTATA AAATTGACTG AGATTAATTT ATACACATTG 1260
ACAATGGGTA AATAGAATTT TTCAGATTAT TAAAAGCTGA AGGATGACCA CGTAAGCAAA 1320
AAAAAAAAAA AAAAAACCAA CAAAAATAAA CCCAAACCCC TCAAACAATT TCGAACACGA 1380
AACATTCTTC TGATGCCGGC ATCCCTGCTT GCAGGTGTGA AGGGGGCAGG AATCAGCGAG 1440
GTGTCCTGGG CTGAGTCCCC GGGGAAGAAT ATGAT
```

Seq ID NO: 2 DNA sequence
Nucleic Acid Accession #: X83301.1

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1      11     21     31     41     51
|      |      |      |      |      |
GCAAAGCCAG CTGGGCTCCT GAGTCCGGTG GGTACTTGGA GAACTTACTA CGTCTAGCTG   60
GAGGATTGTA AATGCACCAA TCAGCATGCT GTGTCTAGCT CAAGATTTTC TCCATCCCCT  120
TATTTTGGGC CAGTGGCTGT CATTACATAT GAGATGAGTC TCTTGAAGAC TACAGATGAA  180
CTCAAGCTCC ATGAGGAGAT GTTTCATTGT CGAGAGCAGT CATGATGGCC TGCACTCCAC  240
ACAATGCAAC AGAGTGAAAG AGCAGGTTCT GCTTCTTTGG TGTAGTCCTG AAGCTTCCTA  300
AGAAACTTCA CATCAGGTGA TGGATAGGAG CAACCCTGTA AAACCAGCCT TAGACTATTT  360
TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAACCAGT TCAAGTTGGA  420
AGTGTGTCTT TTGAATGCAG AGAACAAAGT CGTGGACAAC CAGGCTGGGA CCCAGGGCCA  480
GCTGAAGGTG CTGGGTGCCA ACCTCTGGTG GCCGTACCTG ATGCACGAAC ACCCCGCCTA  540
CCTGTACTCC TGGGAGGATG GTGATTGCTC ACACCAAAGC CTTGGACCCC TCCCAGCCTG  600
TGACCTTTGG GACCAACTCC ACCTACGCAG CAGACAAGGG GGCTCTGTAT GTGGATGTGA  660
TCCGTGTGAA CAGCTACTAC TCTTGGTATC GCAACTACGG GCACCTGGAG TTGATTCGGC  720
TGCAGCTGGC CGCCCAGTTT GAGAATTGGT GTGAGACATC ACAATCCCAT TATTCAGAGC  780
GCGTATGGAG TGGAAACGCT TGTAGGGTTT CACCAGGGCT GGTGAATTAC CAGATCTCCG  840
TCAAGTGCAG TAACCAGTTC AAGTTGGAAG TATGTCTTTT GAATGCAGAA AACAAAGTCG  900
TGGACAACCA GGCTGGGACC CAGGGCCAGC TGAAGGTGCT GGTGCCAACC TCTGGTGGCC  960
GTACCTGATG CACGAACACC CCGCCTACCT GTACTCGTGG GAGGATGGTG ATTGCTCACA 1020
CCAAAGCCTT GGACCCCTCC CAGCCTGTGA CCTTTGGGAC CAACTCCACC TACGCAGCAG 1080
ACAAGGGGGC TCTGTATGTG GATGTGATCC GTGTGAACAG CTACTACTCT TGGTATCGCA 1140
ACTACGGGCA CCTGGAGTTG ATTCGGCTGC AGGCCCTGCA GCTGGCCGCC CAGTTTGTGA 1200
ATTGGTGTAA GACATCACAA TCCCATTATT CAGAGCGCGT ATGGAGTGGA AACGCTTGTA 1260
GGGTTTCACC AGTCTTTCCC AGGGAACTCC GATGAAGTGT TCCAACAAAA TGAGCGAGTG 1320
AACCAAGAAG AGGATGACAT TAGATCCAGG AGATACAACA GAGGAGATAA TCTCCAGGAT 1380
GCCTGTGAAG AAAGATCCCT GGATCCCAGG ATGATTATAG GACAAGTTGT TCATAATCCA 1440
GCAGGCCAGA AGACTTCCAG GGAAACTCAT TTCAAGATGA AAATGGACCA GCCGCAGTGG 1500
CTCACGCCTG TAATACCAGC ACTTTGGGAG GCTGAGGCGG GCGGATCACT TGAGGTCAAG 1560
AGTTTGAAAC TAGCCTGGCC AACGTGGCAA AACTCCATCT CTATTAAAGA TACAAAAATT 1620
AGCCAGGCAT AGTGGTGCAT GCCTGTAGTC CCAGCTACTT GGGATGCTGA GGCAGGAAGA 1680
ATTGCTTGAA CCTGGGAGGC AGAGTCTGCG GTGACCGAGA TCATGCCACT GCACTCCAGC 1740
CTGGGTGACA GAGCCAGACT CCGTCTCTAC TAAAAAAAAA AAAAAAAAAA AAA
```

Seq ID NO: 3 Protein sequence:
Protein Accession #: CAA58280.1

```
1      11     21     31     41     51
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MDRSNPVKPA LDYFSNRLVN YQISVKCSNQ FKLEVCLLNA ENKVVDNQAG TQGQLKVLGA   60
NLWWPYLMHE HPAYLYSWED GDCSHQSLGP LPACDLWDQL HLRSRQGGSV CGCDPCEQLL  120
LLVSQLRAPG VDSAAAGRPV
```

Seq ID NO: 4 DNA sequence
Nucleic Acid Accession #: BC002622.1

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1      11     21     31     41     51
|      |      |      |      |      |
GGCACGAGGC TCCGCCCGCG GCCGGGATGC ACTAGGCAAA GCCAGCTGGG CTCCTGAGTC   60
```

CGGTGGGTAC TTGGAGAACT TACTACGTCT AGCTGGAGGA TTGTAAATGC ACCAATCAGC 120
ATGCTGTGTC TAGCTCAAGA TTTTCTCCAT CCCCTTATTT TGGGCCAGTG GCTGTCATTA 180
CATATGAGAA CTCAAGCTCC ATGAGGAGAT GTTTCATTGT CGAGAGCAGT CATGATGGCC 240
TGCACTCCAC ACAATGCAAC AGAGTGAAAG AGCAGGTTCT GCTTCTTTGG TGTAGTCCTG 300
AAGCTTCCTA AGAAACTTCA CATCAGGTGA TGGATAGGAG CAACCCTGTA AAACCAGCCT 360
TAGACTATTT TTCAAACAGG CTGGTGAATT ACCAGATCTC CGTCAAGTGC AGTAACCAGT 420
TCAAGTTGGA AGTGTGTCTT TTGAATGCAG AAAACAAAGT CGTGGACAAC CAGGCTGGGA 480
CCCAGGGCCA GCTGAAGGTG CTGGGTGCCA ACCTCTGGTG GCCGTACCTG ATGCACGAAC 540
ACCCCGCCTA CCTGTACTCG TGGGAGGATG GTGATTGCTC ACACCAAAGC CTTGGACCCC 600
TCCCAGCCTG TGACCTTTGT GACCAACTCC ACCTACGCAG CAGACAAGGG GGCTCTGTAT 660
GTGGATGTGA TCCGTGTGAA CAGCTACTAC TCTTGGTATC GCAACTACGG GCACCTGGAG 720
TTGATTCAGC TGCAGCTGGC CGCCCAGTTT GAGAATTGGT GTAAGACATC ACAATCCCAT 780
TATTCAGAGC GCGTATGGAG TGGAAACGCT TGTAGGGTTT CACCAGTCTT TCCCAGGGAA 840
CTCCGATGAA GTGTTCCAAC AAAATGAGCG AGTGAACCAA GAAGAGGATG ACATTAGATC 900
CAGGAGATAC AACAGAGGAG ATAATCTCCA GGATGCCTGT GAAGAAAGAT CCCTGGATCC 960
CAGGATGATT ATAGGACAAG TTGTTCATAA TCCAGCAGGC CAGAAGACTT CCAGGGAAAC 1020
TCATTCAAGG AGGTGAAAAT GATGGATGAC TCCTCCAAGA TGAAAATGGA CCAGCCGCAG 1080
TGGCTCACGC CTGTAATACC AGCACTTTGG GAGGCTGAGG CAGGCGGATC ACTTGAGGTC 1140
AGGAGTTTGA AACTAGCCTG GCCAACGTGG CAAAACTCCA TCTCTATTAA AAATACAAAA 1200
ATTAGCCAAG CATAGTGGTG CATGCCTGTA GTCCCAGCTA CTTGGGATGC TGAGGCAGGA 1260
AGAATTGCTT GAACCTGGGA GGCAGAGTCT ACAGTGAGCC GAGATCATGC CACTGCACTC 1320
CAGCCTGGGC AACACAGTGA GACTCCATCT CAAAAAAAAA AAAAAAAAAA AA

Seq ID NO: 5 <u>Protein sequence:</u>
Protein Accession #: AAH02622.1

```
1          11         21         31         41         51
|          |          |          |          |          |
MDRSNPVKPA LDYFSNRLVN YQISVKCSNQ FKLEVCLLNA ENKVVDNQAG TQGQLKVLGA 60
NLWWPYLMHE HPAYLYSWED GDCSHQSLGP LPACDLCDQL HLRSRQGGSV CGCDPCEQLL 120
LLVSQLRAPG VDSAAAGRPV
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Seq ID NO: 6 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

```
1          11         21         31         41         51
|          |          |          |          |          |
ACCTGAGATC AGGAGTTCGA GATCAGCCTG ACCAATAGGG TGAAACCCCG TCTCTACTAA 60
AAATACAAAA AATTAGCTGG ACACGATGGT GGGTGCCTGT GGTCCCGGCT ACTCGGGAGG 120
CTGAGACAGG AGAATCAGTT GACCTGGGAG TTGGTGGTTG CAGTGAGCTG AGATCACACC 180
ATTGCATTCC AAGCCTGGGC AACAAGAGTG AAACTCCATC GCAAAAAAAA AAAAGAAGGG 240
GCATAATTTG TGGATGAGGA TTGGATATAA GGTAAAGGAT GGGACATTCT TGGACTTACA 300
GATGGTGTGA TTGCCTGGCT AGAAGAAGAA TTCCCGGTCA AAAAGAAACC ATCAGCTTTC 360
CAAGTGTGAA AGAGAGATAA ATCTGTGAAG ATTATAGGGA CTACAGGAAA CTTAATCTTT 420
TTCTTTGAAA AAGCAATTGT AGCAAAAAAA AAGAAAATTT CTTACTGTCA TCTAAAATTG 480
ACATGGACAT CTTAGTGGAC TAGAAGTTAA GGGCATAAAT TCTCCCAGTG ATTTTTAATT 540
TTAGCATTGT GATTAACACC TTCTAAAATT GCCAGAACTT AATAAATAAT TGCTTTTCAT 600
TATTAGTATG CCATCAAATT TAGTAGCTGT TTCAGGCTTT AATGTGTCAA GCCTAAAATC 660
CAGATTTTTG AGGATCTTCT CCCTCTTAAA AGAGTATTCA GTTAACTGCC GTAGAAATAC 720
ACATGTATAC AAGGGCACTG TATACATCAG TCTAAAAAAT AAAAATATGT ATACGTTCTG 780
GTGAGTCTAG CACAGCATTG CCCAATAGAA ATACCAATGG AGGTCACAAA TGTGGCCCAT 840
ATAGGTTAAT TGGTAAATTT TCTNATAGNC ACC
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Seq ID NO: 7 DNA sequence
Nucleic Acid Accession #: AK000942
Coding sequence: 1204-1503

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1          11         21         31         41         51
|          |          |          |          |          |
GTAAAGGAAT GTCTTTTTAA TTCAGCTTTT CTTTTCTCCA TGCTAGTGTT ATCAGGTTTT 60
GGTATTTATT TACTTACAGC ATATGTTATG AAGCTGGTTT GAAAATTGGT TTTAGATATA 120
TCTGCAAGTT TACTACTTTG ACTGTAAAAA AAAAAAATGA AAAAGTAGTT GACATCTGTC 180
CTCAGAAGAA GTTTGCAGGT TGCATATTTG TGTGTAAATA CACAGGCTAA AAGGTAATTT 240
ATGTTCCTTG GGAATTGAAA TGGTCAGTGG CCCGTTACAG AAACTTATCA GTCATATATC 300
AGCACCAGTT CATTCTTTTG CACCTTAGGG ACCATCTGTC CCCTGAGGTG ACCTGAGAAA 360
CAACCAGTTG CCCACAGACT GTTATTTCTT CAAGTGAGCC AGGATTTGAT TTCACTGCCT 420
TATATTCTAT TTTTAGTGTA CAGTGCTTTG ATTTTTTGGA AAAACTAAAT TTTAAACATA 480
TTTGAAAAAT GTTATAAGAC TTGGACATTA AGTCTGTTGA TAGCCAAAGT CAGTTTACCA 540
AAGTAAAACA AATAAATTCT ATGCTTCTTC ATTGTCAAAG AGCAGTCTGC CATCATGTGG 600
ATATAAATGG ACTATGTAAA GTGACATGGT GCTTACTCTC TACCTAATAA TAGCCTCCCT 660
CCTGTTCCAA CAAGATAACC AACAGGTATA TTTAATTTAC CAGTTAATAT GTTTTGGATA 720
ATTGGCTGCC TTGAAATGCT ATATGTTTTA TAGTACATCA TAGCTTTAGT TTTCTTCATA 780
AGGAAATTAC AGTTACATCC TGGCTAACAT GGTGAAACTC CATCTCTACT AAAAATACAA 840
AAAATTAGCC GGGCGTGGTG GCGGGCACTT GTAGTCCCAG CTACTCGGGA GGCTGAGGCA 900
GGAGAATGGC GTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATCGT GCCACTGTAC 960
TCTGGCCTGG GAGACAGAGC GAGACTCCAT CTCAAAAAAA AAAAAAAAAA AAAAAAAAGA 1020
GAGAGAGAGA CCTGGAGTAG AGATTCTGTC AAAGAACTTT TTCTTTCTTG AGAAGCATCT 1080
GAAATGGAAT CTGTTGTCTC TTCGAAATAT GTACTGCTGT AACAGTGAAA CAACCCTCAG 1140
AGTATGCCTT CGTGTGGGCT ACTCGTTGTG GTTTTGAACT TGGGGGAACT GTCTGTGTTT 1200
GGGTCAAGAA TATGCAACTG GCTGGGCACA TTGGCTCACG CCTGTAATCC CAGCAATTTG 1260
GGAGGCTGAG GCAGGCGGAT CACCTGAGGT CAGGGCTTCA AGACCAGACT GGCCAACATG 1320
GTGAAACCCC GTCTCTACTG AAAATACAAA AATTAGCTGG GCATGGTGGC AGGTGCCTGT 1380
AATCCCAGCT ACTCGGGAGG CTGACGTGAG AGAATCGCTT GAACCCGGGA GTTGGAGGTT 1440
GCAGTGAGCC GAGATTGCAC CATTGCACTC CAGCTTGGGC AACAAGAGTG AAACTCTTGT 1500
```

CTCAG

Seq ID NO: 8 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

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1         11        21        31        41        51
|         |         |         |         |         |
GACTAGGCTG GGCAACATAG TGAGACCTCA TCTCTAAAAT TAAAAAAATA AAAGCCACCA  60
GAAAAAAACC TAAAAACATG CCAAGTGACA TCAGTCTTTG ATGAAAATGG CAGCAGAAGA  120
GTGATGCCAT GGGTGGGGGT GGGAAATGCT ATTTCAGCAG AGAGGGAGCT GTCATGGAAG  180
ACACCATGTG GCTGGGCACG GTGGCTCACA CCTGTAATCC CAGCACTTTG GGAGATAGAG  240
GCAGGTGGAT CCCTTGAGCT TAGGAATTTG AGACTAGCCT GGGCAATAAG AGTGAAACTC  300
CATCTCAAAA AAAAAAAAAA AAAAAGGTGC ATGAAACATA TGAAGCAAAA AGTGAAAGTC  360
CCCATTCTTT TCCTTTTTCC AGAGGTGATT TTTGTGGCCA ATCTGGTTTC ATTCCCTCCC  420
AGACACTTTT CTAGGCATCT ATGCGCCTCT ATTCACATAT AAACAAAATA GGAGTTTTCC  480
TGTGCTTCCC TTAAATGGCA TATGTATCTT TCACTCTTTT TTTTCACCTA GTGGATCTTT  540
AATACCTTAA AAGCTCAACC TGGGCTTGGT GCGGTGGCTC ATACGTGTAA TCCCAGGCCT  600
TTGGGAGGCC AAGGTGGGAG GATCACTTGA GCTCAGGAGT TCCAGACCAT TCCAAAGCAA  660
AAACAAAAGG ATTTTGAGAT CAGTGTGGGC AACTTAGCAA AACACCATCT CTTAAAAAAA  720
AAAAAAAAAA
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Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: BC010433.1
Coding sequence: 3-335

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1         11        21        31        41        51
|         |         |         |         |         |
GGTCGCCCTC CGTCGTGGTC TGGCGTGTAT TCCGAGCCTT GGTGTCTGGC GGTTTCCGAG  60
CGTTGGTGTC TGGCGGTTTC CGAGCGTTGG TGTCTGGCGG TTTCCGACCG TTGGTGTCTG  120
GCGGTTTCCG ACCGTTGGTG TCTGGCACGC GCCACCCTCT CTTGCTTTGG TTGCGCCATG  180
CCGATGTACC AGACAAGAAG ACAAGAAAAT GATTTGAGGA CAGCTTCAAT CGCGGTGTGA  240
AGAAGAAAGC AGCAAAACGA CCACTGAAAA CAACGCCGGT GGCAAAATAT CCAAAGAAAG  300
GGTCCCAAGC GGTACATCGT CATAGCCGGA AACAGTCAGA GCCACCAGCC AATGATCTTT  360
TCAATGCTGC GAAAGCTGCC AAAAGTGACA TGCAGCACCG AGAAGTCCGC GTGAAGTGCG  420
TGAAGGCTCT GAAAGGGCTG TACGGTAACC GGGACCTGAC CGCACGCCTG GAGCTCTTCA  480
CTGGCCGCTT CAAGGACTGG ATGGTTTCCA TGATCATGGA CAGAGAGTAC AGTGTGGCAG  540
TGGAGGCCGT CAGATTACTG ATACTTATCC TTAAGAACAT GGAAGGGGTG CTGATGGACG  600
TGGACTGTGA GAGCGTCTAC CCCATTGTGT AGGCCTCTAA TTGAGGCCTG GCCTCTGCTG  660
TGGGTGAATT TCTGTACTGG AAACTTTTCT ACCCTGAGTG CGAGATAAGA ACGATGGGTG  720
GAAGAGAGCA ACGCCAGAGC CCAGGTGCCC AGAGGACTTT CTTCCAGCTT CTGCTGTCCT  780
TCTTTGTGGA GAGCAAGCTC CACGACCACG CTGCTTACTT AGTAGACAAC CTGTGGGACT  840
GTGCAGGGAC TCAGCTGAAG GACTGGGAGG GTCTGACAAG CCTGCTGCTG GAGAAGGACC  900
AGAGCACGTG CCACATGGAG CCAGGGCCAG GGACCTTCCA CCTCCTAGGG TGAAACCAGG  960
AGAGATTGCT TGCTTCACTT GTACAAGGCA GGAACGGTGG CATGGGGTGG GGGAAACTTG  1020
GAGTTGGAAG GTGGCTAATC TTTGATTCTA TGTTTTTGAT CCTCCTGGCA CTCCAGACCT  1080
GGGTGATGTG CAGGAGAGCA CACTGATAGA AATCCTTGTG TCCAGTGCCC AGCAACTCCT  1140
GCCTCAGCCT CCCGAGCAGC TGGGACTACA GGCGCCCGCC ACCACGCCTG GCTAACTTTT  1200
TTGTGTTTTT AGTAGAGACG GGTTTCACC GTGTTGGCCA GGATGGTCTT GATCTCTTGA  1260
CCTTGTGATC CACCTGCCTC ATCATCCCAA AGTGCTGGGA TTACAGGCGT GAGCCACTGC  1320
GCCCAGCATG TTAGACAATT TTTAATTCAT CCTCTCTGTG CTGTTGTTTT CTCAGCTGTG  1380
AAAGGAATAT TCTGGTGGGG ACAAGGTTAC AGAGTTGCTG AGAGGGTCTC ATGACATGAA  1440
GGTACTGGCC TTGGCACAGT GCCTGGGGGG GCGGGGACTC CGCACATGCC TGTGATGTCA  1500
CAGTTACTGT CAGTTCACAG CGAACCTTCC CTCCTTTTCC TGTTGACTTT CCCACACTCC  1560
TGTAACCCTC CCTCCCTCCC TTCTTCCTCT CTCTCTCTCT CACTCACGCA CACGCACACA  1620
CACACACACA CACACACACA CACACACTCC ATTCACTGTC TCCATGACTC TGGAGTAAAC  1680
TAACGTCTCG AGTTGCCATT GGAAGCCCCG TTGTCCTCAT TTAGACTTTC ATGGGTTATA  1740
GGCACTTTTG ACTTCCTGGG GTCCTTCTTC AGTTAAAAAA AAAAATTAGA AAATTAGGCC  1800
GGGCGTGGTG GCACATGCCT GTAATCCCAG CACCTTGGCC TCCCAAAGTG CTGGGATTAC  1860
AGGAGTGAGC CACCATGCCC AGCCTCCGTT GTCCTCATTT AGACTTTCAT GGGTTATAGG  1920
CACTTTTGAC TTCCTGGGGT CCTTCTTCAG TTAAAAAAAA AAAAAAAAA
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Seq ID NO: 10 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

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1         11        21        31        41        51
|         |         |         |         |         |
AGTGGNTCCC CCGGNCTGCA GGAATTCGGC ACGAGATCAT GATGGCTAAT ATTTCCTGAG  60
CACCTTTCAT TCAGGCATGA TGCCAGGTGC ACCAACTTAC TTAATCCTCA TAGCCACCAC  120
CTGAGCAAGC TCCTGTTTTA TAAATGGACC AGTTCTTGTT GCTGTTGTAC AAGTTATTTT  180
CTTTCTATAA CGTCCTCCTT GTCCTCCTTC CACATTCTTA AAGAAACTTT CCCTTCCTTT  240
AAAGTACTCA GGGAGCCCTG CATTGCTTCT TGAAGCCTTC TCCAGCTTCA TCATCTCACA  300
GTGGTCTCTC TTTTCACTAA ATGTCCAATA TGCTGCACAT AAGTACCCCA AAGTTAGCAC  360
AGGAATTGTT CCATGGCTGT CATATATGTT AAAAATCATT AAAAGTTCAT TTTTTCTCTC  420
ATTATGGGAA GGATACATGC TCCTACTAGT AAATTTAGTA GGTAGAAAAA AATTATCACT  480
ATCTAGACTG CTTTCCATTT AGTCTTTATG CATAGCTTTC GTGTCTGCCT ATTTTTACCT  540
TGTGTTTGTA ACTTACTATT ATAAAATATG CGTCTCTATG TTCATTGTCA ACGATTATTT  600
ACAATAACAT GGAGTGGATT TACATGTATT CTCTATATTT GGATTAAAGG AGATAGAGTA  660
TGTGAAATTA AATGGGAGAA GTATCTGATA CATAACAGGC AATACAAATA TTATCACATA  720
GCGTCAATTT ATTTGTGAAT ATTGAAAGCT CCAAAAAAGA AAAAAAGTTT TTTTTTAATT  780
CCCGTAATTA CTTATTGCAG TATTGTGTTC ATACAAACTG CTCAGTCATT TTGGAGAAAT  840
AACAATTTTT TTCCTCATCA TGAAGTAAGG TATGCTCACT GCAAAAAAAA TCTAGAAAAT  900
AAAGAGGAAC ATGCTAAAGA AAAGAATACT CCCATATAAT CTCTGTCTTC ATAAATAATC  960
TTTTGTAACG CTTATACACT GCTGGTGGGA ATGTAAATTA GTTCAGCCAT TGTGAAAAGT  1020
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AGCGTAGCAA TTCCTTGAAA AACTTAAAAT AGATTTACCG TTCAACCCAG CAATCCCATT 1080
ATTGGGCATA TACCCAGTGG AATGTAAATC ATCCTGCCAT AAAAACACAT GCACATGTAT 1140
GTTCATTGCA GCACTATTCA CAATAGCAAA GACATGGAAT CAACCTATAT GCCCATCAAT 1200
AGTAGACTGA ATAAAGAAAA TATGGTACAT ATTCACCACA GAATACTAAG CAGCCATAAA 1260
AAAAAA

Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_000582.1
Coding sequence: 88-990

1 11 21 31 41 51
| | | | | |
GCAGAGCACA GCATCGTCGG GACCAGACTC GTCTCAGGCC AGTTGCAGCC TTCTCAGCCA 60
AACGCCGACC AAGGAAAACT CACTACCATG AGAATTGCAG TGATTTGCTT TTGCCTCCTA 120
GGCATCACCT GTGCCATACC AGTTAAACAG GCTGATTCTG GAAGTTCTGA GGAAAAGCAG 180
CTTTACAACA AATACCCAGA TGCTGTGGCC ACATGGCTAA ACCCTGACCC ATCTCAGAAG 240
CAGAATCTCC TAGCCCCACA GACCCTTCCA AGTAAGTCCA ACGAAAGCCA TGACCACATG 300
GATGATATGG ATGATGAAGA TGATGATGAC CATGTGGACA GCCAGGACTC CATTGACTCG 360
AACGACTCTG ATGATGTAGA TGACACTGAT GATTCTCACC AGTCTGATGA GTCTCACCAT 420
TCTGATGAAT CTGATGAACT GGTCACTGAT TTTCCCACGG ACCTGCCAGC AACCGAAGTT 480
TTCACTCCAG TTGTCCCCAC AGTAGACACA TATGATGGCC GAGGTGATAG TGTGGTTTAT 540
GGACTGAGGT CAAAATCTAA GAAGTTTCGC AGACCTGACA TCCAGTACCC TGATGCTACA 600
GACGAGGACA TCACCTCACA CATGGAAAGC GAGGAGTTGA ATGGTGCATA CAAGGCCATC 660
CCCGTTGCCC AGGACCTGAA CGCGCCTTCT GATTGGGACA GCCGTGGGAA GGACAGTTAT 720
GAAACGAGTC AGCTGGATGA CCAGAGTGCT GAAACCCACA GCCACAAGCA GTCCAGATTA 780
TATAAGCGGA AAGCCAATGA TGAGAGCAAT GAGCATTCCG ATGTGATTGA TAGTCAGGAA 840
CTTTCCAAAG TCAGCCGTGA ATTCCACAGC CATGAATTTC ACAGCCATGA AGATATGCTG 900
GTTGTAGACC CCAAAAGTAA GGAAGAAGAT AAACACCTGA AATTTCGTAT TTCTCATGAA 960
TTAGATAGTG CATCTTCTGA GGTCAATTAA AAGGAGAAAA AATACAATTT CTCACTTTGC 1020
ATTTAGTCAA AAGAAAAAAT GCTTTATAGC AAAATGAAAG AGAACATGAA ATGCTTCTTT 1080
CTCAGTTTAT TGGTTGAATG TGTATCTATT TGAGTCTGGA AATAACTAAT GTGTTTGATA 1140
ATTAGTTTAG TTTGTGGCTT CATGGAAACT CCCTGTAAAC TAAAAGCTTC AGGGTTATGT 1200
CTATGTTCAT TCTATAGAAG AAATGCAAAC TATCACTGTA TTTTAATATT TGTTATTCTC 1260
TCATGAATAG AAATTTATGT AGAAGCAAAC AAAATACTTT TACCCACTTA AAAAGAGAAT 1320
ATAACATTTT ATGTCACTAT AATCTTTTGT TTTTTAAGTT AGTGTATATT TTGTTGTGAT 1380
TATCTTTTTG TGGTGTGAAT AAATCTTTTA TCTTGAATGT AATAAGAATT TGGTGGTGTC 1440
AATTGCTTAT TTGTTTTCCC ACGGTTGTCC AGCAATTAAT AAAACATAAC CTTTTTTACT 1500
GCCTAAAAAA AAAAAAAAAA AAAA

Seq ID NO: 12 Protein sequence:
Protein Accession #: NP_000573.1

1 11 21 31 41 51
| | | | | |
MRIAVICFCL LGITCAIPVK QADSGSSEEK QLYNKYPDAV ATWLNPDPSQ KQNLLAPQTL 60
PSKSNESHDH MDDMDDEDDD DHVDSQDSID SNDSDDVDDT DDSHQSDESH HSDESDELVT 120
DFPTDLPATE VFTPVVPTVD TYDGRGDSVV YGLRSKSKKF RRPDIQYPDA TDEDITSHME 180
SEELNGAYKA IPVAQDLNAP SDWDSRGKDS YETSQLDDQS AETHSHKQSR LYKRKANDES 240
NEHSDVIDSQ ELSKVSREFH SHEFHSHEDM LVVDPKSKEE DKHLKFRISH ELDSASSEVN

Seq ID NO: 13 DNA sequence
Nucleic Acid Accession #: NM_001793
Coding sequence: 71-2560

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| | | | | |
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CTGGCTGCAG TGCGCGGCCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
CTTGGAGGCG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
CTGCCCTGGG CAAGAGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
TGAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAAGTCTA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCCGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTCGCTGTA GAGAAGGAGA CAGGCTGGTT GTTGTTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCT CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCCTACCA GGTACTTCTG TGATGCAGGT 780
GACAGCCACG GATGAGGATG ATGCCATCTA CACCTACAAT GGGGTGGTTG CTTACTCCAT 840
CCATAGCCAA GAACCAAAGG ACCCACACGA CCTCATGTTC ACCATTCACC GGAGCACAGG 900
CACCATCAGC GTCATCTCCA GTGGCCTGGA CCGGGAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCCACCACC ACGGCAGTGG CAGTAGTGGA 1020
GATCCTTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATGT 1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGGACGCCCC 1140
CAACTCACCA GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCCACCCTG AGAGCAACCA GGGCATCCTG ACAACCAGGA AGGGTTTGGA 1260
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GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCCACCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCACTGGGGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGCTACCG 1500
CATCCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTCACAGC 1560
TGTGGGCACC CTCGACCGTG AGGATGAGCA GTTTGTGAGG AACAACATCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGACAATG GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGCTAAC 1680

ACTGATTGAT GTCAATGACC ATGGCCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGCGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCCTG AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGTCTGACC ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGCGACTGC CATGGCCATG TCGAAACCTG CCCTGGACCC TGGAAGGGAG GTTTCATCCT 2040
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GAGAAAGAAG CGGAAGATCA AGGAGCCCCT CCTACTCCCA GAAGATGACA CCCGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCGGA GGTGGTTCTC CGCAATGACG TGGCACCAAC 2280
CATCATCCCG ACACCCATGT ACCGTCCTCG GCCAGCCAAC CCAGATGAAA TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCACA GCCCCGCCCT ACGACACCCT 2400
CTTGGTGTTC GACTATGAGG GCAGCGGCTC CGACGCCGCG TCCCTGAGCT CCCTCACCTC 2460
CTCCGCCTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCCTGCC TGCAGGGCTG 2580
GGGACCAAAC GTCAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTCGGAG CTTGTCAGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTTGCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCCTCAG AGGCCAAGTT TCCAGAAGCC 2820
TCTTACCTGC CGTAAAATGC TCAACCCTGT GTCCTGGGCC TGGGCCTGCT GTGACTGACC 2880
TACAGTGGAC TTTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
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GCTGGGCCCA CTGGCCGTCC TGCATTTCTG GTTTCCAGAC CCCAATGCCT CCCATTCGGA 3060
TGGATCTCTG CGTTTTTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTTT TATTTTCCCT 3120
GTTGCGTTGC TATAGATGAA GGGTGAGGAC AATCGTGTAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAAACT TTTCCCAGAA AAAAA

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_001784.2

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QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG  120
KGPFPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLLN KPLDREEIAK  180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT  240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIQA  300
TDMDGDGSTT TAVAVVEILD ANDNAPMFDP QKYEAHVPEN AVGHEVQRLT VTDLDAPNSP  360
AWRATYLIMG GDDGDHFTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL  420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEPVC VYTAEDPDKE NQKISYRILR  480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMVLA MDNGSPPTTG TGTLLLTLID  540
VNDHGPVPEP RQITICNQSP VRQVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD  600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WKGGFILPVL  660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFY YGEEGGGEED QDYDITQLHR  720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APPYDTLLVF  780
DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGGEDD
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Seq ID NO: 15 DNA sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 261-4346

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          |        |        |        |        |        |
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CGGCGCGGGG AGCCAGCGGG GCTGAGCGCG GCCAGGGTCT GAACCCAGAT TTCCCAGACT  120
AGCTACCACT CCGCTTGCCC ACGCCCCGGG AGCTCGCGGC GCCTGGCGGT CAGCGACCAG  180
ACGTCCGGGG CCGCTGCGCT CCTGGCCCGC GAGGCGTGAC ACTGTCTCGG CTACAGACCC  240
AGAGGGAGCA CACTGCCAGG ATGGGAGCTG CTGGGAGGCA GGACTTCCTC TTCAAGGCCA  300
TGCTGACCAT CAGCTGGCTC ACTCTGACCT GCTTCCCTGG GGCCACATCC ACAGTGGCTG  360
CTGGGTGCCC TGACCAGAGC CCTGAGTTGC AACCCTGGAA CCCTGGCCAT GACCAAGACC  420
ACCATGTGCA TATCGGCCAG GGCAAGACAC TGCTGCTCAC CTCTTCTGCC ACGGTCTATT  480
CCATCCACAT CTCAGAGGGA GGCAAGCTGG TCATTAAAGA CCACGACGAG CCGATTGTTT  540
TGCGAACCCG GCACATCCTG ATTGACAACG GAGGAGAGCT GCATGCTGGG AGTGCCCTCT  600
GCCCTTTCCA GGGCAATTTC ACCATCATTT TGTATGGAAG GGCTGATGAA GGTATTCAGC  660
CGGATCCTTA CTATGGTCTG AAGTACATTG GGGTTGGTAA AGGAGGCGCT CTTGAGTTGC  720
ATGGACAGAA AAAGCTCTCC TGGACATTTC TGAACAAGAC CCTTCACCCA GGTGGCATGG  780
CAGAAGGAGG CTATTTTTTT GAAAGGAGCT GGGGCCACCG TGGAGTTATT GTTCATGTCA  840
TCGACCCCAA ATCAGGCACA GTCATCCATT CTGACCGGTT TGACACCTAT AGATCCAAGA  900
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TTGCAGTGAA TGATGAAGGT TCTCGAAATC TGGATGACAT GGCCAGGAAG GCGATGACCA 1020
AATTGGGAAG CAAACACTTC CTGCACCTTG GATTTAGACA CCCTTGGAGT TTTCTAACTG 1080
TGAAAGGAAA TCCATCATCT TCAGTGGAAG ACCATATTGA ATATCATGGA CATCGAGGCT 1140
CTGCTGCTGC CCGGGTATTC AAATTGTTCC AGACAGAGCA TGGCGAATAT TTCAATGTTT 1200
CTTTGTCCAG TGAGTGGGTT CAAGACGTGG AGTGGACGGA GTGGTTCGAT CATGATAAAG 1260
TATCTCAGAC TAAAGGTGGG GAGAAAATTT CAGACCTCTG GAAAGCTCAC CCAGGAAAAA 1320
TATGCAATCG TCCCATTGAT ATACAGGCCA CTACAATGGA TGGAGTTAAC CTCAGCACCG 1380
AGGTTGTCTA CAAAAAAGGC CAGGATTATA GGTTTGCTTG CTACGACCGG GGCAGAGCCT 1440
GCCGGAGCTA CCGTGTACGG TTCCTCTGTG GGAAGCCTGT GAGGCCCAAA CTCACAGTCA 1500
CCATTGACAC CAATGTGAAC AGCACCATTC TGAACTTGGA GGATAATGTA CAGTCATGGA 1560
AACCTGGAGA TACCCTGGTC ATTGCCAGTA CTGATTACTC CATGTACCAG GCAGAAGAGT 1620
TCCAGGTGCT TCCCTGCAGA TCCTGCGCCC CCAACCAGGT CAAAGTGGCA GGGAAACCAA 1680
TGTACCTGCA CATCGGGGAG GAGATAGACG GCGTGGACAT GCGGGCGGAG GTTGGGCTTC 1740
TGAGCCGGAA CATCATAGTG ATGGGGGAGA TGGAGGACAA ATGCTACCCC TACAGAAACC 1800
ACATCTGCAA TTTCTTTGAC TTCGATACCT TTGGGGGCCA CATCAAGTTT GCTCTGGGAT 1860
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TTAAGGCAGC ACACTTGGAG GGCACGGAGC TGAAGCATAT GGGACAGCAG CTGGTGGGTC 1920
AGTACCCGAT TCACTTCCAC CTGGCCGGTG ATGTAGACGA AAGGGGAGGT TATGACCCAC 1980
CCACATACAT CAGGGACCTC TCCATCCATC ATACATTCTC TCGCTGCGTC ACAGTCCATG 2040
GCTCCAATGG CTTGTTGATC AAGGACGTTG TGGGCTATAA CTCTTTGGGC CACTGCTTCT 2100
TCACGGAAGA TGGGCCGGAG GAACGCAACA CTTTTGACCA CTGTCTTGGC CTCCTTGTCA 2160
AGTCTGGAAC CCTCCTCCCC TCGGACCGTG ACAGCAAGAT GTGCAAGATG ATCACAGAGG 2220
ACTCCTACCC GGGGTACATC CCCAAGCCCA GGCAAGACTG CAATGCTGTG TCCACCTTCT 2280
GGATGGCCAA TCCCAACAAC AACCTCATCA ACTGTGCCGC TGCAGGATCT GAGGAAACTG 2340
GATTTTGGTT TATTTTTCAC CACGTACCAA CGGGCCCCTC CGTGGGAATG TACTCCCCAG 2400
GTTATTCAGA GCACATTCCA CTGGGAAAAT TCTATAACAA CCGAGCACAT TCCAACTACC 2460
GGGCTGGCAT GATCATAGAC AACGGAGTCA AAACCACCGA GGCCTCTGCC AAGGACAAGC 2520
GGCCGTTCCT CTCAATCATC TCTGCCAGAT ACAGCCCTCA CCAGGACGCC GACCCGCTGA 2580
AGCCCCGGGA GCCGGCCATC ATCAGACACT TCATTGCCTA CAAGAACCAG GACCACGGGG 2640
CCTGGCTGCG CGGCGGGGAT GTGTGGCTGG ACAGCTGCCG GTTTGCTGAC AATGGCATTG 2700
GCCTGACCCT GGCCAGTGGT GGAACCTTCC CGTATGACGA CGGCTCCAAG CAAGAGATAA 2760
AGAACAGCTT GTTTGTTGGC GAGAGTGGCA ACGTGGGGAC GGAAATGATG GACAATAGGA 2820
TCTGGGGCCC TGGCGGCTTG GACCATAGCG GAAGGACCCT CCCTATAGGC CAGAATTTTC 2880
CAATTAGAGG AATTCAGTTA TATGATGGCC CCATCAACAT CCAAAACTGC ACTTTCCGAA 2940
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GGCAGAGCTG CCCCCATAAC AACGTGACCG GCATTGCCTT TGAGGACGTT CCGATTACTT 3060
CCAGAGTGTT CTTCGGAGAG CCTGGGCCCT GGTTCAACCA GCTGGACATG GATGGGGATA 3120
AGACATCTGT GTTCCATGAC GTCGACGGCT CCGTGTCCGA GTACCCTGGC TCCTACCTCA 3180
CGAAGAATGA CAACTGGCTG GTCCGGCACC CAGACTGCAT CAATGTTCCC GACTGGAGAG 3240
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TGCGAATGAA GATCATCAAG AATGACTTCC CCAGCCACCC TCTTTACCTG GAGGGGCGC 3360
TCACCAGGAG CACCCATTAC CAGCAATACC AACCGGTTGT CACCCTGCAG AAGGGCTACA 3420
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AGGGCGACTG GATCCGAGTG GGGCTCTGCT ACCCGCGAGG CACCACATTC TCCATCCTCT 3540
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ACTCAGGGCT GTTGTTCCTG AAGCTGAAAG CTCAGAACGA GAGAGAGAAG TTTGCTTTCT 3720
GCTCCATGAA AGGCTGTGAG AGGATAAAGA TTAAAGCTCT GATTCCAAAG AACGCAGGCG 3780
TCAGTGACTG CACAGCCACA GCTTACCCCA AGTTCACCGA GAGGGCTGTC GTAGACGTGC 3840
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TGGATGGGAA GAAGTACCCC AGTTCGGAGG ATGGCATCCA GGTGGTGGTG ATTGACGGGA 4020
ACCAAGGGCG CGTGGTGAGC CACACGAGCT TCAGGAACTC CATTCTGCAA GGCATACCAT 4080
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GGGGTCTCAA GTTGAAAGAG CAAATGGCAT TCGTTGGCTT CAAAGGCAGC TTCCGGCCCA 4260
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CAGCAGCTGC CTGGGAAGGC CGTGTTTCAG CCCTGATGGG CCAAGGGAAG GCTATCAGAG 4500
ACCCTGGTGC TGCCACCTGC CCCTACTCAA GTGTCTACCT GGAGCCCCTG GGGCGGTGCT 4560
GGCCAATGCT GGAAACATTC ACTTTCCTGC AGCCTCTTGG GTGCTTCTCT CCTATCTGTG 4620
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GAGGGCCTGG GGAGCCCCAC CCTAGCCCTT GCTGCCACAC CACATTGCCT CAACAACCGG 5760
CCCCAGAGTG CCCAGGCACT CCTGAGGTAG CTTCTGGAAA TGGGGACAAG TCCCCTCGAA 5820
GGAAAGGAAA TGACTAGAGT AGAATGACAG CTAGCAGATC TCTTCCCTCC TGCTCCCAGC 5880
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ACCTGTCAGC CCAGCCTGGG TGCACAGTAG CTGCAACTCC CCATTGGTGC TACCTGGCTC 6000
TCCTGTCTCT GCAGCTCTAC AGGTGAGGCC CAGCAGAGGG AGTAGGGCTC GCCATGTTTC 6060
TGGTGAGCCA ATTTGGCTGA TCTTGGGTGT CTGAACAGCT ATTGGGTCCA CCCCAGTCCC 6120
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TCCCTGGGTC TTGTGATGAA CTACATTTAT CCCCTTTCCT GCCCCAACCA CAAACTCTTT 6300
CCTTCAAAGA GGGCCTGCCT GGCTCCCTCC ACCCAACTGC ACCCATGAGA CTCGGTCCAA 6360
GAGTCCATTC CCCAGGTGGG AGCCAACTGT CAGGGAGGTC TTTCCCACCA AACATCTTTC 6420
AGCTGCTGGG AGGTGACCAT AGGGCTCTGC TTTTAAAGAT ATGGCTGCTT CAAAGGCCAG 6480
AGTCACAGGA AGGACTTCTT CCAGGGAGAT TAGTGGTGAT GGAGAGGAGA GTTAAAATGA 6540
CCTCATGTCC TTCTTGTCCA CGGTTTTGTT GAGTTTTCAC TCTTCTAATG CAAGGGTCTC 6600
ACACTGTGAA CCACTTAGGA TGTGATCACT TTCAGGTGGC CAGGAATGTT GAATGTCTTT 6660
GGCTCAGTTC ATTTAAAAAA GATATCTATT TGAAAGTTCT CAGAGTTGTA CATATGTTTC 6720
ACAGTACAGG ATCTGTACAT AAAAGTTTCT TTCCTAAACC ATTCACCAAG AGCCAATATC 6780
TAGGCATTTT CTTGGTAGCA CAAATTTTCT TATTGCTTAG AAAATTGTCC TCCTTGTTAT 6840
TTCTGTTTGT AAGACTTAAG TGAGTTAGGT CTTTAAGGAA AGCAACGCTC CTCTGAAATG 6900
CTTGTCTTTT TTCTGTTGCC GAAATAGCTG GTCCTTTTTC GGGAGTTAGA TGTATAGAGT 6960
GTTTGTATGT AAACATTTCT TGTAGGCATC ACCATGAACA AAGATATATT TTCTATTTAT 7020

TTATTATATG TGCACTTCAA GAAGTCACTG TCAGAGAAAT AAAGAATTGT CTTAAATGTC

Seq ID NO: 16 Protein sequence:
Protein Accession #: XP_051860.2

1 11 21 31 41 51
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MGAAGRQDFL FKAMLTISWL TLTCFPGATS TVAAGCPDQS PELQPWNPGH DQDHHVHIGQ 60
GKTLLLTSSA TVYSIHISEG GKLVIKDHDE PIVLRTRHIL IDNGGELHAG SALCPFQGNF 120
TIILYGRADE GIQPDPYYGL KYIGVGKGGA LELHGQKKLS WTFLNKTLHP GGMAEGGYFF 180
ERSWGHRGVI VHVIDPKSGT VIHSDRFDTY RSKKESERLV QYLNAVPDGR ILSVAVNDEG 240
SRNLDDMARK AMTKLGSKHF LHLGFRHPWS FLTVKGNPSS SVEDHIEYHG HRGSAAARVF 300
KLFQTEHGEY FNVSLSSEWV QDVEWTEWFD HDKVSQTKGG EKISDLWKAH PGKICNRPID 360
IQATTMDGVN LSTEVVYKKG QDYRFACYDR GRACRSYRVR FLCGKPVRPK LTVTIDTNVN 420
STILNLEDNV QSWKPGDTLV IASTDYSMYQ AEEFQVLPCR SCAPNQVKVA GKPMYLHIGE 480
EIDGVDMRAE VGLLSRNIIV MGEMEDKCYP YRNHICNFFD FDTFGGHIKF ALGFKAAHLE 540
GTELKHMGQQ LVGQYPIHFH LAGDVDERGG YDPPTYIRDL SIHHTFSRCV TVHGSNGLLI 600
KDVVGYNSLG HCFFTEDGPE ERNTFDHCLG LLVKSGTLLP SDRDSKMCKM ITEDSYPGYI 660
PKPRQDCNAV STFWMANPNN NLINCAAAGS EETGFWFIFH HVPTGPSVGM YSPGYSEHIP 720
LGKFYNNRAH SNYRAGMIID NGVKTTEASA KDKRPFLSII SARYSPHQDA DPLKPREPAI 780
IRHFIAYKNQ DHGAWLRGGD VWLDSCRFAD NGIGLTLASG GTFPYDDGSK QEIKNSLFVG 840
ESGNVGTEMM DNRIWGPGGL DHSGRTLPIG QNFPIRGIQL YDGPINIQNC TFRKFVALEG 900
RHTSALAFRL NNAWQSCPHN NVTGIAFEDV PITSRVFFGE PGPWFNQLDM DGDKTSVFHD 960
VDGSVSEYPG SYLTKNDNWL VRHPDCINVP DWRGAICSGC YAQMYIQAYK TSNLRMKIIK 1020
NDFPSHPLYL EGALTRSTHY QQYQPVVTLQ KGYTIHWDQT APAELAIWLI NFNKGDWIRV 1080
GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDSGLLFL 1140
KLKAQNEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKFTERAV VDVPMPKKLF 1200
GSQLKTKDHF LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS 1260
HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE 1320
QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L

Seq ID NO: 17 DNA sequence
Nucleic Acid Accession #: NM_015515.1
Coding sequence: 61-1329

1 11 21 31 41 51
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ATGAACTCCG GACACAGCTT CAGCCAGACC CCCTCGGCCT CCTTCCATGG CGCCGGAGGT 120
GGCTGGGGCC GGCCCAGGAG CTTCCCCAGG GCTCCCACCG TCCATGGCGG TGCGGGGGGA 180
GCCCGCATCT CCCTGTCCTT CACCACGCGG AGCTGCCCAC CCCCTGGAGG GTCTTGGGGT 240
TCTGGAAGAA GCAGCCCCCT ACTAGGCGGA AATGGGAAGG CCACCATGCA GAATCTCAAC 300
GACCGCCTGG CCTCCTACCT GGAGAAGGTT CGCGCCCTGG AGGAGGCCAA CATGAAGCTG 360
GAAAGCCGCA TCCTGAAATG GCACCAGCAG AGAGATCCTG GCAGTAAGAA AGATTATTCC 420
CAGTATGAGG AAAACATCAC ACACCTGCAG GAGCAGATAG TGGATGGTAA GATGACCAAT 480
GCTCAGATTA TTCTTCTCAT TGACAATGCC AGGATGGCAG TGGATGACTT CAACCTCAAG 540
TATGAAAATG AACACTCCTT TAAGAAAGAC TTGGAAATTG AAGTCGAGGG CCTCCGAAGG 600
ACCTTAGACA ACCTGACCAT TGTCACAACA GACCTAGAAC AGGAGGTGGA AGGAATGAGG 660
AAAGAGCTCA TTCTCATGAA GGAGCACCAT GAGCAGGAAA TGGAGGAGCA TCATGTGCCA 720
AGTGACTTCA ATGTCAATGT GAAGGTGGAT ACAGGTCCCA GGGAAGATCT GATTAAGGTC 780
CTGGAGGATA TGAGACAAGA ATATGAGCTT ATAATAAAGA AGAAGCATCG AGACTTGGAC 840
ACTTGGTATA AAGAACAGTC TGCAGCCATG TCCCAGGAGG CAGCCAGTCC AGCCACTGTG 900
CAGAGCAGAC AAGGTGACAT CCACGAACTG AAGCGCACAT TCCAGGCCCT GGAGATTGAC 960
CTGCAGGCAC AGTACAGCAC GAAATCTGCT TTGGAAAACA TGTTATCCGA GACCCAGTCT 1020
CGGTACTCCT GCAAGCTCCA GGACATGCAA GAGATCATCT CCCACTATGA GGAGGAACTG 1080
ACGCAGCTAC GCCACGAACT GGAGCGGCAG AACAATGAAT ACCAAGTGCT GCTGGGCATC 1140
AAAACCCACC TGGAGAAGGA AATCACCACG TACCGACGGC TCCTGGAGGG AGAGAGTGAA 1200
GGGACACGGG AAGAATCAAA GTCGAGCATG AAAGTGTCTG CAACTCCAAA GATCAAGGCC 1260
ATAACCCAGG AGACCATCAA CGGAAGATTA GTTCTTTGTC AAGTGAATGA AATCCAAAAG 1320
CACGCATGAG ACCAATGAAA GTTTCCGCCT GTTGTAAAGT CTATTTTCCC CCAAGGAAAG 1380
TCCTTGCACA GACACCAGTG AGTGAGTTCT AAAAGATACC CTTGGAATTA TCAGACTCAG 1440
AAACTTTTAT TTTTTTTTT CTGTAACAGT CTCACCAGAC TTCTCATAAT GCTCTTAATA 1500
TATTGCACTT TTCTAATCAA AGTGCGAGTT TATGAGGGTA AAGCTCTACT TTCCTACTGC 1560
AGCCTTCAGA TTCTCATCAT TTTGCATCTA TTTTGTAGCC AATAAAACTC CGCACTAGC

Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_056330.1

1 11 21 31 41 51
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MNSGHSFSQT PSASFHGAGG GWGRPRSFPR APTVHGGAGG ARISLSFTTR SCPPPGGSWG 60
SGRSSPLLGG NGKATMQNLN DRLASYLEKV RALEEANMKL ESRILKWHQQ RDPGSKKDYS 120
QYEENITHLQ EQIVDGKMTN AQIILLIDNA RMAVDDFNLK YENEHSFKKD LEIEVEGLRR 180
TLDNLTIVTT DLEQEVEGMR KELILMKEHH EQEMEEHHVP SDFNVNVKVD TGPREDLIKV 240
LEDMRQEYEL IIKKKHRDLD TWYKEQSAAM SQEAASPATV QSRQGDIHEL KRTFQALEID 300
LQAQYSTKSA LENMLSETQS RYSCKLQDMQ EIISHYEEEL TQLRHELERQ NNEYQVLLGI 360
KTHLEKEITT YRRLLEGESE GTREESKSSM KVSATPKIKA ITQETINGRL VLCQVNEIQK 420
HA

Seq ID NO: 19 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | | |

TTTTTTTTTT TTAAAAAAAA GAGGCTTGGT AAGTTTTTGA TACTTAGTTG ACTTTTAGCA 60
TTATCCAGCA TTTGTATTAT GAACCAGTGA GTACTGTAAT TTTTCTTTCC CTTTCAGAAA 120
GACTCAAAGG GAACATATAA ATGTTTCCTA TTTTTNNNNN NNNNNNNNNN NNNNNNNNNN 180
NNNNACCCAT CGTGCGATGA TCNNNNNNNN NNNNNNNNNN NNNNNTTGGG ATCCAGTTTC 240
AAATAAGGTA TGGGAAAAAC AGATGTTTTC ATTATCGCCA CTTAATCCTT ACTTCCGATT 300
ATAATTATAC ATGTTTGGCT GTAATAACTA TACTAAAGCA TGCTTGTGAA AGTAGACTTC 360
TACAAGGACA GAAAACCCAC AACAACAAAG ATCGATCACG AAAGACAAGG CATATTCATT 420
CATTAATTTA CTTCTCTTAG ACCCGGGACA TGTGGGACAA ATACTTTTGT CCTCATGGAT 480
GGCTTGATAA TTTATTTATA TGTTCTAGAG TCTGAGGATT TTCTTTCAGT GGCAGACAAC 540
AAAGGATGTT ACAATTTACT TCAAAATAAT ACAATCATGG TTTAATTTAC AGTGTAAATC 600
CATAACTATT TTATAGAGAT GGATTATCAT ACATGGGATT ATAAAAATAA CTTACCCATA 660
TGCTTGCAAA ATAGACTTTT CCTATTGGGA GGAACATCTT TTAACCTAAA ACGGATTTAT 720
TTCAGATGAA TTAGACAGTA CATTTTTCAG GAGAACCAGC CTTACTGGAT GATCTTTTGT 780
CAGGTTTGGA GGCCTCTTCT TTGTCTTTGC AACCATAACC CCTTTTCAGC TGAAGACCAC 840
TGGCCTTCAA CCCAAGCCAG GAGTTTGGCT CAAATGA

Seq ID NO: 20 DNA sequence
Nucleic Acid Accession #: D32051.1
Coding sequence: 72-1373

1 11 21 31 41 51
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TGGCCTGGAA ACTTGCACAG TCTCATCATG TCAAACAAGT GTTGGTTGCC CCAGGAAACG 180
CAGGCACTGC CTGCTCTGAA AAGATTTCAA ATACCGCCAT CTCAATCAGT GACCACACTG 240
CCCTTGCTCA ATTCTGCAAA GAGAAGAAAA TTGAATTTGT AGTTGTTGGA CCAGAAGCAC 300
CTCTGGCTGC TGGGATTGTT GGGAACCTGA GGTCTGCAGG AGTGCAATGC TTTGGCCCAA 360
CAGCAGAAGC GGCTCAGTTA GAGTCCAGCA AAAGGTTTGC CAAAGAGTTT ATGGACAGAC 420
ATGGAATCCC AACCGCACAA TGGAAGGCTT TCACCAAACC TGAAGAAGCC TGCAGCTTCA 480
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GGGTGATTGT TGCAAAGAGC AAAGAAGAGG CCTGCAAAGC TGTACAAGAG ATCATGCAGG 600
AGAAAGCCTT TGGGGCAGCT GGAGAAACAA TTGTCATTGA AGAACTTCTT GACGGAGAAG 660
AGGTGTCGTG TCTGTGTTTC ACTGATGGCA AGACTGTGGC CCCCATGCCC CCAGCACAGG 720
ACCATAAGCG ATTACTGGAG GGAGATGGTG GCCCTAACAC AGGGGGAATG GGAGCCTATT 780
GTCCAGCCCC TCAGGTTTCT AATGATCTAT TACTAAAAAT TAAAGATACT GTTCTTCAGA 840
GGACAGTGGA TGGCATGCAG CAAGAGGGTA CTCCATATAC AGGTATTCTC TATGCTGGAA 900
TAATGCTGAC CAAGAATGGC CCAAAAGTTC TAGAGTTTAA TTGCCGTTTT GGTGATCCAG 960
AGTGCCAAGT AATCCTCCCA CTTCTTAAAA GTGATCTTTA TGAAGTGATT CAGTCCACCT 1020
TAGATGGACT GCTCTGCACA TCTCTGCCTG TTTGGCTAGA AAACCACACC GCCCTAACTG 1080
TTGTCATGGC AAGTAAAGGT TATCCTGGAG ACTACACCAA GGGTGTAGAG ATAACAGGGT 1140
TTCCTGAGGC TCAAGCTCTA GGACTGGAGG TGTCCCATGC AGGCACTGCC CTCAAAAATG 1200
GCAAAGTAGT AACTCATGGG GGTAGAGTTC TTGCAGTCAC AGCCATCCGG GAAAATCTCA 1260
TATCAGCCCT TGAGGAAGCC AAGAAAGGAC TAGCTGCTAT AAAGTTTGAG GGAGCAATTT 1320
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TTAACCCTAT AAGTCATTCA GTATTCTTTT CTCTCTGTGG GAGTGATACA GTCTTGGTTT 1500
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TGCCTCAGCC TCCCAAATAG CTGGGACTAC AGGCACAGGC CACCACACCT GGCTAATTTT 1740
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CTCAAGTGAT CCTCCTGCTT TGGCCTCCCA AAATGCTGGG ACTATAGGCA TGAGGCGCTG 1860
CACTTGGCCT GATACTGATT TTTATTCCTT GCGTTATCAC ATAGTGTTGT ATTTGAAACA 1920
TAGTTCATGG TTTTATCAAA GAACTGAAGA TGAGAATACT GGTCATCTAA CTTTGTAATT 1980
TGATTTGATT ATACTGTAAA GTTTGACAGT CCCATTTTAA CCTGCGTTTG TATCTATTAC 2040
TAAAATGTAT TTTTTGACCT CTTACTGATT CATGGTTGGT ATGTACAAAC TGTTGACTTG 2100
TAAAATCAAT AAAGTCTTAG TTGG

Seq ID NO: 21 Protein sequence:
Protein Accession #: BAA06809.1

1 11 21 31 41 51
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MAARVLIIGS GGREHTLAWK LAQSHHVKQV LVAPGNAGTA CSEKISNTAI SISDHTALAQ 60
FCKEKKIEFV VVGPEAPLAA GIVGNLRSAG VQCFGPTAEA AQLESSKRFA KEFMDRHGIP 120
TAQWKAFTKP EEACSFILSA DFPALVVKAS GLAAGKGVIV AKSKEEACKA VQEIMQEKAF 180
GAAGETIVIE ELLDGEEVSC LCFTDGKTVA PMPPAQDHKR LLEGDGGPNT GGMGAYCPAP 240
QVSNDLLLKI KDTVLQRTVD GMQQEGTPYT GILYAGIMLT KNGPKVLEFN CRFGDPECQV 300
ILPLLKSDLY EVIQSTLDGL LCTSLPVWLE NHTALTVVMA SKGYPGDYTK GVEITGFPEA 360
QALGLEVSHA GTALKNGKVV THGGRVLAVT AIRENLISAL EEAKKGLAAI KFEGAIYRKD 420
IGFRAIAFLQ QPR

Seq ID NO: 22 DNA sequence
Nucleic Acid Accession #: EOS cloned
Coding sequence: 1-2424

1 11 21 31 41 51
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ATGCCCCCTT TCCTGTTGCT GGAGGCCGTC TGTGTTTTCC TGTTTTCCAG AGTGCCCCCA 60
TCTCTCCCTC TCCAGGAAGT CCATGTAAGC AAAGAAACCA TCGGGAAGAT TTCAGCTGCC 120
AGCAAAATGA TGTGGTGCTC GGCTGCAGTG GACATCATGT TTCTGTTAGA TGGGTCTAAC 180

AGCGTCGGGA AAGGGAGCTT TGAAAGGTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
CTGGACATCA GCCCCGAGAG GGTCAGAGTG GGAGCATTCC AGTTCAGTTC CACTCCTCAT 300
CTGGAATTCC CCTTGGATTC ATTTTCAACC CAACAGGAAG TGAAGGCAAG AATCAAGAGG 360
ATGGTTTTCA AAGGAGGGCG CACGGAGACG GAACTTGCTC TGAAATACCT TCTGCACAGA 420
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AAGTCCCAGG GGGATGTGGC ACTGCCATCC AAGCAGCTGA AGGAAAGGGG TGTCACTGTG 540
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AGAGGGCAGC ACGTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CCTCTTCAGC 660
ACCCTCAGCA GCTCGGCCAT CTGCTCCAGC GCCACGCCAG ACTGCAGGGT CGAGGCTCAC 720
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AGAGGATCGC GGCGGACCCT TGCGGTGCTG GCTGCACACT GTCCCTTCTA CAGCTGGAAG 840
AGAGTGTTCC TAACCCACCC TGCCACCTGC TACAGGACCA CCTGCCCAGG CCCCTGTGAC 900
TCGCAGCCCT GCCAGAATGG AGGCACATGT GTTCCAGAAG GACTGGACGG CTACCAGTGC 960
CTCTGCCCGC TGGCCTTTGG AGGGGAGGCT AACTGTGCCC TGAAGCTGAG CCTGGAATGC 1020
AGGGTCGACC TCCTCTTCCT GCTGGACAGC TCTGCGGGCA CCACTCTGGA CGGCTTCCTG 1080
CGGGCCAAAG TCTTCGTGAA GCGGTTTGTG CGGGCCGTGC TGAGCGAGGA CTCTCGGGCC 1140
CGAGTGGGTG TGGCCACATA CAGCAGGGAG CTGCTGGTGG CGGTGCCTGT GGGGGAGTAC 1200
CAGGATGTGC CTGACCTGGT CTGGAGCCTC GATGGCATTC CCTTCCGTGG TGGCCCCACC 1260
CTGACGGGCA GTGCCTTGCG GCAGGCGGCA GAGCGTGGCT TCGGGAGCGC CACCAGGACA 1320
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GAGGCCGTGC GGGCAGAGCT GGAGGAGATC ACAGGCAGCC CAAAGCATGT GATGGTCTAC 1500
TCGGATCCTC AGGATCTGTT CAACCAAATC CCTGAGCTGC AGGGGAAGCT GTGCAGCCGG 1560
CAGCGGCCAG GGTGCCGGAC ACAAGCCCTG GACCTCGTCT TCATGTTGGA CACCTCTGCC 1620
TCAGTAGGGC CCGAGAATTT TGCTCAGATG CAGAGCTTTG TGAGAAGCTG TGCCCTCCAG 1680
TTTGAGGTGA ACCCTGACGT GACACAGGTC GGCCTGGTGG TGTATGGCAG CCAGGTGCAG 1740
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GCCCCCTACC TAGGTGGGGT GGGCTCAGCC GGCACCGCCC TGCTGCACAT CTATGACAAA 1860
GTGATGACCG TCCAGAGGGG TGCCCGGCCT GGTGTCCCCA AAGCTGTGGT GGTGCTCACA 1920
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TCTGTCTTGG TCGTGGGCGT GGGGCCTGTC CTAAGTGAGG GTCTGCGGAG GCTTGCAGGT 2040
CCCCGGGATT CCCTGATCCA CGTGGCAGCT TACGCCGACC TGCGGTACCA CCAGGACGTG 2100
CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCG 2160
TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT 2220
GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280
CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340
CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400
AATGTCTGTG CCCCAGGTCC TTAG

Seq ID NO: 23 Protein sequence:
Protein Accession #: EOS cloned

```
1      11     21     31     41     51
|      |      |      |      |      |
MPPFLLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN   60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR  120
MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIVTDG KSQGDVALPS KQLKERGVTV  180
FAVGVRFPRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH  240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCPGPCD  300
SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLLDS SAGTTLDGFL  360
RAKVFVKRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT  420
LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLTESHSEDE VAGPARHARA RELLLLGVGS  480
EAVRAELEEI TGSPKHVMVY SDPQDLFNQI PELQGKLCSR QRPGCRTQAL DLVFMLDTSA  540
SVGPENFAQM QSFVRSCALQ FEVNPDVTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ  600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPKAVVVLT GGRGAEDAAV PAQKLRNNGI  660
SVLVVGVGPV LSEGLRRLAG PRDSLIHVAA YADLRYHQDV LIEWLCGEAK QPVNLCKPSP  720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS  780
RTPPSNYREG LGTEMVPTFW NVCAPGP
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Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

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1      11     21     31     41     51
|      |      |      |      |      |
AGGTCGGCTG GTTATCGGGA GTTGGAGGGC TGAGGTCGGG AGGGTGGTGT GTACAGAGCT   60
CTAGGACTCA CGCACCAGGC CAGTCGCGGG TTTTGGGCCG AGGCCTGGGT TACAAGCAGC  120
AAGTGCGCGG TTGGGGCCAC TGCGAGGCCG TTTTAGAAAA CTGTTTAAAA CAAAGAGCAA  180
TTGATGGATA AATCAGGAAT AGATTCTCTT GACCATGTGA CATCTGATGC TGTGGAACTT  240
GCAAATCGAA GTGATAACTC TTCTGATAGC AGCTTATTTA AAACTCAGTG TATCCCTTAC  300
TCACCTAAAG GGGAGAAAAG AAACCCCATT CGAAAATTTG TTCGTACACC TGAAAGTGTT  360
CACGCAAGTA TTCATCAAGT GACTCATCTT TTGAACCAGT ACCATTGACT ATAAAAGCTA  420
TTTTTGAAAG ATTCAAGAAC AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGAGGTACC  480
AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTCACTAA  540
TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTTA GAATCAGAGA  600
ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT  660
TTTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCT GAAAGAATCA TTGAAGCAAA  720
TGAATGTTGG TGAAGATTTA GAAAATGAAG ATTTTGACAG TCGTAGATAC AAATTTTTGG  780
ATGATGATGG ATCCATTTCT CCTATTGAGG AGTCAACGCT TTTATCTTGA GGACATGGTG  840
TCTGGAGTTA AAGGTATTGG CATACTCCAC ACATCTGTAC CATTCTTGAG TGATCGCTTA  900
GGAATGAATG TGATTTGGAC TCATTCATGT ATGAGAGTAA GCAATGCTTT TTTTTCCAGG  960
GTGTCAAATT GAGAACCAGG TAGATCCCCA CCACCTACAG TAAAAAGGAC CCTAAAGTAA 1020
ATTGGTTGAA GAAATTAGAT CCCAAAGATT CTTGGTGAAT TTTGAAGTCT TCATCAGTAT 1080
ATCCATATTA AAACGAGATG ACAGAAGCCA AAGTAATTAT GGGCTGACAG GACAACTGGA 1140
TCAGTTTCAT TAAAAAGGGC AAACTTGAAG ATAAATCTTT TGACTCCAGC TCTTTAGAGG 1200
ATCTAAAGTG ACCTTGATGG ACAGTGGAAG AAATCACAAC ATGGAATTCC TCGAATAACA 1260
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ATTTATTGAC TTTAAATAAT TTTGTCTAAT GCTACATATA CACAATTAAA AAACCTTTAC 1320
ACTATTTCTA GAAAGTCAGC ATGTATTTTT GGCTCGAAGT TTCTCTAGTG TTTTCTGTGG 1380
AAGGAATAAA AATTTGAGGT TTCAATACAA AAACAAAACA AACAACACGA AACACGAAAA 1440
ACAATCTGTT GTGCGGCGCC CCTGGGCCCC TTGAGAGAAA ACTTTTTAGA ACCCCTTTTG 1500
CGTTGTGGCG GCCCGGGGGC CCCACAGTTG GGTTTAGGTG GGCACCCTTG TGTCTACAAG 1560
TGGTGTCTCC CCAAGAGAGA GAACACCTCC GGGGTCAAGC GGACAACAAG AGTGCGTCGT 1620
GAGGACTCTT CACCCAAAGT ATATAAAACC CGCCCCGCGG GGGAACCACC GGCCGCTTTT 1680
CTGTAGACAC AACCCCCACA GTGGGAACCT CTGAGGGCGC ACACACAGGG CGAGCCTTAT 1740
CAACAAGGGG TGCCCAACAG AAACCCCGAG TTAAAAATCG

Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: BC001972.1
Coding sequence: 183-1019

1 11 21 31 41 51
GGTCGGCTGG TTATCGGGAG TTGGAGGGCT GAGGTCGGGA GGGTGGTGTG TACAGAGCTC 60
TAGGACTCAC GCACCAGGCC AGTCGCGGGT TTTGGGCCGA GGCCTGGGTT ACAAGCAGCA 120
AGTGCGCGGT TGGGGCCACT GCGAGGCCGT TTTAGAAAAC TGTTTAAAAC AAAGAGCAAT 180
TGATGGATAA ATCAGGAATA GATTCTCTTG ACCATGTGAC ATCTGATGCT GTGGAACTTG 240
CAAATCGAAG TGATAACTCT TCTGATAGCA GCTTATTTAA AACTCAGTGT ATCCCTTACT 300
CACCTAAAGG GGAGAAAAGA AACCCCATTC GAAAATTTGT TCGTACACCT GAAAGTGTTC 360
ACGCAAGTGA TTCATCAAGT GACTCATCTT TTGAACCAAT ACCATTGACT ATAAAAGCTA 420
TTTTTGAAAG ATTCAAGAAC AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGAGGTACC 480
AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTCACTAA 540
TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTTA GAATCAGAGA 600
ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT 660
TTTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCT GAAAGAATCA TTGAAGCAAA 720
TGAATGTTGG TGAAGATTTA GAAAATGAAG ATTTTGACAG TCGTAGATAC AAATTTTTGG 780
ATGATGATGG ATCCATTTCT CCTATTGAGG AGTCAACAGC AGAGGATGAG GATGCAACAC 840
ATCTTGAAGA TAACGAATGT GATATCAAAT TGGCAGGGGA TAGTTTCATA GTAAGTTCTG 900
AATTCCCTGT AAGACTGAGT GTATACTTAG AAGAAGAGGA TATTACTGAA GAAGCTGCTT 960
TGTCTAAAAA GAGAGCTACA AAAGCCAAAA ATACTGGACA GAGAGGCCTG AAAATGTGAC 1020
AGGATCATGA ATGTCAAAGG CTTTTATCTT GAGAACATGG TGTCTGGAGT TAAAGGACTA 1080
TTGTTAGATC TGTGGGAAGG AATTACAAGA CAGTTGCTAA AAGTTTGAAA AAGACGGTTG 1140
CTAAACGTTA TGAAAAACCA GATAATCTAC TTTTTTACCT TAGGTATTGG CATACTCCAC 1200
ACATCTGTAC CATTCTTGAG TGATCGCTTA GGAATGAATG TGATTTGAAC TCATTCATGT 1260
TGAGAGGGTG TCAAATTGAG AACCAGGTAG ATCCCCACCA CCTACAGTAA AAAGGACCCT 1320
AAAGTAAATT GGTTGAAGAA ATTAGATCCC AAAGATTCTT GGTGAATTTT GAAGTCTTCA 1380
TCAGTATATC CATATTAAAA CGAGATGACA GAAGCCAAAG TAATTATGGG CTGACAGGAC 1440
AACTGGATCA GTTTCATTAA AAAGGGCAAA CTTGAAGATA AATCTTTTGA CTCCAGCTCT 1500
TTAGAGGATC TAAAGTGACC TTGATGGACA GTGGAAGAAA TCACAACATG GAATTCCTCG 1560
AATAACAATT TATTGACTTT AAATAATTTT GTCTAATGCT ACATATACAC AATTAAAAAA 1620
CCTTTACACT AAAAAAAAAA AAAAAA

Seq ID NO: 26 Protein sequence:
Protein Accession #: AAH01972.1

1 11 21 31 41 51
MDKSGIDSLD HVTSDAVELA NRSDNSSDSS LFKTQCIPYS PKGEKRNPIR KFVRTPESVH 60
ASDSSSDSSF EPIPLTIKAI FERFKNRKKR YKKKKKRRYQ PTGRPRGRPE GRRNPIYSLI 120
DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF FNYIEKLKYE HHLKESLKQM 180
NVGEDLENED FDSRRYKFLD DDGSISPIEE STAEDEDATH LEDNECDIKL AGDSFIVSSE 240
FPVRLSVYLE EEDITEEAAL SKKRATKAKN TGQRGLKM

Seq ID NO: 27 DNA sequence
Nucleic Acid Accession #: AK027016
Coding sequence: 207-1043

1 11 21 31 41 51
CTTTTCTTCC GCACGGTTGG AGGAGGTCGG CTGGTTATCG GGAGTTGGAG GGCTGAGGTC 60
GGGAGGGTGG TGTGTACAGA GCTCTAGGAC TCACGCACCA GGCCAGTCGC GGATTTTGGG 120
CCGAGGCCTG GGTTACAAGC AGCAAGTGCG CGGTTGGGGC CACTGCGAGG CCGTTTTAGA 180
AAACTGTTTA AAACAAAGAG CAATTGATGG ATAAATCAGG AATAGATTCT CTTGACCATG 240
TGACATCTGA TGCTGTGGAA CTTGCAAATC GAAGTGATAA CTCTTCTGAT AGCAGCTTAT 300
TTAAAACTCA GTGTATCCCT TACTCACCTA AAGGGGAGAA AAGAAACCCC ATTCGAAAAT 360
TTGTTCGTAC ACCTGAAAGT GTTCACGCAA GTGATTCATC AAGTGACTCA TCTTTTGAAC 420
CAATACCATT GACTATAAAA GCTATTTTTG AAAGATTCAA GAACAGGAAA AAGAGATATA 480
AAAAAAAGAA AAAGAGGAGG TACCAGCCAA CAGGAAGACC ACGGGGAAGA CCAGAAGGAA 540
GGAGAAATCC TATATACTCA CTAATAGATA AGAAGAAACA ATTTAGAAGC AGAGGATCTG 600
GCTTCCCATT TTTAGAATCA GAGAATGAAA AAAACGCACC TTGGAGAAAA ATTTTAACGT 660
TTGAGCAAGC TGTTGCAAGA GGATTTTTTA ACTATATTGA AAAGCTGAAG TATGAACACC 720
ACCTGAAAGA ATCATTGAAG CAAATGAATG TTGGTGAAGA TTTAGAAAAT GAAGATTTTG 780
ACAGTCGTAG ATACAAATTT TTGGATGATG ATGGATCCAT TTCTCCTATT GAGGAGTCAA 840
CAGCAGAGGA TGAGGATGCA ACACATCTTG AAGATAACGA ATGTGATATC AAATTGGCAG 900
GGGATAGTTT CATAGTAAGT TCTGAATTCC CTGTAAGACT GAGTGTATAC TTAGAAGAAG 960
AGGATATTAC TGAAGAAGCT GCTTTGTCTA AAAAGAGAGC TACAAAAGCC AAAAATACTG 1020
GACAGAGAGG CCTGAAAATG TGACAGGATC ATGAATGTCA AAGGCTTTTA TCTTGAGAAC 1080
ATGGTGTCTG GAGTTAAAGG TATTGGCATA CTCCACACAT CTGTACCATT CTTGAGTGAT 1140
CGCTTAGGAA TGAATGTGAT TTGAACTCAT TCATGTTGAG AGGGTGTCAA ATTGAGAACC 1200
AGGTAGATCC CCACCACCTA CAGTAAAAAG GACCCTAAAG TAAATTGGTT GAAGAAATTA 1260
GATCCCAAAG ATTCTTGGTG AATTTTGAAG TCTTCATCAG TATATCCATA TTAAAACGAG 1320

ATGACAGAAG CCAAAGTAAT TATGGCAAGT AATGGTTTTT ATCTTAACTA TAAGTTATTT 1380
GCTCAAGGGT GTAATGGTCA TTACCAAGGC TTTTAGAATG CAGTTTCTCA TTTGCTGTGG 1440
ACATGACCAT AAAAAAAAAT TTCCCAGTAG GTTTTCTATC TGCTACGTTG CTAGCAATCA 1500
GCTTATTGGG AACAGTTGAT TAACTGTAAT AGAAATGCAA TACAAATAAA ATGTGAACCA 1560
CATGTGATTT TTCTTTAAAA TCAGTGAGAT TTGAAAATTC TCCTAGATCT CTTGAATCAT 1620
GCAAATTTGC TTTGCCTTTA TATTGTAACC CTTGTGGGTT GCTAATAACC AAGCAGTTTG 1680
TAGTAGAGTT AACTCAGGCT CGTTCTAGGG ACTCATTCAT GTTCACTCAC TGTACACTCA 1740
TCTCTGGAAA TGTAAAATTT ACTTTTATAC TATTGTTATG TAGGGCTGAC AGGACAACTG 1800
GATCAGTTTC ATTAAAAAGG TATGTATGCA TTAGAAAAGA CATTTGTATG GGTCATTTCA 1860
AAGAGGGCTT ATGAGGCTGT GAAACCCAGA GCTCTTAACG CTGTGACCAA AGATGGAAGT 1920
TCTCTATAGG AAGCCATAGC ACTCCTAATG TTTGGTGCTA TGTTTTCCTG AGGAGATATA 1980
AAACGTAATA ATCCATGATT GTTGCCATGT GAGAGTTTTA AAGGTTAATC AAAATTTCTC 2040
TTCTTCAGGG CAAACTTGAA GATAAATCTT TTGACTCCAG CTCTTTAGAG GATCTAAAGT 2100
GACCTTGATG GACAGTGGAA GAAATCACAA CATGGAATTC CTCGAATAAC AATTTATTGA 2160
CTTTAAATAA TTTTGTCTAA TGCTACATAT ACACAATTAA AAAACCTTTA CACTATTTCT 2220
AGAAAGTCAG CATGTATTTT TGGCTCGAAG TTTCTCTAGT GTTTTCTGTG GAAGGAATAA 2280
AAATTTGAGT TTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

Seq ID NO: 28 Protein sequence:
Protein Accession #: BAB15628.1

1 11 21 31 41 51
| | | | | |
MDKSGIDSLD HVTSDAVELA NRSDNSSDSS LFKTQCIPYS PKGEKRNPIR KFVRTPESVH 60
ASDSSSDSSF EPIPLTIKAI FERFKNRKKR YKKKKKRRYQ PTGRPRGRPE GRRNPIYSLI 120
DKKKQFRSRG SGFPFLESEN EKNAPWRKIL TFEQAVARGF FNYIEKLKYE HHLKESLKQM 180
NVGEDLENED FDSRRYKFLD DDGSISPIEE STAEDEDATH LEDNECDIKL AGDSFIVSSE 240
FPVRLSVYLE EEDITEEAAL SKKRATKAKN TGQRGLKM

Seq ID NO: 29 DNA sequence
Nucleic Acid Accession #: NM_004289.3
Coding sequence: 493-1695

1 11 21 31 41 51
| | | | | |
GCCGCCGCCT CGTCCACCGG AGGAGCCGGC GCCAGCGTGG ACGGCGGCAG CCAGGCTGTG 60
CAGGGGGGCG GCGGGGACCC CCGAGCGGCT CGGAGTGGCC CCTTGGACGC CGGGGAAGAG 120
GAGAAGGCAC CCGCGGAACC GACGGCTCAG GTGCCGGACG CTGGCGGATG TGCGAGCGAG 180
GAGAATGGGG TACTAAGAGA AAAGCACGAA GCTGTGGATC ATAGTTCCCA GCATGAGGAA 240
AATGAAGAAA GGGTGTCAGC CCAGAAGGAG AACTCACTTC AGCAGAATGA TGATGATGAA 300
AACAAAATAG CAGAGAAACC TGACTGGGAG GCAGAAAAGA CCACTGAATC TAGAAATGAG 360
AGACATCTGA ATGGGACAGA TACTTCTTTC TCTCTGGAAG ACTTATTCCA GTTGCTTTCA 420
TCACAGCCTG AAAATTCACT GGAGGGCATC TCATTGGGAG ATATTCCTCT TCCAGGCAGT 480
ATCAGTGATG GCATGAATTC TTCAGCACAT TATCATGTAA ACTTCAGCCA GGCTATAAGT 540
CAGGATGTGA ATCTTCATGA GGCCATCTTG CTTTGTCCCA ACAATACATT TAGAAGAGAT 600
CCAACAGCAA GGACTTCACA GTCACAAGAA CCATTTCTGC AGTTAAATTC TCATACCACC 660
AATCCTGAGC AAACCCTTCC TGGAACTAAT TTGACAGGAT TTCTTTCACC GGTTGACAAT 720
CATATGAGGA ATCTAACAAG CCAAGACCTA CTGTATGACC TTGACATAAA TATATTTGAT 780
GAGATAAACT TAATGTCATT GGCCACAGAA GACAACTTTG ATCCAATCGA TGTTTCTCAG 840
CTTTTTGATG AACCAGATTC TGATTCTGGC CTTTCTTTAG ATTCAAGTCA CAATAATACC 900
TCTGTCATCA AGTCTAATTC CTCTCACTCT GTGTGTGATG AAGGTGCTAT AGGTTATTGC 960
ACTGACCATG AATCTAGTTC CCATCATGAC TTAGAAGGTG CTGTAGGTGG CTACTACCCA 1020
GAACCCAGTA AGCTTTGTCA CTTGGATCAA AGTGATTCTG ATTTCCATGG AGATCTTACA 1080
TTTCAACACG TATTTCATAA CCACACTTAC CACTTACAGC CAACTGCACC AGAATCTACT 1140
TCTGAACCTT TTCCGTGGCC TGGGAAGTCA CAGAAGATAA GGAGTAGATA CCTTGAAGAC 1200
ACAGATAGAA ACTTGAGCCG TGATGAACAG CGTGCTAAAG CTTTGCATAT CCCTTTTTCT 1260
GTAGATGAAA TTGTCGGCAT GCCTGTTGAT TCTTTCAATA GCATGTTAAG TAGATATTAT 1320
CTGACAGACC TACAAGTCTC ACTTATCCGT GACATCAGAC GAAGAGGGAA AAATAAAGTT 1380
GCTGCGCAGA ACTGTCGTAA ACGCAAATTG GACATAATTT TGAATTTAGA AGATGATGTA 1440
TGTAACTTGC AAGCAAAGAA GGAAACTCTT AAGAGAGAGC AAGCACAATG TAACAAAGCT 1500
ATTAACATAA TGAAACAGAA ACTGCATGAC CTTTATCATG ATATTTTTAG TAGATTAAGA 1560
GATGACCAAG GTAGGCCAGT CAATCCCAAC CACTATGCTC TCCAGTGTAC CCATGATGGA 1620
AGTATCTTGA TAGTACCCAA AGAACTGGTG GCCTCAGGCC ACAAAAAGGA AACCCAAAAG 1680
GGAAAGAGAA AGTGAGAAGA AACTGAAGAT GGACTCTATT ATGTGAAGTA GTAATGTTCA 1740
GAAACTGATT ATTTGGATCA GAAACCATTG AAACTGCTTC AAGAATTGTA TCTTTAAGTA 1800
CTGCTACTTG AATAACTCAG TTAACGCTGT TTTGAAGCTT ACATGGACAA ATGTTTAGGA 1860
CTTCAAGATC ACACTTGTGG GCAATCTGGG GGAGCCACAA CTTTTCATGA AGTGCATTGT 1920
ATACAAAATT CATAGTTATG TCCAAAGAAT AGGTTAACAT GAAAACCCAG TAAGACTTTC 1980
CATCTTGGCA GCCATCCTTT TTAAGAGTAA GTTGGTTACT TCAAAAAGAG CAAACACTGG 2040
GGATCAAATT ATTTTAAGAG GTATTTCAGT TTTAAATGCA AAATAGCCTT ATTTTCATTT 2100
AGTTTGTTAG CACTATAGTG AGCTTTTCAA ACACTATTTT AATCTTTATA TTTAACTTAT 2160
AAATTTTGCT TTCT

Seq ID NO: 30 Protein sequence:
Protein Accession #: NP_004280

1 11 21 31 41 51
| | | | | |
MNSSAHYHVN FSQAISQDVN LHEAILLCPN NTFRRDPTAR TSQSQEPFLQ LNSHTTNPEQ 60
TLPGTNLTGF LSPVDNHMRN LTSQDLLYDL DINIFDEINL MSLATEDNFD PIDVSQLFDE 120
PDSDSGLSLD SSHNNTSVIK SNSSHSVCDE GAIGYCTDHE SSSHHDLEGA VGGYYPEPSK 180
LCHLDQSDSD FHGDLTFQHV FHNHTYHLQP TAPESTSEPF PWPGKSQKIR SRYLEDTDRN 240
LSRDEQRAKA LHIPFSVDEI VGMPVDSFNS MLSRYYLTDL QVSLIRDIRR RGKNKVAAQN 300
CRKRKLDIIL NLEDDVCNLQ AKKETLKREQ AQCNKAINIM KQKLHDLYHD IFSRLRDDQG 360

RPVNPNHYAL QCTHDGSILI VPKELVASGH KKETQKGKRK

Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: NM_033260.1
Coding sequence: 1-1208

1 11 21 31 41 51
| | | | | |
ATGAAGTTGG AGGTGTTCGT CCCTCGCGCG GCCCACGGGG ACAAGCAGGG CAGTGACCTG 60
GAGGGCGCGG GCGGCAGCGA CGCGCCGTCC CCGCTGTCGG CGGCGGGAGA CGACTCCCTG 120
GGCTCAGATG GGGACTGCGC GGCCAAGCCG TCCGCGGGCG GCGGCGCCAG AGATACGCAG 180
GGCGACGGCG AACAGAGTGC GGGAGGCGGG CCGGGCGCGG AGGAGGCGAT CCCGGCAGCA 240
GCTGCTGCAG CGGTGGTGGC GGAGGGCGCG GAGGCCGGGG CGGCGGGGCC AGGCGCGGGC 300
GGCGCGGGGA GCGGCGAGGG TGCACGCAGC AAGCCATATA CGCGGCGGCC CAAGCCCCCC 360
TACTCGTACA TCGCGCTCAT CGCCATGGCC ATCCGCGACT CGGCGGGCGG GCGCTTGACG 420
CTGGCGGAGA TCAACGAGTA CCTCATGGGC AAGTTCCCCT TTTTCCGCGG CAGCTACACG 480
GGCTGGCGCA ACTCCGTGCG CCACAACCTT TCGCTCAACG ACTGCTTCGT CAAGGTGCTG 540
CGCGACCCCT CGCGGCCCTG GGGCAAGGAC AACTACTGGA TGCTCAACCC CAACAGCGAG 600
TACACCTTCG CCGACGGGGT CTTCCGCCGC CGCCGCAAGC GCCTCAGCCA CCGCGCGCCG 660
GTCCCCGCGC CCGGGCTGCG GCCCGAGGAG GCCCCGGGCC TCCCCGCCGC CCCGCCGCCC 720
GCGCCCGCCG CCCCGGCCTC GCCCCGCATG CGCTCGCCCG CCCGCCAGGA GGAGCGCGCC 780
AGCCCCGCGG GCAAGTTCTC CAGCTCCTTC GCCATCGACA GCATCCTGCG CAAGCCCTTC 840
CGCAGCCGTC GCCTCAGGGA CACGGCCCCC GGGACGACGC TTCAGTGGGG CGCCGCGCCC 900
TGCCCGCCGC TGCCCGCGTT CCCCGCGCTC CTCCCCGCGG CGCCCTGCAG GGCCCTGCTG 960
CCGCTCTGCG CGTACGGCGC GGGCGAGCCG GCGCGGCTGG GCGCGCGCGA GGCCGAGGTG 1020
CCACCGACCG CGCCGCCCCT CCTGCTTGCA CCTCTCCCGG CGGCGGCCCC CGCCAAGCCA 1080
CTCCGAGGCC CGGCGGCCGG CGGCGCGCAC CTGTACTGCC CCCTGCGGCT GCCCGCAGCC 1140
CTGCAGGCGG CCTTAGTCCG NCGTCCTGGC CCGCACCTGT CGTACCCGGT GGAGACGCTC 1200
CTAGCTTGA

Seq ID NO: 32 Protein sequence:
Protein Accession #: NP_150285.1

1 11 21 31 41 51
| | | | | |
MKLEVFVPRA AHGDKQGSDL EGAGGSDAPS PLSAAGDDSL GSDGDCAAKP SAGGGARDTQ 60
GDGEQSAGGG PGAEEAIPAA AAAAVVAEGA EAGAAGPGAG GAGSGEGARS KPYTRRPKPP 120
YSYIALIAMA IRDSAGGRLT LAEINEYLMG KFPFFRGSYT GWRNSVRHNL SLNDCFVKVL 180
RDPSRPWGKD NYWMLNPNSE YTFADGVFRR RRKRLSHRAP VPAPGLRPEE APGLPAAPPP 240
APAAPASPRM RSPARQEERA SPAGKFSSSF AIDSILRKPF RSRRLRDTAP GTTLQWGAAP 300
CPPLPAFPAL LPAAPCRALL PLCAYGAGEP ARLGAREAEV PPTAPPLLLA PLPAAAPAKP 360
LRGPAAGGAH LYCPLRLPAA LQAALVRRPG PHLSYPVETL LA

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: NM_012128.2
Coding sequence: 43-2796

1 11 21 31 41 51
| | | | | |
GAACAAACCA ACATTTGAGC CAGGAATAAC TAGAGAGGAA CAATGGGGTT ATTCAGAGGT 60
TTTGTTTTCC TCTTAGTTCT GTGCCTGCTG CACCAGTCAA ATACTTCCTT CATTAAGCTG 120
AATAATAATG GCTTTGAAGA TATTGTCATT GTTATAGATC CTAGTGTGCC AGAAGATGAA 180
AAAATAATTG AACAAATAGA GGATATGGTG ACTACAGCTT CTACGTACCT GTTTGAAGCC 240
ACAGAAAAAA GATTTTTTTT CAAAAATGTA TCTATATTAA TTCCTGAGAA TTGGAAGGAA 300
AATCCTCAGT ACAAAAGGCC AAAACATGAA AACCATAAAC ATGCTGATGT TATAGTTGCA 360
CCACCTACAC TCCCAGGTAG AGATGAACCA TACACCAAGC AGTTCACAGA ATGTGGAGAG 420
AAAGGCGAAT ACATTCACTT CACCCCTGAC CTTCTACTTG GAAAAAAACA AAATGAATAT 480
GGACCACCAG GCAAACTGTT TGTCCATGAG TGGGCTCACC TCCGGTGGGG AGTGTTTGAT 540
GAGTACAATG AAGATCAGCC TTTCTACCGT GCTAAGTCAA AAAAAATCGA AGCAACAAGG 600
TGTTCCGCAG GTATCTCTGG TAGAAATAGA GTTTATAAGT GTCAAGGAGG CAGCTGTCTT 660
AGTAGAGCAT GCAGAATTGA TTCTACAACA AAACTGTATG GAAAAGATTG TCAATTCTTT 720
CCTGATAAAG TACAAACAGA AAAAGCATCC ATAATGTTTA TGCAAAGTAT TGATTCTGTT 780
GTTGAATTTT GTAACGAAAA AACCCATAAT CAAGAAGCTC CAAGCCTACA AAACATAAAG 840
TGCAATTTTA GAAGTACATG GGAGGTGATT AGCAATTCTG AGGATTTTAA AAACACCATA 900
CCCATGGTGA CACCACCTCC TCCACCTGTC TTCTCATTGC TGAAGATCCG TCAAAGAATT 960
GTGTGCTTAG TTCTTGATAA GTCTGGAAGC ATGGGGGGTA AGGACCGCCT AAATCGAATG 1020
AATCAAGCAG CAAAACATTT CCTGCTGCAG ACTGTTGAAA ATGGATCCTG GGTGGGGATG 1080
GTTCACTTTG ATAGTACTGC CACTATTGTA AATAAGCTAA TCCAAATAAA AAGCAGTGAT 1140
GAAAGAAACA CACTCATGGC AGGATTACCT ACATATCCTC TGGGAGGAAC TTCCATCTGC 1200
TCTGGAATTA AATATGCATT TCAGGTGATT GGAGAGCTAC ATTCCCAACT CGATGGATCC 1260
GAAGTACTGC TGCTGACTGA TGGGGAGGAT AACACTGCAA GTTCTTGTAT TGATGAAGTG 1320
AAACAAAGTG GGGCCATTGT TCATTTTATT GCTTTGGGAA GAGCTGCTGA TGAAGCAGTA 1380
ATAGAGATGA GCAAGATAAC AGGAGGAAGT CATTTTTATG TTTCAGATGA AGCTCAGAAC 1440
AATGGCCTCA TTGATGCTTT TGGGGCTCTT ACATCAGGAA ATACTGATCT CTCCCAGAAG 1500
TCCCTTCAGC TCGAAAGTAA GGGATTAACA CTGAATAGTA ATGCCTGGAT GAACGACACT 1560
GTCATAATTG ATAGTACAGT GGGAAAGGAC ACGTTCTTTC TCATCACATG GAACAGTCTG 1620
CCTCCCAGTA TTTCTCTCTG GGATCCCAGT GGAACAATAA TGGAAAATTT CACAGTGGAT 1680
GCAACTTCCA AAATGGCCTA TCTCAGTATT CCAGGAACTG CAAAGGTGGG CACTTGGGCA 1740
TACAATCTTC AAGCCAAAGC GAACCCAGAA ACATTAACTA TTACAGTAAC TTCTCGAGCA 1800
GCAAATTCTT CTGTGCCTCC AATCACAGTG AATGCTAAAA TGAATAAGGA CGTAAACAGT 1860
TTCCCCAGCC CAATGATTGT TTACGCAGAA ATTCTACAAG GATATGTACC TGTTCTTGGA 1920
GCCAATGTGA CTGCTTTCAT TGAATCACAG AATGGACATA CAGAAGTTTT GGAACTTTTG 1980
GATAATGGTG CAGGCGCTGA TTCTTTCAAG AATGATGGAG TCTACTCCAG GTATTTTACA 2040
GCATATACAG AAAATGGCAG ATATAGCTTA AAAGTTCGGG CTCATGGAGG AGCAAACACT 2100
GCCAGGCTAA AATTACGGCC TCCACTGAAT AGAGCCGCGT ACATACCAGG CTGGGTAGTG 2160

AACGGGGAAA TTGAAGCAAA CCCGCCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC 2220
TTGGAGGATT TCAGCCGAAC AGCATCCGGA GGTGCATTTG TGGTATCACA AGTCCCAAGC 2280
CTTCCCTTGC CTGACCAATA CCCACCAAGT CAAATCACAG ACCTTGATGC CACAGTTCAT 2340
GAGGATAAGA TTATTCTTAC ATGGACAGCA CCAGGAGATA ATTTTGATGT TGGAAAAGTT 2400
CAACGTTATA TCATAAGAAT AAGTGCAAGT ATTCTTGATC TAAGAGACAG TTTTGATGAT 2460
GCTCTTCAAG TAAATACTAC TGATCTGTCA CCAAAGGAGG CCAACTCCAA GGAAAGCTTT 2520
GCATTTAAAC CAGAAAATAT CTCAGAAGAA AATGCAACCC ACATATTTAT TGCCATTAAA 2580
AGTATAGATA AAAGCAATTT GACATCAAAA GTATCCAACA TTGCACAAGT AACTTTGTTT 2640
ATCCCTCAAG CAAATCCTGA TGACATTGAT CCTACTCCTA CTCCTACTCC TACTCCTGAT 2700
AAAAGTCATA ATTCTGGAGT TAATATTTCT ACGCTGGTAT TGTCTGTGAT TGGGTCTGTT 2760
GTAATTGTTA ACTTTATTTT AAGTACCACC ATTTGAACCT TAACGAAGAA AAAAATCTTC 2820
AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACAATGT AAGTAAAGGA TATTTCTGAA 2880
TCTTAAAATT CATCCCATGT GTGATCATAA ACTCATAAAA ATAATTTTAA GATGTCGGAA 2940
AAGGATACTT TGATTAAATA AAAACACTCA TGGATATGTA AAAACTGTCA AGATTAAAAT 3000
TTAATAGTTT CATTTATTTG TTATTTTATT TGTAAGAAAT AGTGATGAAC AAAGATCCTT 3060
TTTCATACTG ATACCTGGTT GTATATTATT TGATGCAACA GTTTTCTGAA ATGATATTTC 3120
AAATTGCATC AAGAAATTAA AATCATCTAT CTGAGTAGTC AAAATACAAG TAAAGGAGAG 3180
CAAATAAACA ACATTTGGAA AAAAAAAAAA AAAAAAAA

Seq ID NO: 34 Protein sequence:
Protein Accession #: NP_036260.1

1 11 21 31 41 51
| | | | | |
MGLFRGFVFL LVLCLLHQSN TSFIKLNNNG FEDIVIVIDP SVPEDEKIIE QIEDMVTTAS 60
TYLFEATEKR FFFKNVSILI PENWKENPQY KRPKHENHKH ADVIVAPPTL PGRDEPYTKQ 120
FTECGEKGEY IHFTPDLLLG KKQNEYGPPG KLFVHEWAHL RWGVFDEYNE DQPFYRAKSK 180
KIEATRCSAG ISGRNRVYKC QGGSCLSRAC RIDSTTKLYG KDCQFFPDKV QTEKASIMFM 240
QSIDSVVEFC NEKTHNQEAP SLQNIKCNFR STWEVISNSE DFKNTIPMVT PPPPPVFSLL 300
KIRQRIVCLV LDKSGSMGGK DRLNRMNQAA KHFLLQTVEN GSWVGMVHFD STATIVNKLI 360
QIKSSDERNT LMAGLPTYPL GGTSICSGIK YAFQVIGELH SQLDGSEVLL LTDGEDNTAS 420
SCIDEVKQSG AIVHFIALGR AADEAVIEMS KITGGSHFYV SDEAQNNGLI DAFGALTSGN 480
TDLSQKSLQL ESKGLTLNSN AWMNDTVIID STVGKDTFFL ITWNSLPPSI SLWDPSGTIM 540
ENFTVDATSK MAYLSIPGTA KVGTWAYNLQ AKANPETLTI TVTSRAANSS VPPITVNAKM 600
NKDVNSFPSP MIVYAEILQG YVPVLGANVT AFIESQNGHT EVLELLDNGA GADSFKNDGV 660
YSRYFTAYTE NGRYSLKVRA HGGANTARLK LRPPLNRAAY IPGWVVNGEI EANPPRPEID 720
EDTQTTLEDF SRTASGGAFV VSQVPSLPLP DQYPPSQITD LDATVHEDKI ILTWTAPGDN 780
FDVGKVQRYI IRISASILDL RDSFDDALQV NTTDLSPKEA NSKESFAFKP ENISEENATH 840
IFIAIKSIDK SNLTSKVSNI AQVTLFIPQA NPDDIDPTPT PTPTPDKSHN SGVNISTLVL 900
SVIGSVVIVN FILSTTI

Seq ID NO: 35 DNA sequence
Nucleic Acid Accession #: NM_000901.1
Coding sequence: 217-3171

1 11 21 31 41 51
| | | | | |
CGCGGGAGCC AACTTCAGGC TGCTCAGAGG AAGCCCGTGC AGTCAGTCAC CTGGGTGCAA 60
GAGCGTTGCT GCCTCGGGCT CTCCCGCTGC AGGGAGAGCG GCACTCGCTG GCCTGGATGT 120
GGTTGGATTT AGGGGGGCTC CGCAGCAGGG GTTTCGTGGC GGTGGCAAGC GCTGCAACAG 180
GTAGACGGCG AGAGACGGAC CCCGGCCGAG GCAGGGATGG AGACCAAAGG CTACCACAGT 240
CTCCCTGAAG GTCTAGATAT GGAAAGACGG TGGGGTCAAG TTTCTCAGGC TGTGGAGCGT 300
TCTTCCCTGG GACCTACAGA GAGGACCGAT GAGAATAACT ACATGGAGAT TGTCAACGTA 360
AGCTGTGTTT CCGGTGCTAT TCCAAACAAC AGTACTCAAG GAAGCAGCAA AGAAAAACAA 420
GAACTACTCC CTTGCCTTCA GCAAGACAAT AATCGGCCTG GGATTTTAAC ATCTGATATT 480
AAAACTGAGC TGGAATCTAA GGAACTTTCA GCAACTGTAG CTGAGTCCAT GGGTTTATAT 540
ATGGATTCTG TAAGAGATGC TGACTATTCC TATGAGCAGC AGAACCAACA AGGAAGCATG 600
AGTCCAGCTA AGATTTATCA GAATGTTGAA CAGCTGGTGA AATTTTACAA AGGAAATGGC 660
CATCGTCCTT CCACTCTAAG TTGTGTGAAC ACGCCCTTGA GATCATTTAT GTCTGACTCT 720
GGGAGCTCCG TGAATGGTGG CGTCATGCGC GCCATTGTTA AAAGCCCTAT CATGTGTCAT 780
GAGAAAAGCC CGTCTGTTTG CAGCCCTCTG AACATGACAT CTTCGGTTTG CAGCCCTGCT 840
GGAATCAACT CTGTGTCCTC CACCACAGCC AGCTTTGGCA GTTTTCCAGT GCACAGCCCA 900
ATCACCCAGG GAACTCCTCT GACATGCTCC CCTAATGCTG AAAATCGAGG CTCCAGGTCG 960
CACAGCCCTG CACATGCTAG CAATGTGGGC TCTCCTCTCT CAAGTCCGTT AAGTAGCATG 1020
AAATCCTCAA TTTCCAGCCC TCCAAGTCAC TGCAGTGTAA AATCTCCAGT CTCCAGTCCC 1080
AATAATGTCA CTCTGAGATC CTCTGTGTCT AGCCCTGCAA ATATTAACAA CTCAAGGTGC 1140
TCTGTTTCCA GCCCTTCGAA CACTAATAAC AGATCCACGC TTTCCAGTCC GGCAGCCAGT 1200
ACTGTGGGAT CTATCTGTAG CCCTGTAAAC AATGCCTTCA GCTACACTGC TTCTGGCACC 1260
TCTGCTGGAT CCAGTACATT GCGGGATGTG GTTCCCAGTC CAGACACGCA GGAGAAAGGT 1320
GCTCAAGAGG TCCCTTTTCC TAAGACTGAG GAAGTAGAGA GTGCCATCTC AAATGGTGTG 1380
ACTGGCCAGC TTAATATTGT CCAGTACATA AAACCAGAAC CAGATGGAGC TTTTAGCAGC 1440
TCATGTCTAG GAGGAAATAG CAAAATAAAT TCGGATTCTT CATTCTCAGT ACCAATAAAG 1500
CAAGAATCAA CCAAGCATTC ATGTTCAGGC ACCTCTTTTA AAGGGAATCC AACAGTAAAC 1560
CCGTTTCCAT TTATGGATGG CTCGTATTTT TCCTTTATGG ATGATAAAGA CTATTATTCC 1620
CTATCAGGAA TTTTAGGACC ACCTGTGCCC GGCTTTGATG GTAACTGTGA AGGCAGCGGA 1680
TTCCCAGTGG GTATTAAACA AGAACCAGAT GACGGGAGCT ATTACCCAGA GGCCAGCATC 1740
CCTTCCTCTG CTATTGTTGG GGTGAATTCA GGTGGACAGT CCTTCCACTA CAGGATTGGT 1800
GCTCAAGGTA CAATATCTTT ATCACGATCG GCTAGAGACC AATCTTTCCA ACACCTGAGT 1860
TCCTTTCCTC CTGTCAATAC TTTAGTGGAG TCATGGAAAT CACACGGCGA CCTGTCGTCT 1920
AGAAGAAGTG ATGGGTATCC GGTCTTAGAA TACATTCCAG AAAATGTATC AAGCTCTACT 1980
TTACGAAGTG TTTCTACTGG ATCTTCAAGA CCTTCAAAAA TATGTTTGGT GTGTGGGGAT 2040
GAGGCTTCAG GATGCCATTA TGGGGTAGTC ACCTGTGGCA GCTGCAAAGT TTTCTTCAAA 2100
AGAGCAGTGG AAGGGCAACA CAACTATTTA TGTGCTGGAA GAAATGATTG CATCATTGAT 2160
AAGATTCGAC GAAAGAATTG TCCTGCTTGC AGACTTCAGA AATGTCTTCA AGCTGGAATG 2220
AATTTAGGAG CACGAAAGTC AAAGAAGTTG GGAAAGTTAA AAGGGATTCA CGAGGAGCAG 2280
CCACAGCAGC AGCAGCCCCC ACCCCCACCC CCACCCCCGC AAAGCCCAGA GGAAGGGACA 2340

ACGTACATCG CTCCTGCAAA AGAACCCTCG GTCAACACAG CACTGGTTCC TCAGCTCTCC 2400
ACAATCTCAC GAGCGCTCAC ACCTTCCCCC GTTATGGTCC TTGAAAACAT TGAACCTGAA 2460
ATTGTATATG CAGGCTATGA CAGCTCAAAA CCAGATACAG CCGAAAATCT GCTCTCCACG 2520
CTCAACCGCT TAGCAGGCAA ACAGATGATC CAAGTCGTGA AGTGGGCAAA GGTACTTCCA 2580
GGATTTAAAA ACTTGCCTCT TGAGGACCAA ATTACCCTAA TCCAGTATTC TTGGATGTGT 2640
CTATCATCAT TTGCCTTGAG CTGGAGATCG TACAAACATA CGAACAGCCA ATTTCTCTAT 2700
TTTGCACCAG ACCTAGTCTT TAATGAAGAG AAGATGCATC AGTCTGCCAT GTATGAACTA 2760
TGCCAGGGGA TGCACCAAAT CAGCCTTCAG TTCGTTCGAC TGCAGCTCAC CTTTGAAGAA 2820
TACACCATCA TGAAAGTTTT GCTGCTACTA AGCACAATTC CAAAGGATGG CCTCAAAAGC 2880
CAGGCTGCAT TTGAAGAAAT GAGGACAAAT TACATCAAAG AACTGAGGAA GATGGTAACT 2940
AAGTGTCCCA ACAATTCTGG GCAGAGCTGG CAGAGGTTCT ACCAACTGAC CAAGCTGCTG 3000
GACTCCATGC ATGACCTGGT GAGCGACCTG CTGGAATTCT GCTTCTACAC CTTCCGAGAG 3060
TCCCATGCGC TGAAGGTAGA GTTCCCCGCA ATGCTGGTGG AGATCATCAG CGACCAGCTG 3120
CCCAAGGTGG AGTCGGGGAA CGCCAAGCCG CTCTACTTCC ACCGGAAGTG ACTGCCCGCT 3180
GCCCAGAAGA ACTTTGCCTT AAGTTTCCCT GTGTTGTTCC ACACCCAGAA GGACCCAAGA 3240
AAACCTGTTT TTAACATGTG ATGGTTGATT CACACTTGTT CAACAGTTTC TCAAGTTTAA 3300
AGTCATGTCA GAGGTTTGGA GCCGGGAAAG CTGTTTTTCC GTGGATTTGG CGAGACCAGA 3360
GCAGTCTGAA GGATTCCCCA CCTCCAATCC CCCAGCGCTT AGAAACATGT TCCTGTTCCT 3420
CGGGATGAAA AGCCATATCT AGTCAATAAC TCTGATTTTG ATATTTTCAC AGATGGAAGA 3480
AGTTTTAACT ATGCCGTGTA GTTTCTGGTA TCGTTCGCTT GTTTTAAAAG GGTTCAAGGA 3540
CTAACGAACG TTTTAAAGCT TACCCTTGGT TTGCACATAA AACGTATAGT CAATATGGGG 3600
CATTAATATT CTTTTGTTAT TAAAAAAACA CAAAAAAATA ATAAAAAAAT ATATACAGAT 3660
TCCTGTTGTG TAATAACAGA ACTCGTGGCG TGGGGCAGCA GCTGCCTCTG AGCCCTCGCT 3720
CGTCCACGGT CTTCTGCATC ACTGGTATAC ACACTCGTTA GCGTCCATTT CTTATTTAAT 3780
TAGAATGGAT AAGATGATGT TAAATGCCTT GGTTTGATTT CTAGTATCTA TTGTGTTGGC 3840
TTTACAAATA ATTTTTTGCA GTCTTTTGCT GTGCTGTACA TTACTGTATG TATAAATTAT 3900
GAAGGACCTG AAATAAGGTA TAAGGATCTT TTGTAAATGA GACACATACA AAAAAAATCT 3960
TTAATGGTTA ATAGGATGAA TGGGAAAGTA TTTTTGAAAG AATTCTATTT TGCTGGAGAC 4020
TATTTAAGTA CTATCTTTGT CTAAACAAGG TAATTTTTTT TTGTAAAGTG CAATGTCCTG 4080
CATGCATAAT GAACCGTTTA CAGTGTATTT AAGAAAGGGA AAGCTGTGCC TTTTTTAGCT 4140
TCATATCTAA TTTACCATTA TTTTACAGTC TCTGTTGTAA ATAACCACAC TGAAACCTCT 4200
TCGGTTGTCT TGAAACCTTT CTACTTTTTC TGTACTTTTT GTTTTGTTCT TGGTCTCCCG 4260
CTTGGGGCAT TTGTGGGACT CCAGCACGTT TTCTGGCTTC TGCTTCATCC TGCTCCATCG 4320
GGGAATGACA CACTGCGGTG TCTGCAGCTC CTGGAAGGTG TCATTTGACA ACACATGTGG 4380
GAGAGGAGGT CCTTGGAGTG CTGCAGCTTT GGGAAAGCCT GCCTCGTTTC CCTTTTCCTC 4440
TAGAAGCAGA ACCAGCTCTA CGAGAGTGAG ACTGGGAACT TGATGGCTCA GAGAGCATCT 4500
TTTCCTCCCA TTTTAGAAAA TCAGATTTTC TCCTGTGGGA AAAAAAAATT CCATGCACTC 4560
TCTCTCTGTT AAAGATCAGC TATTCCCTTC TGATCTTGGA AAGAGGTTCT GCACTCCTGG 4620
AACCGGTCAC AGGAACGCAC AGATCATGGC AGGATGCGCT GGGACGGCCC ATCTTGGCAA 4680
GGTTCAGTCT GAATGGCATG GAGACCGGGA GATAGAGGGG TTTTAGATTT TTAAAAGGTA 4740
GGTTTTAAAA ATAAGTTTTA TACATAAACA GTTTTGGAGA AAAATTACAG ATCATATAAG 4800
CAAGACAGTG GCACTAAAAT GTTTAATTCA TTAATCTGTT TGTTTGGCAC TGATGCAATG 4860
TATGGCTTTT CTCTTGCCCC AAATCACAAA CATATGTATC TTTGGGGAAA CTAACAATAT 4920
GATTGCACTA AATAAACTAC TTTGAATAGA GGCCAAATTA ATCTTTTAAA AATGATGATA 4980
ATCATCAGGT TTACTCAGTG AAATCATATT AATTATTTTC CAAAATCTAA AAGCTGTAGC 5040
TGGAGAAGCC CATGGCCACG AGGAAGCAGC AATTAATTAG ATCAACACTT TTCTCCAGGG 5100
TTCACCATGC AGGCAACATT ACCTTGTCTT TCAAAAGACA CCTGCCTTAG TGCAAGGGGA 5160
AACCTGTGAA AGCTGCACTC AGAGGGAGGA GTCTTTCTTA CATAATTTGC AATTTCAGGA 5220
ATTTAATTTA TAGGCAGATC TTTAAATACA GTCAACTTAC GGTGCACAGT AATATGAAAG 5280
CCACACTTTG AAGGTAATAA ATACACAGCA TGCAGACTGG GAGTTGCTAG CAAACAAATG 5340
GCTTACTTAC AAAAGCAGCT TTTAGTTCAG ACTTAGTTTT TATAAAATGA GAATTCTGAC 5400
TTACTTAACC AGGTTTGGGA TGGAGATGGT CTGCATCAGC TTTTTGTATT AACAAAGTTA 5460
CTGGCTCTTT GTGTGTCTCC AGGTAACTTT GCTTGATTAA ACAGCAAAGC CATATTCTAA 5520
ATTCACTGTT GAATGCCTGT CCCAGTCCAA ATTGTCTGTC TGCTCTTATT TTTGTACCAT 5580
ATTGCTCTTA AAAATCTTGG TTTGGTACAG TTCATAATTC ACCAAAAAGT TCATATAATT 5640
TAAAGAAACA CTAAATTAGT TTAAAATGAA GCAATTTATA TCTTTATGCA AAAACATATG 5700
TCTGTCTTTG CAAAGGACTG TAAGCAGATT ACAATAAATC CTTTACTTT

Seq ID NO: 36 Protein sequence:
Protein Accession #: NP_000892.1

1 11 21 31 41 51

METKGYHSLP EGLDMERRWG QVSQAVERSS LGPTERTDEN NYMEIVNVSC VSGAIPNNST 60
QGSSKEKQEL LPCLQQDNNR PGILTSDIKT ELESKELSAT VAESMGLYMD SVRDADYSYE 120
QQNQQGSMSP AKIYQNVEQL VKFYKGNGHR PSTLSCVNTP LRSFMSDSGS SVNGGVMRAI 180
VKSPIMCHEK SPSVCSPLNM TSSVCSPAGI NSVSSTTASF GSFPVHSPIT QGTPLTCSPN 240
AENRGSRSHS PAHASNVGSP LSSPLSSMKS SISSPPSHCS VKSPVSSPNN VTLRSSVSSP 300
ANINNSRCSV SSPSNTNNRS TLSSPAASTV GSICSPVNNA FSYTASGTSA GSSTLRDVVP 360
SPDTQEKGAQ EVPFPKTEEV ESAISNGVTG QLNIVQYIKP EPDGAFSSSC LGGNSKINSD 420
SSFSVPIKQE STKHSCSGTS FKGNPTVNPF PFMDGSYFSF MDDKDYYSLS GILGPPVPGF 480
DGNCEGSGFP VGIKQEPDDG SYYPEASIPS SAIVGVNSGG QSFHYRIGAQ GTISLSRSAR 540
DQSFQHLSSF PPVNTLVESW KSHGDLSSRR SDGYPVLEYI PENVSSSTLR SVSTGSSRPS 600
KICLVCGDEA SGCHYGVVTC GSCKVFFKRA VEGQHNYLCA GRNDCIIDKI RRKNCPACRL 660
QKCLQAGMNL GARKSKKLGK LKGIHEEQPQ QQQPPPPPPP PQSPEEGTTY IAPAKEPSVN 720
TALVPQLSTI SRALTPSPVM VLENIEPEIV YAGYDSSKPD TAENLLSTLN RLAGKQMIQV 780
VKWAKVLPGF KNLPLEDQIT LIQYSWMCLS SFALSWRSYK HTNSQFLYFA PDLVFNEEKM 840
HQSAMYELCQ GMHQISLQFV RLQLTFEEYT IMKVLLLLST IPKDGLKSQA AFEEMRTNYI 900
KELRKMVTKC PNNSGQSWQR FYQLTKLLDS MHDLVSDLLE FCFYTFRESH ALKVEFPAML 960
VEIISDQLPK VESGNAKPLY FHRK

Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: see Table 25 & 25A for complete list

1 11 21 31 41 51
| | | | | |
CCTACCAGGT TCAAGCAACT CTGCTGCCTC AGCTCCCAAG TAGCTGGGAT TACAGGTGCA 60
TGCCACTACA CCTGGCTTTT TGTATTTTTA GTAGAGATGG TTTTCACTAT GTTGGCCAGG 120
CTGATCTTGA ATTCCTGGCC TGAAGTAATC TGCCTGCCTC AGCCTCCCAA AGTGCTGGGA 180
TTATAGGAGC CACCACACCT GGCATAACTG GTATTTTTTA TATGCTTCCT GGGCAACTTA 240
AAAAATTGAT TACTCTGTTG TTTCTTCCTT TTTTTTTTTT TTTTGGCTTT GACCAATTTG 300
TGAGACCCAA GTATCTCCTA CCTAGAAAAA AAACACACTA AACAGTAAAT GATTACCAAC 360
CTATTTGGAA CAAATCTCAA TTAATTAACA TATACTTCAA GGAGAAGACT TAACAAAATC 420
TTACTTTTCA TTCTTAATAG CTCTTTCCAT AAAAATGTTC CACAAGTGTA TCAAATTAGT 480
CCTAACAACT ACTGTTAAGT GATTAATGAA ACAGGAGTGA CAGGAGTGAA TTTAATAATA 540
GCAATAAATA CAGATGGGAC TACATAAATT GTGGAGGTCC TGATGCAAAA CTCTCTCTGT 600
ATTCGATGGC ATCTCAGCTT TCTCATAGAG CTGTTTCACT GTGAGGGTCT TTATCCTTCA 660
TGCAGAGCTT CATTATTTTC TTTCTTCTAG CAATCAGTCC AAAGCACAAT GTCAGAAAGA 720
TCACAACACA TGCAGCAATA ATGGGCTCTA TTGGTACACC CACAGTTTTA TCTTTAACAA 780
TC

Seq ID NO: 38 DNA sequence
Nucleic Acid Accession #: NM_001192.1
Coding sequence: 219-773

1 11 21 31 41 51
| | | | | |
AAGACTCAAA CTTAGAAACT TGAATTAGAT GTGGTATTCA AATCCTTACG TGCCGCGAAG 60
ACACAGACAG CCCCCGTAAG AACCCACGAA GCAGGCGAAG TTCATTGTTC TCAACATTCT 120
AGCTGCTCTT GCTGCATTTG CTCTGGAATT CTTGTAGAGA TATTACTTGT CCTTCCAGGC 180
TGTTCTTTCT GTAGCTCCCT TGTTTTCTTT TTGTGATCAT GTTGCAGATG GCTGGGCAGT 240
GCTCCCAAAA TGAATATTTT GACAGTTTGT TGCATGCTTG CATACCTTGT CAACTTCGAT 300
GTTCTTCTAA TACTCCTCCT CTAACATGTC AGCGTTATTG TAATGCAAGT GTGACCAATT 360
CAGTGAAAGG AACGAATGCG ATTCTCTGGA CCTGTTTGGG ACTGAGCTTA ATAATTTCTT 420
TGGCAGTTTT CGTGCTAATG TTTTTGCTAA GGAAGATAAG CTCTGAACCA TTAAAGGACG 480
AGTTTAAAAA CACAGGATCA GGTCTCCTGG GCATGGCTAA CATTGACCTG GAAAAGAGCA 540
GGACTGGTGA TGAAATTATT CTTCCGAGAG GCCTCGAGTA CACGGTGGAA GAATGCACCT 600
GTGAAGACTG CATCAAGAGC AAACCGAAGG TCGACTCTGA CCATTGCTTT CCACTCCCAG 660
CTATGGAGGA AGGCGCAACC ATTCTTGTCA CCACGAAAAC GAATGACTAT TGCAAGAGCC 720
TGCCAGCTGC TTTGAGTGCT ACGGAGATAG AGAAATCAAT TTCTGCTAGG TAATTAACCA 780
TTTCGACTCG AGCAGTGCCA CTTTAAAAAT CTTTTGTCAG AATAGATGAT GTGTCAGATC 840
TCTTTAGGAT GACTGTATTT TTCAGTTGCC GATACAGCTT TTTGTCCTCT AACTGTGGAA 900
ACTCTTTATG TTAGATATAT TTCTCTAGGT TACTGTTGGG AGCTTAATGG TAGAAACTTC 960
CTTGGTTTCA TGATTAAAGT CTTTTTTTTT CCTGA

Seq ID NO: 39 Protein sequence:
Protein Accession #: NP_001183.1

1 11 21 31 41 51
| | | | | |
MLQMAGQCSQ NEYFDSLLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK GTNAILWTCL 60
GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA NIDLEKSRTG DEIILPRGLE 120
YTVEECTCED CIKSKPKVDS DHCFPLPAME EGATILVTTK TNDYCKSLPA ALSATEIEKS 180
ISAR

Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_025087.1
Coding sequence: 183-2282

1 11 21 31 41 51
| | | | | |
ACACTGCCTC GGTTCGGCAA GTGGGTCAGT TGGCTGGGGC TCACTTGGCA ACGGGACGCG 60
GGAACGAGGG GCGCGGACGC AGGCCCGGGA GGACGCGGCG GCGGGAACCT GGGGGCGCAG 120
GGCTAGGGCA GCGGGCCCGA CCCGCACGGC TTTCCTGGAA AGCGCTGCCC CTCGCCGCGG 180
CGATGACCTC GCTGTGGAGA GAAATCCTCT TGGAGTCGCT GCTGGGATGT GTTTCTTGGT 240
CTCTCTACCA TGACCTGGGA CCGATGATCT ATTACTTTCC TTTGCAAACA CTAGAACTCA 300
CTGGGCTTGA AGGTTTTAGT ATAGCATTTC TTTCTCCAAT ATTCCTAACA ATTACTCCTT 360
TCTGGAAATT GGTTAACAAG AAGTGGATGC TAACCCTGCT GAGGATAATC ACTATTGGCA 420
GCATAGCCTC CTTCCAGGCT CCAAATGCCA AACTTCGACT GATGGTTCTT GCGCTTGGGG 480
TGTCTTCCTC ACTGATAGTG CAAGCTGTGA CTTGGTGGTC AGGAAGTCAT TTGCAAAGGT 540
ACCTCAGAAT TTGGGGATTC ATTTTAGGAC AGATTGTTCT TGTTGTTCTA CGCATATGGT 600
ATACTTCACT AAACCCAATC TGGAGTTATC AGATGTCCAA CAAAGTGATA CTGACATTAA 660
GTGCCATAGC CACACTTGAT CGTATTGGCA CAGATGGTGA CTGCAGTAAA CCTGAAGAAA 720
AGAAGACTGG TGAGGTAGCC ACGGGGATGG CCTCTAGACC CAACTGGCTG CTGGCAGGGG 780
CTGCTTTTGG TAGCCTTGTG TTCCTCACCC ACTGGGTTTT TGGAGAAGTC TCTCTTGTTT 840
CCAGATGGGC AGTGAGTGGG CATCCACATC CAGGGCCAGA TCCTAACCCA TTTGGAGGTG 900
CAGTACTGCT GTGCTTGGCA AGTGGATTGA TGCTTCCATC TTGTTTGTGG TTTCGTGGTA 960
CTGGTTTGAT CTGGTGGGTT ACAGGAACAG CTTCAGCTGC GGGGCTCCTT TACCTGCACA 1020
CATGGGCAGC TGCTGTGTCT GGCTGTGTCT TCGCCATCTT TACTGCATCC ATGTGGCCCC 1080
AAACACTTGG ACACCTTATT AACTCAGGGA CAAACCCTGG GAAAACCATG ACCATTGCCA 1140
TGATATTTTA TCTTCTAGAA ATATTTTTCT GTGCCTGGTG CACAGCTTTT AAGTTTGTCC 1200
CAGGAGGTGT CTACGCTAGA GAAAGATCAG ATGTGCTTTT GGGGACAATG ATGTTAATTA 1260
TCGGGCTGAA TATGCTATTT GGTCCTAAGA AAAACCTTGA TTTGCTTCTT CAAACAAAAA 1320
ACAGTTCTAA AGTGCTTTTC AGAAAGAGTG AAAAATACAT GAAACTTTTT CTGTGGCTGC 1380
TTGTTGGTGT GGGATTGTTG GGATTAGGAC TACGGCATAA AGCCTATGAG AGAAAACTGG 1440
GCAAAGTGGC ACCAACCAAA GAGGTCTCTG CTGCCATCTG GCCTTTCAGG TTTGGATATG 1500
ACAATGAAGG GTGGTCTAGT CTAGAAAGAT CAGCTCACCT GCTCAATGAA ACAGGTGCAG 1560
ATTTCATAAC AATTTTGGAG AGTGATGCTT CTAAGCCCTA TATGGGGAAC AATGACTTAA 1620

CCATGTGGCT AGGGGAAAAG TTGGGTTTCT ATACAGACTT TGGTCCAAGC ACAAGGTATC 1680
ACACTTGGGG GATTATGGCT TTGTCAAGAT ACCCAATTGT GAAATCTGAG CATCACCTTC 1740
TTCCGTCACC AGAGGGCGAG ATCGCACCAG CCATCACATT GACCGTTAAC ATTTCGGGCA 1800
AGCTGGTGGA TTTTGTCGTG ACACACTTTG GGAACCACGA AGATGACCTC GACAGGAAAC 1860
TGCAGGCTAT TGCTGTTTCA AAACTACTGA AAAGTAGCTC TAATCAAGTG ATATTTCTGG 1920
GATATATCAC TTCAGCACCT GGCTCCAGAG ATTATCTACA GCTCACTGAA CATGGCAATG 1980
TGAAGGATAT CGACAGCACT GATCATGACA GATGGTGTGA ATACATTATG TATCGAGGGC 2040
TGATCAGGTT GGGTTATGCA AGAATCTCCC ATGCTGAACT GAGTGATTCA GAAATTCAGA 2100
TGGCAAAATT TAGGATCCCT GATGACCCCA CTAATTATAG AGACAACCAG AAAGTGGTCA 2160
TAGACCACAG AGAAGTTTCT GAGAAAATTC ATTTTAATCC CAGATTTGGA TCCTACAAAG 2220
AAGGACACAA TTATGAAAAC AACCATAATT TTCATATGAA TACTCCCAAA TACTTTTTAT 2280
GAAACATTTA AAACAAGAAG TTATTGGCTG GGAAAATCTA AGAAAAAAAG TATGTAAGAT 2340
AAAAAGAAGA GATTAATGAA AGTGGGAAAA TACACATGAA GAACCTCAAC TTAAAAAACA 2400
CATGGTATCT ATGCAGTGGG AAATTACCTC CATTTGTAAA CTATGTTGCT TAATAAAAAC 2460
ATTTCTCTAA AAAAAAAAAA AAAAAA

Seq ID NO: 41 Protein sequence:
Protein Accession #: NP_079363.1

1 11 21 31 41 51

MTSLWREILL ESLLGCVSWS LYHDLGPMIY YFPLQTLELT GLEGFSIAFL SPIFLTITPF 60
WKLVNKKWML TLLRIITIGS IASFQAPNAK LRLMVLALGV SSSLIVQAVT WWSGSHLQRY 120
LRIWGFILGQ IVLVVLRIWY TSLNPIWSYQ MSNKVILTLS AIATLDRIGT DGDCSKPEEK 180
KTGEVATGMA SRPNWLLAGA AFGSLVFLTH WVFGEVSLVS RWAVSGHPHP GPDPNPFGGA 240
VLLCLASGLM LPSCLWFRGT GLIWWVTGTA SAAGLLYLHT WAAAVSGCVF AIFTASMWPQ 300
TLGHLINSGT NPGKTMTIAM IFYLLEIFFC AWCTAFKFVP GGVYARERSD VLLGTMMLII 360
GLNMLFGPKK NLDLLLQTKN SSKVLFRKSE KYMKLFLWLL VGVGLLGLGL RHKAYERKLG 420
KVAPTKEVSA AIWPFRFGYD NEGWSSLERS AHLLNETGAD FITILESDAS KPYMGNNDLT 480
MWLGEKLGFY TDFGPSTRYH TWGIMALSRY PIVKSEHHLL PSPEGEIAPA ITLTVNISGK 540
LVDFVVTHFG NHEDDLDRKL QAIAVSKLLK SSSNQVIFLG YITSAPGSRD YLQLTEHGNV 600
KDIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRIPDDPT NYRDNQKVVI 660
DHREVSEKIH FNPRFGSYKE GHNYENNHNF HMNTPKYFL

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.